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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. BACKGROUND OF THE INVENTION

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1.1 TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

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1.2 BACKGROUND

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

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Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

30 2. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as

allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1 – 948. The polypeptide sequences are designated SEQ ID NOS: 949-1896. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-948 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-948. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-948 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-948. The sequence information can be a segment of any one of SEQ ID NO: 1-948 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-948.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The

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array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

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In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-948 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-948 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 949-1896; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1–948; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1–948. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1–948; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include

polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-948; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

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Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

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In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the

polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

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In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention

provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

3. DETAILED DESCRIPTION OF THE INVENTION

3.1 DEFINITIONS

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

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The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and

N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

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The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 500 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-948.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOs: 1-948. The sequence information can be a segment of any one of SEQ ID NOs: 1-948 that uniquely identifies or

represents the sequence information of that sequence of SEQ ID NO: 1-948. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids,

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more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected

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in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

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Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

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The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers.

Recombinant expression systems as defined herein will express polypeptides or proteins

endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

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The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" or "substantially similar" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the

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corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity. more preferably at least 95% sequence identity, more preferably at least 98% sequence identity, and most preferably at least 99% sequence identity. Substantially equivalent nucleotide sequence of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, the nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least about 95% sequence identity, more preferably at least 98% sequence identity, and most preferably at least 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

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The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

3.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEO ID NO: 1-948; a polynucleotide encoding any one of the peptide sequences of SEO ID NO: 949-1896; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polynucleotides of any one of SEO ID NO: 1 - 948. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1 – 948; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing as SEQ ID NO: 949-1896; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 949-1896. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1 – 948 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1 – 948 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1 – 948 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99% sequence identity to a polynucleotide recited above.

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Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1 - 948, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1 - 948, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NOs: 1 - 948 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

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The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NOs: 1 - 948, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

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Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

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The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

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The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with

more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

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In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are

capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-948, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 948 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NOs: 1 - 948 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one

of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed

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recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intra-muscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

3.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 - 948, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a

double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO: 949-1896 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1 - 948 are additionally provided.

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In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO: 1 - 948, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of an mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of an mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of an mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine,

inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methylguanine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et*

al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

3.4 RIBOZYMES AND PNA MOIETIES

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In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of an mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO: 1 - 948). For example, a derivative of Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742.

Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

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Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

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In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

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PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to

another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

3.5 HOSTS

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The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

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Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

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Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include

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Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but

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configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

3.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 949-1896 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NOs: 1 - 948 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NOs: 1-948 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 949-1896 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 949-1896 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 949-1896.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S.

McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

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The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

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Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

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The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

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The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well

known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 949-1896.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

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The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

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Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

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The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego,

Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

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Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

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Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability.

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Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

3.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

3.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active

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portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus, or to the middle.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprise one or more domains fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, e.g., cancer as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) Current Protocols in Molecular Biology, John Wiley & Sons, 1992). Moreover, many

expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

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3.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

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Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

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The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the

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polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.

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Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

3.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals,

preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

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In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

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Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

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3.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

3.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA

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sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

3.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the

polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

3.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

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A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current

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Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immunol. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

3.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal

cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells.

Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium.

Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for

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inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

3.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines,

thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are

cited above.

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Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures

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in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

3.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention

contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

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The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

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Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

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Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

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A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

3.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the

treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

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Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation

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may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in

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cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

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Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of

Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

3.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

3.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts,

neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

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A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

3.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of

thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

3.10.11 CANCER DIAGNOSIS AND THERAPY

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Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma. astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system.

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bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

3.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

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Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

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3.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

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Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

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The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

3.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays

can be used to identify polynucleotides encoding binding partners. As another example,

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affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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3.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation

associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

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3.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

3.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;

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- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

3.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition

(including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

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3.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

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Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect

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the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

3.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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3.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

3.11.1 EXAMPLE

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One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about $0.1\mu g/kg$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

ROUTES **OF** AND **FORMULATIONS** PHARMACEUTICAL 3.12 ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2,

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G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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3.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in

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the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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3.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

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When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition

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for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene

glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable

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polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a cosolvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia,

trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg

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(preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize

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a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a

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mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

3.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of

administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

3.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

3.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

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An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 949-1896, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

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In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of alpha-2-macroglobulin-like protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more

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domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

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The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (i.e., able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, S. aureus protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow et al. (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full-length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention. Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells,

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neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. et al., "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. et al., Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

3.13.1 POLYCLONAL ANTIBODIES

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g.,

aluminum hydroxide), surface-active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants that can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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3.13.2 MONOCLONAL ANTIBODIES

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

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Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

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The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-

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103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol.</u>, <u>133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a nonimmunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

3.13.3 HUMANIZED ANTIBODIES

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539). In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues that are found neither in the recipient antibody will comprise

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substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

3.13.4 HUMAN ANTIBODIES

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al, (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

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Human antibodies may additionally be produced using transgenic nonhuman animals that are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells that secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

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In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

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3.13.5 FAB FRAGMENTS AND SINGLE CHAIN ANTIBODIES

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_{v} fragments.

3.13.6 BISPECIFIC ANTIBODIES

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

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Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion

preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are cotransfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

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According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was

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able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary V_L and \dot{V}_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

3.13.7 HETEROCONJUGATE ANTIBODIES

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Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

3.13.8 EFFECTOR FUNCTION ENGINEERING

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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3.13.9 IMMUNOCONJUGATES

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

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Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain,

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alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

3.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer

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readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NOs: 1 - 948 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NOs: 1 - 948 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means

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having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif.

There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

3.15 TRIPLE HELIX FORMATION

WO 02/070539

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

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3.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

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In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

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In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

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In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

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Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound

antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

3.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

3.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NOs: 1 - 948, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

 In general, therefore, such methods for identifying compounds that bind to a
 polynucleotide of the invention can comprise contacting a compound with a polynucleotide
 of the invention for a time sufficient to form a polynucleotide/compound complex, and
 detecting the complex, so that if a polynucleotide/compound complex is detected, a
 compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the

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complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or

rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

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Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

3.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOs: 1 - 948. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NOs: 1 - 948 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used

in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

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Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

3.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be

achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

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Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

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Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

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The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

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More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours

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at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

3.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.*

(1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods.

Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

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Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

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One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviJI*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

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The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

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As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

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Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

3.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and

methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

4.0 EXAMPLES

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4.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

4.2 EXAMPLE 2

Novel Nucleic Acids

The novel nucleic acids of the present invention of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The nucleic acids were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 119, gb pri

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119, and UniGene version 119) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 121, gb pri 121, UniGene version 121, Genpept release 121). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and cg-zip-2 (Hyseq, Inc.). The full-length nucleotide and amino acid sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1-948.

Table 1 shows the various tissue sources of SEQ ID NO: 1-1896.

The nearest neighbor results for polypeptides encoded by SEQ ID NO: 1-948 (i.e. SEQ ID NO: 949-1896) were obtained by a BLASTP (version 2.0a1 19MP-WashU) search against Genpept, Geneseq and SwissProt databases using BLAST algorithm. The nearest neighbor result showed the closest homologue with functional annotation for SEQ ID NO: 1-948. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1-948 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), polypeptides encoded by SEQ ID NO: 1-948 (i.e. SEQ ID NO: 949-1896) were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the Pfam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) polypeptides encoded by SEQ ID NO: 1-948 (i.e. SEQ ID NO: 949-1896) were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the product of all the e-value of similar domains found, the pFam score for the identified domain within

the sequence, number of similar domains found, and the position of the domain in the SEQ ID NO: being interrogated.

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The GeneAtlas™ software package (Molecular Simulations Inc. (MSI), San Diego, CA) was used to predict the three-dimensional structure models for the polypeptides encoded by SEQ ID NO: 1-948 (i.e. SEQ ID NO: 949-1896). Models were generated by (1) PSI-BLAST which is a multiple alignment sequence profile-based searching developed by Altschul et al., (Nucl. Acids res. 25, 3389-3408 (1997)), (2) High Throughput Modeling (HTM) (Molecular Simulations Inc. (MSI) San Diego, CA) which is an automated sequence and structure searching procedure (http://www.msi.com/), and (3) SeqFold™ which is a fold recognition method described by Fischer and Eisenberg (J. Mol. Biol. 209, 779-791 (1998)). This analysis was carried out, in part, by comparing the polypeptides of the invention with the known NMR (nuclear magnetic resonance) and x-ray crystal three-dimensional structures as templates. Table 5 shows, "PDB ID", the Protein DataBase (PDB) identifier given to template structure; "Chain ID", identifier of the subcomponent of the PDB template structure; "Compound Information", information of the PDB template structure and/or its subcomponents; "PDB Function Annotation" gives function of the PDB template as annotated by the PDB files (http://www.rcsb.org/PDB/); start and end amino acid position of the protein sequence aligned; PSI-BLAST score, the verify score, the SeqFold score, and the Potential(s) of Mean Force (PMF). The verify score produced by GeneAtlas™ software (MSI), is based on Dr. Eisenberg's Profile-3D threading program developed in Dr. DavidEisenberg's laboratory (US patent no. 5,436,850 and Luthy, Bowie, and Eisenberg, Nature, 356:83-85 (1992)) and a publication by R. Sanchez and A. Sali, Proc. Natl. Acad. Sci. USA, 95:12502-13597. The verify score produced by GeneAtlas™ normalizes the verify score for proteins with different lengths so that a unified cutoff can be used to select good models as follows:

Verify score (normalized) = (raw score $-\frac{1}{2}$ high score)/(1/2 high score)

The PMF score, produced by GeneAtlas™ software (MSI), is a composite scoring function that depends in part on the compactness of the model, sequence identity in the alignment used to build the model, pairwise and surface mean force potential (MFP). As given in Table 5, a verify score between 0 to 1.0, with 1 being the best, represents a good model. Similarly, a PMF score between 0 to 1.0, with 1 being the best, represents a good model. A SeqFold™ score of more than 50 is considered significant. A good model may

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also be determined by one of skill in the art based on all the information in Table 5 taken in totality.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determined from using Neural Network SignalP V1.1 program(from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et al., as reference, were obtained for the polypeptide sequences. Table 6 shows the position of the last amino acid of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 7 correlates each of SEQ ID NO: 1-948 to a specific chromosomal location.

Table 8 is a correlation table of the novel polynucleotide sequences SEQ ID NO: 1-948, novel polypeptide sequences SEQ ID NO: 949-1896, and their corresponding priority nucleotide sequences in the priority application USSN 09/799,451, herein incorporated by reference in its entirety.

20 TABLE 1

Tissue Origin	Library/RNA Source	HYSEQ Library Name	SEQ ID NOS:
Nuli	mix tissues library	CTL016	52 137 189-192 316-325 529 591
Null	enriched libray	CTL021	65 84 169 189-192 311 316-325 406 676 727 782 850
Null	mix tissues library	CTL028	65
Null	PCR products	PCR2V1	34 51 134 189 191-192 224 232 260 3,11 388 606 623 806
Null	mix tissues library	SUP002	51 96 103 163 216 272 294 311 316-325 328 378 383 388 446-448 450 453 474 481 500 516 610 774 780 885 904 922
adipocytes	Stratagene	ADP001	2 43 51 73 76 88 97 142 166 181 186 188 208 257 262-263 267-270 282 311 316-325 383 386 427-429 459 463 465 493 507 514 522 545 552 572 643 651 667 700 721 740 754 758 778 795 872 881 883 888 947
adrenal gland	Clontech	ADR002	3-6 10-11 13 16 20-21 24 27-28 33 38 48-49 51 53-54 58 66-67 75 88 97 99 124-125 130 140 157-158 179 188 197-198 200 212-214 216 218 224 229 231 237 257 267 279 281-282 288 302 311 326 362 376-377 381 383 396 398-403 429 443 453-454 456 459-460 474 489 515 526 531-

Tissue Origin	Library/RNA Source	HYSEQ Library Name	
			532 540 545 550 559 564 568 577 581 586 589
•	1	}	599 605 610 613 631-632 643 648 651 667 670
	1		672 681 684 699 703 706 708 717-718 734 736
			751 779 785-786 795 813 817 837 871 876 887-
adult brain	BioChain	ABR012	888 897 904 907 916 921 924-926 948
edult brain	BioChain	ABR013	140 208 311 748 810
adult brain	Clontech	ABR001	51 245 311 316-325 436 717 810 936
·		ADROOT	12 51 87 142 169 178 180 245 263 286 288 290
			295 304 308 311-313 375 379-380 403 425 428 431 458 486 499 503 512 557-558 567-568 606
			610 641 651 695 704 730 741 754 766 810 822
			827 841 850 864 871 884 897 917 920 925-927
			934 946
adult brain	Clontech	ABR006	2 14-15 22-23 29 32-33 49 66-68 83 99 111-112
			115 129 131 142 147 153 157 163 169 189-192
	1	1	200 205 207 212-214 218 221 229 234 256-257
		1	263 272 276 279 282 292-299 301 311 315 340-
			343 349 376-377 383-386 388 403 405 407 410
			425 438 453-454 460 463 469 474 489 495 499-
			500 511 522 531-532 539 541 545-546 551 556
			563 565 571 579-583 591 594 606 626 628 631-
	1		632 643 647 651 678 684 691-692 700 717 721
			726 730 732 741 744 754 757 769 772 774 782
	1		788 793 810 820 827-828 853 867 869 875 879
adult brain	Clontech	ABR008	897 913 921-922 925-926 933-934 939-941 947
	Cionicon	ABRUUS	1-2 9-10 13 16-18 23 27-28 30-32 37 39 42-43
			46 49-51 66 70 76 80 83 86-87 95-97 109 111-
	1		112 116-117 124 130-131 133-134 136-137 141-
			142 146-147 152-157 160 162 169 171 179 184 189-192 195 200-201 206 211-212 216-218 239
	}		247-248 250 252 254-258 261-263 271-272 276
		1	278 282 288 293-295 297 300 302 307 309 311
			314-326 328 333 337-341 343 347 349 351-354
			358 360-361 367 374 376-378 381 384 388-390
			393 395-396 400-403 405 407 409 411 414 418-
			420 422 427-429 433 438 440-441 445-447 450
			453-455 458 460-461 463 466-470 474 476 486
			491-493 496 498-500 507 511 514 520-521 525
			527-529 531-532 534-535 542 546 548-549 551-
			552 557-558 560 562 564-566 568 571-572 578-
ļ)	583 586-587 590-591 594 599 602 606 618-619
			621 626 629 631-634 643-644 647 651 656-660
ļ			664 670 672 677 680 684 687-688 691-695 697
			706 709-710 712-714 716-718 721-722 724-725
j			727-728 730 733 740-741 745 751-752 754 761
1			765 774 777-779 787 790 792-793 799 801-804
j			808 810 812 820 822 824 827 831-832 834 836
			845 850 858-861 868-869 871-872 875-876 883
			887 891 897 900 904 907 910 913 917-920 925-
dult brain	Clontech	ABR011	927 929 931-934 938-941 946-947
dult brain	GIBCO	AB3001	51 133 810 892
1		1	16-17 19 40 66 92-94 97 124 131 134 163 186
	ĺ		188 208 213 231 268-270 284 288 295 297 299 311 315-325 340 373 387 396 407 429 469 489
			495 498-499 533 542 545 562 568 587 589 618-
			619 643 664 687-688 694-695 730 748 836 876
			882 884 902 925-926 948
lult brain	GIBCO		2 22-24 29 33 43 45 50-51 66 71 75 77 82 87-88

Tissue Origin	Library/RNA	HYSEQ Library Name	SEQ ID NOS:
	Source	Ivame	91-92 95 131 140 157 179 188-192 200 208 213
			220 225 247 252 257 261 263-265 277 284 288
		1	295 299 301 315-325 355-356 373 387-389 392
		1	395-396 407 423 431 443-444 450-451 457 459
		}	468 476 489 495 499-500 514 520-522 532-533
			541-542 545-546 557-558 562 564 576-577 581-
		1	583 588-589 591 595 597 599 601 610 619 631-
			632 639 643-644 654-655 658-660 664 667 676
	1		682 687-688 693 696 700 704 711 713-714 746
			758 765-766 774-775 780 800 802 804 807 810
			827 829 834 842 850 854-855 866 870-871 878
			892-893 897 899 910 916 920-921 929 931-932
	· · · · · · · · · · · · · · · · · · ·	ABR014	934 2 51 65 84 86 134 311 316-325 384 422 445 460
adult brain	Invitrogen	ADKUI4	503 525 564 634 651 721 794 804 810 922
1 11 1	Touitegaan	ABR015	37 134 263 272 277 294 311 443 467 500 514
adult brain	Invitrogen	ADKOIS	582-583 619 651 694 850 871-872 883 888 936
a dula huain	Invitrogen	ABR016	19 22 57 134 188 233 271 277 299 373 440 444
adult brain	Invitrogen	ADROIG	459 469 514 640 717 882 890 920
adula busin	Invitrogen	ABT004	1-2 18 28 51 55-57 67 87-88 115 119 137-139
adult brain	IllAltioBell	AD1004	142 163 200 204 213 218 257 263 271 282 288
		[299 301 311 341 358 370 378 402 407 422-423
			427 458 460 463 499 504 534-535 551 557-558
			571 586 605-606 610 618 627-628 640 643 680
			687 691-692 697 701-702 715 719-721 725 727
		-	753-754 758 771 782 810 827 859 871-872 881
			913 920 925-926 938-941 944 946
adult heart	GIBCO	AHR001	1-2 5-6 14-18 20-21 23 28 32 37 41 45 51 53 55-
adult ileait	GIBCO	7 II IKOO	56 62 66 69-70 80-81 85 87 91 97 107 120-121
]			124 134 140-141 156 163 165-166 172 188-192
ļ ·			195 197-198 200 208 213 216 221 229 231 235
			261-265 267 271 276 284 288 302 305 308 311
			316-325 328 333-334 337-338 347 368-369 373
		.[376-377 379-380 389 396 420 440 445 453-454
ł			459-460 465 468 478 483-484 489 491-493 495
		ì	501 504 507 514 524 529 533 539 541-543 545
			549 552-553 564 566 568 574 577 581-583 587
			589-591 596 599 602 605 608-609 618-619 623
[625 629-632 643 645 647 651 664 672 676 678
			683-684 707 714 716-717 732 735 740 743-744
1	1	1	751 754 757 765 775 778 784-786 788 807-808
			810 826 828-829 842 850 860 876 878-880 890
1	1	_	894 897 899 902 916 923-927 933 939-941
adult kidney	GIBCO	AKD001	1-2 5-6 13 16-17 19-23 26 28 33 38-39 43 45 48-
			51 55-57 60 66-67 69-73 79 82-83 87 90 94 96-
1			97 100 103 126 131 134 140 148-149 157 163
			166 179 184 186 188-192 200-203 213-216 220-
1	1		221 224 226-229 232 235 245 252 257 261-263
}			268-270 272-274 276-277 279 282 288 290 294
			299 308 311 316-325 332 335 339-340 358 360-
			363 373 375 379-380 386 388-389 392 395-396
1			402 413 421 423-424 428-429 431 436 440 444
	1		450 454 457 459-460 468-469 476 489 492-493
	1	}	499 504 511 513-514 520-521 524-526 531 533
		ļ	538-542 544-547 552 564 567-568 574 577-578
			582-583 590-591 595-596 598 602 607 610 613
			618-619 622 631-632 639-642 644 647 651 654-
		1	655 658-659 664 667-669 673 678 680-682 684

Tissue Origin	Library/RNA Source	HYSEQ Library Name	SEQ ID NOS:
			687 689 693 696 706-707 712 714-715 717-718
			721 729-731 734-736 740 744 748 754 760 771
		İ	774 782 784 789 795 807 809-810 819 825 834
	1	ĺ	836-837 842 850 859 870 872 876 878-879 884
			887 890 895 897-899 902 905 910 919-921 925-
adult kidney	Tasitus	AYEMAA	926 933 936 944
addit kidiley	Invitrogen	AKT002	1 14-15 28 30 35-37 53-54 73 88 112 114 129
			134 137 140 149 157 166 172 186-188 191-192
			203-204 213 235 245 257 262-263 266 268-270
			273-274 288-289 297 299 302 310-313 315-325
			335 340 358 373 378-381 395 413 423 441 450
			453 456 459-460 470 477 491-494 500 513 540
			542 545 554 556 564 567 587 591 619 622 627 633 643 668-669 677 684 689 693 701-702 704
			714 729-730 754 758 760 777 781 785-786 788-
			789 807 836-837 840 849-850 872 876 881 890
		İ	895 905-906 913 923 925-926 931-933 944
adult liver	Clontech	ALV003	159 179 189-192 201 219 257 349 392 568 664
			753 796 887 934
adult liver	Invitrogen	ALV002	5-6 28 35-36 52 54 70 72 86-87 103 112 127 134
		· ·	140 159 179 188 200-201 213 218-219 225 239-
			240 257 263 271 275 311 315 367 373 388 392
			444 459-460 464 468 497-499 512 527 532 542
			545 562 599 605 629 640 657 680 684 687-688
			706 713 715 717-718 721 742 754 758 771 791-
		1	793 818 829 843 854-855 871 878-879 887 921
adult lung	GIBCO	47.0001	933-934
acuit fullg	GIBCO	ALG001	5-6 16 28 38 51 74 97 122 124 134 140 163 188-
		1.	192 200 218 221 262-263 268-272 294 311 316-
	i		325 379-380 429 463 468 493 511 520-522 537-
			538 542 545 568-569 595 622 643-644 664 667 711 714 721 730 754 775 850 860 863 879 887
			897 925-926 944
adult lung	Invitrogen	LGT002	2 5-8 13 16-17 29-31 35-39 43 46 57 67 72 76
			78 81 85 87 90 94 97 100 110 119 122 130-131
			134 137 140 146 149 167 172 174 179 188 197-
			198 201 213 216 218 220-221 223 231 245-246
			251-252 256-257 262-263 267-270 277 284 288
			296 299 301-302 311 316-325 340 354 373 379-
			380 388 392 395 400-401 410 413 421 431 436
]	441-443 445 451 455 457 460 463-464 467 469
			475 478 489 491 493 497 499 504 507 514 518-
			519 524 529 534-535 537 542 545-546 548 552
			555 559 568 578 581-583 592 597 602-603 605-
			607 613 615 619 621-622 636-637 642-643 646-
			647 654-655 679-681 684 687-689 693 701-702
			704 706 711 713 715-716 718 727 732-734 738
1			748 753-754 757-758 760 762 766 769 774 782
			785-786 802 817 829 834 850 853 859-860 866-
ļ			867 870-871 878-879 887 890 899 902 904 910
dult spleen	Clontech	SPLc01	917 923 925-926 936-937
		OI LOUI	33 38 57 67 75 87 134 142 163 216 221 229 244
]			257 304 307 311 316-325 340 355-356 378 441 468 525 538 545 560 564 500 721 754 766 722
		ł	468 525 538 545 560 564 599 721 754 766 780 794 827 841 850 866
dult spleen	GIBCO	ASP001	2 14-15 20-22 29 38 43 48 51 53-56 65 67 72 74
-			84 87 131-132 134 137 140 172 188-192 200
			212 221 256 263 271 282 308 311 316-325 343

Tissue Origin	Library/RNA Source	HYSEQ Library Name	SEQ ID NOS:
	Source	Name	383 389 423 436 441 443 459-460 467 469 495 499-500 505 514 520-522 524 529 537 539 545 552 585 619 631-632 639 643 664 673 707 723 735 742-744 758 771 799 810 817 836 850 878 925-926 934 936
bladder	Invitrogen	BLD001	5-6 8 20-21 28 72 91 122 126 130 166 188 197 200 213-214 225 257 262 315-325 341 409 486 491 572 593 622 650 673 691-692 810 813 861 870 877 883 887 904
bone marrow	Clonetech	BMD007	65 76 84 245 516
bone marrow	Clontech	BMD001	8 13-16 28 38 43 45-48 50-51 57 62-63 65 67 84-85 97 100 104 118 122-124 131 134 140 163 188 214 216 221 224 231 245 252 261-263 268-270 273-274 279 288 290 311 373 378 389-391 395 414 428 431 436 440-441 443 451 455 459-460 465 469-470 475 495 497-498 502 507 514-519 529 537-538 542 546 550 552 556 560-561 563-564 568 576-577 580 587 589 596 601-602 610-613 619-620 626 642-643 647 651 664 666 668 676 678 681-682 684 696 704 706-707 715 727 730 732-735 740 748 753 758 761 764 771 775 780 794 800-801 830 834 836 842 850 863 871-872 878-879 882 884 888 897 900-901 904 910 921 923 929 934 947
bone marrow	Clontech	BMD004	65
bone marrow	GF	ВМD002	1-2 5-6 10 13 16-21 27 31 38 42-43 46 57 65-66 76 80 84 87 97 99 110 112 118 131 134 137 140 145 161 163 165 172 195 206 208 221 229 231 237 244 247 252 256 267-270 272 276 278-279 282 284 288 294 301 304 307 311 316-327 333-334 337-338 345-347 352 360-361 368 373 376-378 381 383 388 414 436 441 443 450 452 454-455 457 469-470 483-484 486 490 498 516 519-521 524 530-531 539 542-543 545-546 551 553 555 559 564 571 576-577 580 585 591 594 602 604-605 607-608 610-612 619-621 625-626 629 631-632 639-640 644 650-651 664-665 684 687-688 693 699 703 714 723-724 727 733 735 740 742 745 748 750-752 754-755 777-780 784 787 794-795 802 809 817 824 827 831-832 834 846-847 850-851 854-855 861 867 875 878 883 886 891 894 897 900 902 910 914 919 921 925-926 929 936 939-941 944
cervix	BioChain	CVX001	3-4 14-16 20-23 25 33 42-43 45 48-50 54 57 67 69 75 85 87 91 95-97 107 110 114 124 126-127 131 134 137 140 150 157 163 165 172 185-188 200 204 212-213 216 225 229 245 252 257 261-263 266-270 276 282 288 290 301-302 308 316-325 327 340 363-364 372-373 378 383 388-392 394 396 409 413-414 421 428-429 438-440 443-444 454 456-457 459 463 467 475 486 489 493 495 507 514-515 522 534-537 556 568 572 574 577 582-583 587 594 600 608 610 613 622 626 633 639 643 647-648 651 653 667 680 683 685-686 693 696 703-704 706 711 721 723-725 727 730-731 734-735 742-743 748 754-757 762 771 776 785-786 788 794 800 802 807 809-810 817 827 829 834-835 842 850 857 860 862-863 868

Tissue Origin	Library/RNA Source	HYSEQ Library Name	SEQ ID NOS:
			870 873 876-877 879-880 884 887 891 897 904- 905 910 916-917 921 925-926 933 937 947
colon	Invitrogen	CLN001	19-21 53 55-57 72 88 133-134 168 213 245 252
ļ			311-313 316-325 340 443 459 469 483-484 486
			497 515-516 597 606 622 643 667 676 706 718
diaphragm	BioChain	DIA002	742-743 753 766 829 833 872 887 902 923 929 305 311
endothelial cells	Strategene	EDT001	1-2 7-8 14-16 19-22 24 28-29 32-33 41 43 45 51
			57 61 74 83 87-88 97 105 112 116-117 131 134
			137 140 148 165 172 179 188-192 197-198 208
			212-213 220-221 225 229 231 237 246 252 256-
			258 261-265 268-272 276-277 279 281-282 284
			286 288 294 297 299 302 307-308 311-313 326 334-335 340 355-356 358 360-361 364 375 383
			386 389 392 403 413 423-424 429 440 443 445
			451 453 455-456 459-460 462-463 465-466 468-
			470 475 491 495 497-499 504 514 520-522 524-
			526 528 532-536 539-540 546 551-552 554 556
			564 566-567 571 574-577 581-583 587 591-593
			597-599 601 607 615 618 622 625 633 639 641-
			644 651 667 677 680 684 691-692 701-702 704 716-717 720-721 726 732-733 735 743-744 754
			758 765 785-786 795 802 806 809,819 826 828-
			830 832 834 836 846-847 850 867 871 877-878
ozanka za	D: CI		890-891 897 902 907 921 923 925-926 944 946
esophagus fetal brain	BioChain Clontech	ESO002	188
Total Orall	Ciontech	FBR001	33 49 51 126 134 197-198 264-265 360-361 413 460 647 810 819 871
fetal brain	Clontech	FBR004	137 156 205 282 284 405 424 480 489 701-702
			820 921
fetal brain	Clontech	FBR006	2 9-10 18-19 22 28 30-32 37 39-40 42-43 46-47
			49 57 66-67 76 80 83 96 109 112 116-117 120
•			124 131 133-134 136 142-143 146 152 155 160
		!	162 165 169 173 184 189-198 200-201 205 215-
			216 238 244 248 254-255 257-258 260-263 272- 274 276-277 282 288 293-294 307 309 311 314-
			328 343 347 351-352 354 357-358 360-361 373-
			375 378-381 390 392 400-401 403 405 407 410-
			411 413 420 424 429 445 450 452-453 458 460
			463 467-469 472 474 477 479 483-484 491 499
			507 520-521 525 527 529 531 533 538 545 551
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lung	Ctuata and	7 PP 004	936 943
ung	Strategene	LFB001	2-4 22 28 32-33 47 51 79 120 129 134 140 163
			172 188 208 220-221 231 252 257 263 276-277
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			463 486 491 493 495 499 539 571 591 601 607
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ymph node	Clautach	4737001	735 748 782 828 850 870-871
Juiph node	Clontech	ALN001	43 98 131 140 163 188 221 245 277 299 311 491
		1	515 546 564 593 603 610 615 630 682 694 707
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Prince , Braine	Cionicen	F11004	41-42 83 85 97 134 193-194 204 208 213 224
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saliva gland	Clontech	SALS03	460
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			436 441 459 476 514-515 520-521 532 543 568
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		1	754 777 824 836 864 867 878 883 897 901-902
skeletal muscle	Clontech		916-917 933 938-941
			42 98 156 163 191-192 200 261 305 311 395 415 462 468 504 531 542 566 583 583 583 583
j			415 462 468 504 531 543 566 582-583 585 594 680 740 853 875 927 933 935
keletal muscle	Clontech		850
kin fibroblast	ATCC		379-380 850
kin fibroblast	ATCC		742 850

Tissue Origin Library/RNA HYSEQ Library	SEQ ID NOS:
Source Name	
skin fibroblast ATCC SFB003	87
small intestine Clontech SIN001	27-29 31 38 40 46 48 51 54 57-58 62 65 67 75
	77 85 97 110 112 116-117 119 131-132 134 137
	140 161 163 166 168 177 188 197-198 208 213
	220 224 229 246 257 261-262 264-265 276-277 288 295 297 299 311 316-326 328-330 337-338
	288 295 297 299 311 316-326 326-330 337-338 340 360-361 373 375 382 390-391 410 413 428-
	429 436 438 440 453-454 459 468 476-477 497
	507 511 522 531 536 538 542 545-546 548 552
	556 564 570-571 576 580-581 586-587 591 596
	599 605 610 613 619 625-626 643-644 651-653
	664-666 668-670 677 680 684 693 700-702 706-
	707 713-715 723-724 729-730 735 740 746 748
	753-754 757-758 764 777-778 784-786 818 822
	824 826-829 833-837 842 862-863 865-867 877-
	878 886 897 900-902 906 913 916 921 925-926
	936 939-941
CT 1 CT CT CT CT CT CT CT CT CT CT CT CT CT	18 23 33 37 42 51 67 87 92 94 97 100 140 162
spinal cord Clontech SPC001	184 188 191-192 208 213 220 231 248 262 268-
	271 273-274 282 287-288 290 307 311 316-325
	358 364 376-377 383 387 389-390 402 412 422
	444 455 476 483-484 489 504 522 534-535 556
	562 587-588 591 597 603-604 618-619 643 651
	667-670 677 693 703-704 717-718 727 746 757
	773 808 810 827 834-835 837 850 871-872 875
	904 910 931-932 939-941
stomach Clontech STO001	18 65 88 163 188 208 213 261 272 277 286 294
Stomach Cronteen 310001	336 373 396 412 459 514 553 602 610 647 651-
·	652 671 673 714 774 790 831 833 842 850 876
testis GIBCO ATS001	1 3-4 14-16 28 31 45-46 66 85 90 95 97 103 112
lesus Gibeo	128-130 134 140 163 166 188 191-192 199-200
	213 226-228 261-265 267-271 284 302 311 316-
	325 327 379-380 391 413 421 428 444 454 457
	459-460 467 491 493 495 500 505 519 525 529
	532 534-535 545 552 556 566 568 575 596 599
	613 616-617 647 649 651 680 684 703 707 716
	719 721 727 734 738 740 744 748 758 765-766
	774 777 782 802 810 817 827-828 834 842 846-
	847 850 862-863 871-872 878 880 892 901 916-
	917 921
thalamus Clontech THA002	2 87 96 103 106 189-192 208 252 258 295 308
	311 367 376-377 383-384 445 455 459-460 498
	529 587 598 602 629 654-655 705-706 715 717
	723 754 775 810 817 822 864 867 881 892 927
	930
thymus Clonetech THM001	3-4 8 18 28 54 57 63 65 68 84 97 100 116-117
	122 134 142 151 169 171-172 188 195 197-198
	201 213 221 237 245 261 287 311 316-325 360-
	361 376-377 423 441 444 459 489 491-493 495
	498 504 507 514 527 532 534-536 539 553 556
	568 571-572 590 595-596 599 610 618 622 631-
	632 643 647 651 654-655 664 687-688 691-693
	703 715 721 733-735 748 760 762 765 781 794
	799 802 831 834 836 842 850 860-861 863 871
	878 885 896-897 903 910 923 925-926 928 939-
	941
thymus Clontech THMc02	2-4 17 20-22 37-38 42-43 46 63 65-68 76 88 95
	103 118 120 124 134 137 140-141 143 163 165

Source Name 171 179 182 189-194 1 228 231 244 257 262 2 299 307 316-325 341 3 377 379-381 389 391 3	ID NOS: 198 200 212-215 221 226- 266 276-277 287-288 297 352 358 360-361 373 376- 394-396 403 410-411 436
228 231 244 257 262 2 299 307 316-325 341 3 377 379-381 389 391 3	266 276-277 287-288 297 352 358 360-361 373 376- 394-396 403 410-411 436
228 231 244 257 262 2 299 307 316-325 341 3 377 379-381 389 391 3	266 276-277 287-288 297 352 358 360-361 373 376- 394-396 403 410-411 436
377 379-381 389 391 3	394-396 403 410-411 436
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440 445 450 459 463-4	164 469 478 491 495 500
563 576 581 597 505 5	532 539 542 550 555 560 OI 610-611 613-614 618
622 625-626 631-632 6	638 642-644 657 664 667
670 673 680 683 687 6	91-693 699 715-716 721
740 743-744 747-754 7	61 763-765 771 777 780-
781 784-787 790 794 8	05 811 820 826 831 834
841 845 861 867-868 8	78 881 883 891 893-894
896-897 902 904 910 9	12-914 918 923 936-941
45-947	
1-2 10-21 27 32 38 42 4	46 49 51 53-56 66 72 77-
78 87-88 97 115 119 12	24 130-131 134 136 152
103-105 172 183 188-19	92 202 212-213 216 221
224 229 233 241-243 23	52 257-258 261 263-265
267 277 279 297 301 30 357 363 373 376-377 38	JD 308 311 316-325 327 R1 393 390 307 400 401
410 413-414 427-428 44	01 303 309 397 400-401 43-444 446 447 467 460
463 467-469 475 482 48	89 495 499-500 504 500
513 519-522 526 529 53	33 537-538 542 545-546
548 556 564 567-568 58	32-583 589 592 599 605
608 611 621 623 630 64	2-644 648 651-652 654-
655 664 672-676 684-68	36 691-694 700 706-708
713 717-718 721-722 72	25 729 731 734-735 740
748 753-754 760 764 76	66 771 774 777 781 792
797-800 802 805 826 82	8-829 834 842 850 861
863 868 876 879 897 899 939-941	9 901 910 913 929 937
trachea Clontech TRC001 20-21 38 112 161 163 18	88 263 267 327 413 420
457 459-460 471 514 54	0-541 552 572 574 622
639 654-655 676-677 69	1-692 707 725 743 748
765 777-778 862 868 89°	7 905 908 944
1-2 29 32 46 67 83 87 94	134 136 140 148 160
163 166 172 181 186-192	2 197-198 208 213 216
225-231 237 252 261-26	5 267-270 279 282 288
295 302 308 311 316-320	6 339-340 365 376-377
379-380 384 392-397 42 452 459 461 463-464 470	1 423 428 433 440 445
500 507 517-518 522 525	5-526 528 524 525 540
545-546 556-558 564 566	6 568 571-572 577 502
599 601 605 610 618 623	644 651 661 668-669
673 678 680 685-686 696	5 706 709 718 735-736
748 754 769 772-777 782	2 792 797-799 802 807
809 815 817 824 850 854	-855 870 876 881 888
891 897 899 901 913 921	928 930-932
51 6/ 126 130 133 140 18	88-192 229 267 329
373 440 491 514 599 685	-686 693 713 716-717
young liver GIBCO ALV001 3-4 17 20-21 32 43 55-56	70 100
3-4 17 20-21 32 43 55-56	70 100 134 137 163
172 174 179 186 188-192 229 232 252 275 301 311	200 213 216 219 221
441 459-460 497 499-500	514 524 526 522 520
550 568 571 588-589 595	619 622 631 622 642
658-659 664 677 680 693	700 707 713 710 742
754 757-758 766 807 834	863 867 876 884 887

Tissue Origin	Library/RNA Source	HYSEQ Library Name	SEQ ID NOS:
			904 907

TABLE 2

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
949	AAM253 84	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:899.	644	99
949	AAY275 81	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 15.	644	99
949	gi137856 18	Mus musculus	sideroflexin 4	396	60
950	gi127691 2	Homo sapiens	Human putative ubiquitin C- terminal hydrolase (UHXI) mRNA, complete cds.	3719	100
950	gi126531 65	Homo sapiens	ubiquitin specific protease 11, clone MGC:8620 IMAGE:2961383, mRNA, complete cds.	3709	99
950	gi135294 94	Mus musculus	Similar to ubiquitin specific protease 11	3167	83
951	AAY116 96	Homo sapiens	MITU LckSH3 domain- combining protein.	4131	99
951	AAG786 48	Homo sapiens	SHAN- Human Ra1BPI related protein 82.	3875	99
951	gi136251 66	Homo sapiens	RALBP1 mRNA, complete cds.	3875	99
952	AAY116 96	Homo sapiens	MITU LckSH3 domain- combining protein.	3953	96
952	AAG786 48	Homo sapiens	SHAN- Human Ra 1BPI related protein 82.	3697	96
952	gi136251	Homo sapiens	RALBP1 mRNA, complete cds.	3697	96
953	gi104371	Homo sapiens	cDNA: FLJ21146 fis, clone CAS09305.	2190	94
953	gi128432	Mus musculus	putative	1672	77
953	gi157788 93	Homo sapiens	Similar to hypothetical protein FLJ20967, clone MGC:11140 IMAGE:3837082, mRNA, complete cds.	1328	99
954	gi104371	Homo sapiens	cDNA: FLJ21146 fis, clone CAS09305.	2359	100
954	gi128432	Mus musculus	putative	1643	72
954	gi157788 93	Homo sapiens	Similar to hypothetical protein FLJ20967, clone MGC:11140 IMAGE:3837082, mRNA, complete cds.	1409	99
955	gi158253	Mus musculus	NIMA-related kinase 8	2009	89
955	gi158253	Danio rerio	NIMA-related kinase 8	1439	70
955	AAO019	Homo sapiens	HYSE- Human polypeptide SEQ	548	85

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	74		ID NO 15866.	 	identity
956	AAW886 60		HUMA- Secreted protein encoded by gene 127 clone HSUBW09.	175	97
956	AAO001 87	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 14079.	70	55
956 	gi138154 29	Suifolobus solfataricus	Sugar transport related protein	70	40
957	AAB939 66	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14027.	1133	100
957	gi104338 35	Homo sapiens	cDNA FLJ12377 fis, clone MAMMA1002524, weakly similar to HYPOTHETICAL 117.8 KD PROTEIN IN STE2- FRS2 INTERGENIC REGION.	1133	100
957	AAO043 81	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 18273.	594	100
958	AAB952 97	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17525.	885	100
958	gi104349 41	Homo sapiens	cDNA FLJ13087 fis, clone NT2RP3002099.	885	100
958	gi167405 66	Homo sapiens	Similar to hypothetical protein FLJ13087, clone MGC:15009 IMAGE:3536735, mRNA, complete cds.	807	95
959	AAY276 76	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 110.	474	100
959	gi529595 1	Oryza sativa	Similar to Herpesvirus papio BRRF2 homolog gene, partial cds.(U23857)	69	41
960	AAG892 62	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 382.	352	98
960	AAY307 21	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	352	98
960	AAB236 15	Homo sapiens	ALPH- Human secreted protein SEQ ID NO: 30.	343	97
961	AAY726 05	Homo sapiens	INCY- Human Electron Transfer Protein, ETRN-3.	579	100
961	AAO116 27	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 25519.	579	100
961	AAG039 41	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 8022.	570	98
962	gi146034 55	Homo sapiens	ubiquitin-conjugating enzyme E2A (RAD6 homolog), clone MGC:20175 IMAGE:3051041, mRNA, complete cds.	599 .	79
962	gi488377 3	Gallus gallus	ubiquitin-conjugating enzyme	599	79
962	gi144852 44	Mus musculus	ubiquitin-conjugating enzyme HR6A	599	79
963	gi146034 · 55	Homo sapiens	ubiquitin-conjugating enzyme E2A (RAD6 homolog), clone MGC:20175 IMAGE:3051041, mRNA, complete cds.	699	90
963	gi488377 3	Gallus gallus	ubiquitin-conjugating enzyme	699	90
63	gi144852	Mus musculus	ubiquitin-conjugating enzyme	699	90

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	44		HR6A		
964	gi168770 66	Homo sapiens	clone MGC:24447 IMAGE:4077762, mRNA, complete cds.	362	100
964	gi168770 59	Homo sapiens	clone MGC:24437 IMAGE:4075637, mRNA, complete cds.	362	100
964	AAY949 59	Homo sapiens	GEMY Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	204	97
965	AAB929 93	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11723.	2879	97
965	AAG813 64	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:246.	2879	97
965	gi140423 80	Homo sapiens	cDNA FLJ14690 fis, clone NT2RP2005270.	2879	97
966	AAB957 69	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18703.	2841	99
966	gi104366 07	Homo sapiens	cDNA FLJ14207 fis, clone NT2RP3003185, weakly similar to TROPOMYOSIN 1, FUSION PROTEIN 33.	2841	99
966	gi128331 93	Mus musculus	putative	2375	85
967	AAM254 13	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:928.	799	100
967	AAW678 63	Homo sapiens	HUMA- Human secreted protein encoded by gene 57 clone HFEBF41.	551	98
967	gi135438	Mus musculus	Unknown (protein for IMAGE:3591061)	95	33
968	gi104379 60	Homo sapiens	cDNA: FLJ21792 fis, clone HEP00441.	5865	99
968	AAE0618 6	Homo sapiens	HUMA- Human gene 58 encoded secreted protein fragment, SEQ ID NO:248.	3088	98
968	AAE0609 8	Homo sapiens	HUMA- Human gene 58 encoded secreted protein HSLCX03, SEQ ID NO:160.	3088	98
969	gi126980	Homo sapiens	mRNA for KIAA1767 protein, partial cds.	4441	98
969	AAM255 78	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1093.	3898	98
969	AAE0618 6	Homo sapiens	HUMA- Human gene 58 encoded secreted protein fragment, SEQ ID NO:248.	3464	98
970	AAY483 59	Homo sapiens	META- Human prostate cancerassociated protein 56.	403	98
970	gi152159 66	Homo sapiens	DL8Q12 gene for hypothetical protein, exons 1-2.	92	53
970	AAR992 56	Homo sapiens	UYAR- Natural killer lytic associated protein.	75	37
971	gi656182	Mus musculus	Kif21a	5684	76
971	gi656182	Mus musculus	Kif21b	4944	60
971	gi126979	Homo sapiens	mRNA for KIAA1708 protein,	4656	99

SEQ	Hit ID	Speicies	Description	S score	Percent
	61		partial cds.	 	identity
972	AAW750 79		HUMA- Human secreted protein encoded by gene 23 clone HBMCT32.	148	100
973	AAY359 21	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 170.	548	99
973	86 86	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:901.	494	96
973	AAY359 23	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 172.	494	96
974	AAY275 87	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 21.	448	100
974	gi128025 61	Bovine herpesvirus 4	unknown	74	42
975	AAU162 97	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1250.	2420	98
975	AAB944 86	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15170.	1761	74
975	AAM940 18	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 106.	1761	74
976	AAM412 64	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6195.	903	99
976	AAM394 78	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2623.	903	99
976	AAB437 71	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1216.	903	99
977	gi117616 11	Homo sapiens	kinesin-like protein RBKIN1 (RBKIN) mRNA, complete cds, alternatively spliced.	9290	99
977	gil 17616 13	Homo sapiens	kinesin-like protein RBKIN2 (RBKIN) mRNA, complete cds, alternatively spliced.	9055	98
977	gi120540 30	Homo sapiens	mRNA for KINESIN-13A1 (KIN13A gene).	8955	97
978	gi759580 2	Mus musculus	ELKL motif kinase 2 short form	188	48
978	gi759580 0	Mus musculus	ELKL motif kinase 2 long form	188	48
978	AAM939 56	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4158.	187	48
979	gi161984 56	Homo sapiens	Similar to RIKEN cDNA 0610040E02 gene, clone MGC:17973 IMAGE:3919892, mRNA, complete cds.	1050	100
979	gi167406 89	Mus musculus	RIKEN cDNA 0610040E02 gene	891	76
979	gi128413 15	Mus musculus	putative	891	76
980	gi147149 27	Homo sapiens	amino acid transporter system A1, clone MGC:17722 IMAGE:3871101, mRNA, complete cds.	2466	100
980	gi116407	Homo sapiens		2466	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	43		A1 mRNA, complete cds.		
980	AAB935 56	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12942.	2459	99
981	AAW750 90	Homo sapiens	HUMA- Human secreted protein encoded by gene 34 clone HTEGA81.	507	100
981	AAW751 52	Homo sapiens	HUMA- Human secreted protein encoded by gene 34 clone HKMLK44.	507	100
981	AAW751 51	Homo sapiens	HUMA- Human secreted protein encoded by gene 34 clone HTEGA81.	507	100
982	AAB947 54	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15811.	4658	99
982	gi140428 59	Homo sapiens	cDNA FLJ14964 fis, clone PLACE4000581, moderately similar to FIBROPELLIN I PRECURSOR.	4658	99
982	gi111771 64	Mus musculus	polydom protein	3880	81
983	AAB652 78	Homo sapiens	GETH Human PRO1185 (UNQ599) protein sequence SEQ ID NO:401.	993	100
983	AAM253 16	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:831.	993	100
983	AAM238 05	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1330.	993	100
984	AAY359 96	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 381.	589	66
984	AAB652 78	Homo sapiens	GETH Human PRO1185 (UNQ599) protein sequence SEQ ID NO:401.	567	65
984	AAM253 16	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:831.	567	65
985	gi168770 39	Homo sapiens	hypothetical protein FLJ22688, clone MGC:2438 IMAGE:2819805, mRNA, complete cds.	1952	91
985	gi133252 53	Homo sapiens	Similar to hypothetical protein FLJ22688, clone MGC:4098 IMAGE:2819805, mRNA, complete cds.	1952	91
985	gi104391	Homo sapiens	cDNA: FLJ22688 fis, clone HSI11003.	1695	89
986	gi512469	Homo sapiens	H.sapiens HLA-DMA gene.	1285	92
986	gi218187 6		Human DNA sequence from clone XX-O27 on chromosome 6. Contains the BRD2 gene encoding bromodomain-containing 2 protein, the HLA-DMA gene encoding major histocompatibility complex class II DM alpha, two CpG islands,	1285	92
986	gi150303	Homo sapiens	ESTs, STSs and GSSs, complete sequence. clone MGC:13532	1285	92

SEQ ID		Speicies	Description	S score	Percent identity
	36		IMAGE:4245221, mRNA, complete cds.		lucitaty
987	AAB425 29	Homo sapiens	CURA- Human ORFX ORF2293 polypeptide sequence SEQ ID NO:4586.	2683	99
987	gi126978 93	Homo sapiens	mRNA for KIAA1674 protein, partial cds.	2683	99
987	AAM905 36	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:18129.	1512	98
988	gi222453 9	Homo sapiens	Human mRNA for KIAA0299 gene, partial cds.	9903	99
988	AAY165 88	Homo sapiens	RHON A protein that interacts with presenilins.	4733	97
988	gi730171 0	Drosophila melanogaster	CG11754 gene product	3074	43
989	AAW748 87	Homo sapiens	HUMA- Human secreted protein encoded by gene 160 clone HCELB21.	203	100
989	AAM244 01	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1926.	183	85
989	gi929400 3	Arabidopsis thaliana	cytochrome P450-like protein	70	39
990	gi119904 20	Homo sapiens	mRNA for MOP-3, complete cds.	4359	93
990	AAB932 29	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12223.	3950	99
990	gi702311 4	Homo sapiens	cDNA FLJ10833 fis, clone NT2RP4001206, moderately similar to Drosophila melanogaster strawberry notch mRNA.	3950	99
991	gi433710 5	Homo sapiens	MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds.	668	100
991	gi29969	Homo sapiens	Human gene for casein kinase II subunit beta (EC 2.7.1.37).	668	100
991	gi29967	Homo sapiens	Human mRNA for phosvitin/casein kinase type II beta subunit (EC 2.7.1.37).	668	100
992	AAY108 40	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	349	100
993	AAM259 27	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1442.	824	100
993	AAY733 25	Homo sapiens	INCY- HTRM clone 001106 protein sequence.	820	99
993	AAG038 70	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7951.	819	99
994	AAB940 43	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14201.	5698	99
	gi104339 76	Homo sapiens	cDNA FLJ12471 fis, clone NT2RM1000894, highly similar to DNA-DIRECTED RNA	5698	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	·		POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6).	·	
994	gi162159 4	Mus musculus	second largest subunit of RNA polymerase I	5095	84
995	AAU158 80	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 833.	1091	100
995	ABB0334 5	Homo sapiens	HUMA- Human musculoskeletal system related polypeptide SEQ ID NO 1292.	1091	100
995	gi138794 42	Mus musculus	Similar to RIKEN cDNA 2310035M22 gene	1056	93
996	gi669260	Mus musculus	MGA protein	3446	77
996	gi304356	Homo sapiens	mRNA for KIAA0518 protein,	3272	100
996	AAB945 60	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15332.	1933	99
997	gi577139 2	Homo sapiens	RAB-like protein 2B (RABL2B) mRNA, complete cds.	718	99
997	gi159288 38	Homo sapiens	RAB, member of RAS oncogene family-like 2B, clone MGC:10160 IMAGE:3906749, mRNA, complete cds.	718	99
997	gi726396	Homo sapiens	Human DNA sequence from clone RP11-395L14. Contains (part of) up to six novel genes or pseudogenes, the gene for a novel forkhead protein similar to FOXD4 (forkhead box D4, FREAC5), the gene for a novel phosphoglucomutase like protein, a pseudogene similar to part of DEAD/H (Asp-Glu-Ala-Asp/His) box (S.cerevisiae CHL1-like helicase), an RPL23A (60S ribosomal protein L23A) pseudogene, the RABL2A gene for RAB-like 2A, the gene for a novel protein similar to small nuclear ribonucleoprotein polypeptide A' (SNRPA1) and the 3' part of the gene for a novel protein similar to acrosin (ACR). Contains ESTs, STSs, GSSs and nine putative CpG islands, complete sequence.		
998	gi104402 02	Homo sapiens	cDNA: FLJ23495 fis, clone LNG02228.	2398	99
998	AAU172 89	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 854.	487	97
998	AAM926 81	Homo sapiens	HUMA- Human digestive system antigen SEQ ID NO: 2030.	487	97
999	gi126532 49	Homo sapiens	Similar to CAAX box 1, clone MGC:8471 IMAGE:2821721, mRNA, complete cds.	450	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
999	AAY322 07		INCY- Human receptor molecule (REC) encoded by Incyte clone 2936050.	429	95
999	gi757623 2		Human DNA sequence from clone RP4-809E13 on chromosome Xq26.1-27.1. Contains the gene for a putative prenylated protein, two putative prenylated protein pseudogenes, ESTs, STSs, GSSs and three putative CpG islands, complete sequence.	397	87
1000	gi157785 56		alpha-1-B glycoprotein precursor (A1BG) mRNA, complete cds.	1487	98
1000	gi 118773 48	Rattus norvegicus	putative alpha 1B-glycoprotein	518	40
1000	AAY646 70	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:831.	430	76
1001	AAY873 15	Homo sapiens	INCY- Human signal peptide containing protein HSPP-92 SEQ ID NO:92.	2817	100
1001	AAM937 93	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3821.	2527	99
1001	gi128045 27	Homo sapiens	hypothetical protein FLJ22405, clone MGC:2543 IMAGE:2961594, mRNA, complete cds.	2194	100
1002	gi416030 4	Mus musculus	HS1 binding protein 3	1449	75
1002	AAB958 01	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18781.	1082	100
1002	gi104366 60	Homo sapiens	cDNA FLJ14249 fis, clone OVARC1001200, weakly similar to Mus musculus mRNA for HS1 binding protein 3.	1082	100
1003	AAY873 15	Homo sapiens	INCY- Human signal peptide containing protein HSPP-92 SEQ ID NO:92.	1837	100
1003	gi128045 27	Homo sapiens	hypothetical protein FLJ22405, clone MGC:2543 IMAGE:2961594, mRNA, complete cds.	1837	100
1003	gi104387 80	Homo sapiens	cDNA: FLJ22405 fis, clone HRC08294.	1837	100
1004	AAM937 93	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3821.	3401	99
1004	gi173906 94	Mus musculus	Similar to hypothetical protein FLJ22405	2543	90
1004	AAY873 15	Homo sapiens	INCY- Human signal peptide containing protein HSPP-92 SEQ ID NO:92.	2535	100
1005	AAY873 27	Homo sapiens	INCY- Human signal peptide containing protein HSPP-104 SEQ ID NO:104.	584	100
1005	AAY597 05	Homo sapiens	GEST Secreted protein 51-41-1- F10-FL1.	554	95

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1005	AAY128 65	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:455.	208	100
1006	AAY362 37	Homo sapiens	HUMA- Human secreted protein encoded by gene 14.	177	100
1007	AAY873 10	Homo sapiens	INCY- Human signal peptide containing protein HSPP-87 SEQ ID NO:87.	370	100
1007	AAG773 44	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:8110.	201	79
1007	gi141981 25	Homo sapiens	clone MGC:18053 IMAGE:4148889, mRNA, complete cds.	68	61
1008	AAB941 08	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14340.	1844	96
1008	AAU045 57	Homo sapiens	GETH Human Stra6 homologue, PRO10282.	1844	96
1008	gi135609 66	Homo sapiens	STRA6 isoform 1 mRNA, complete cds, alternatively spliced.	1844	96
1009	AAY383 94	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 9.	213	100
1010	gi104323 82	Homo sapiens	Human DNA sequence from clone RP4-717123 on chromosome 1p21.2-22.3 Contains ESTs, STSs and GSSs. Contains part of a novel gene for a protein similar to Xenopus laevis Sojo protein, a novel gene and a 60S ribosomal protein L39 (RPL39) pseudogene, complete sequence.	3267	100
1010	gi569043 5	Xenopus laevis	nuclear protein Sojo	1386	44
1010	AAG750 36	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5800.	557	98
1011	AAG005	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4598.	160	48
1011	AAO024 74	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 16366.	153	45
1011	gi854065	Human herpesvirus 6	U88	145	50
1012	AAY195 61	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	514	100
1012	AAB381 57	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 39 SEQ ID NO:96.	70	30
1012	AAU049 58	Homo sapiens	GETH Human Interleukin 17 receptor, IL-17RH4.	69	60
1013	AAR152 22	Homo sapiens	TEXA Chronic myelogenous leukaemia-derived myeloid-related protein.	635	100
1013	gi32402	Homo sapiens	Human mRNA for HP-1, a member of the corticostatin/defensin family.	493	100
1013	gi292363	Homo sapiens	Human neutrophil peptide-1	493	100

SEQ	Hit ID	Speicies	Description	S score	Percent
ID.					identity
1014	gi633017	Homo sapiens	gene, complete cds.	1050	
	6		mRNA for KIAA1167 protein, partial cds.	4079	99
1014	ĺ	norvegicus	GRIP-associated protein 1 long form	3814	92
1014	63		Similar to GRIP-associated protein 1	3646	89
1015	gi104430 47	Homo sapiens	Human DNA sequence from clone RP11-465L10 on chromosome 20. Contains 10 CpG islands, ESTs, STSs and GSSs. Contains the gene for a novel protein similar to Drosophila CG11399, the gene for a novel C2H2 type zinc finger protein similar to chicken FZF-1, a Ferritin light polypeptide (FTL) pseudogene, the MMP9 gene for matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase) (CLG4B), a novel gene, the SLC12A5 gene for solute carrier family 12, (potassium-chloride transporter) member 5 (KIAA1176) and the 3' end of gene KIAA1637, complete sequence.	6471	99
1015	gi104389 18	Homo sapiens	cDNA: FLJ22504 fis, clone HRC11430.	4392	98
1015	gi984814	Gallus gallus	zinc finger protein	2127	58
1016	AAE0607 7	L	HUMA- Human gene 37 encoded secreted protein HDPCJ91, SEQ ID NO:139.	267	100
1016	AAY871 00	Homo sapiens	HUMA- Human secreted protein sequence SEQ ID NO:139.	267	100
1016	gi127188 12	Yarrowia lipolytica	ND3 protein	69	48
1017	AAY864 63	Homo sapiens	HUMA- Human gene 47- encoded protein fragment, SEQ ID NO:378.	361	100
1017	AAY863 20	Homo sapiens	HUMA- Human secreted protein HPRBC80, SEQ ID NO:235.	361	100
1017	gi754963 3	Arabidopsis thaliana	hypothetical protein	70	31
1018	AAM253 84	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:899.	1126	100
1018	AAY275 81	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 15.	774	100
018	gi137856 18	Mus musculus	sideroflexin 4	660	60
019	gi452890	Cricetulus migratorius	serum amyloid P; SAP; female protein; FP	158	71
019	gi387051	Cricetulus Iongicaudatus	FP	157	71
019	gi347257	Mesocricetus auratus	serum amyloid P component	157	71

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1020	gi174287 83	Ralstonia solanacearum	PROBABLE NADP- DEPENDENT OXIDOREDUCTASE OXIDOREDUCTASE PROTEIN	68	29
1020	gi151592 26	Agrobacterium tumefaciens str. C58 (Cereon)	AGR_L_1604p	67	28
1020	gi177425 00	Agrobacterium tumefaciens str. C58 (Dupont)	succinoglycan biosynthesis protein	67	28
1021	gi165539 33	Homo sapiens	cDNA FLJ25217 fis, clone REC08938, highly similar to Oryctolagus cuniculus Na+/glucose cotransporter- related protein mRNA.	1477	100
1021	AAE0661 4	Homo sapiens	SAGA Human protein having hydrophobic domain, HP03974.	1394	100
1021	gi152098 08	Homo sapiens	unnamed protein product	1394	100
1022	AAY167 81	Homo sapiens	GEMY Human secreted protein (clone bh157_7).	1258	100
1022	gi126540 11	Homo sapiens	similar to rat nuclear ubiquitous casein kinase 2, clone MGC:5494 IMAGE:3452665, mRNA, complete cds.	1258	100
1022	gi120536	Homo sapiens	mRNA for NUCKS protein.	1258	100
1023	AAB832 46	Homo sapiens	MILL- Human FATP1 SEQ ID NO: 47.	3372	100
1023	AAB832 39	Homo sapiens	MILL- Human FATP1 SEQ ID NO: 38.	3372	100
1023	AAB832 34	Homo sapiens	MILL- Human FATP1 SEQ ID NO: 32.	3372	100
1024	gi159299 04	Homo sapiens	Similar to dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit, clone MGC:21559 IMAGE:4181887, mRNA, complete cds.	366	100
1024	AAY579 05	Homo sapiens	INCY- Human transmembrane protein HTMPN-29.	153	100
1024	gi379036	Homo sapiens	mRNA for DPM2, complete cds.	153	100
1025	AAY257 32	Homo sapiens	HUMA- Human secreted protein encoded from gene 22.	212	100
1026	AAG770 16	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:7780.	291	100
1026	AAS0319 3_aa1	Homo sapiens	GEHO Human lymphocyte cell surface antigen CD53 cDNA sequence.	116	95
1026	AAV812 20 aa1	Homo sapiens	GEHO Human CD53 antigen cDNA.	116	95
1027	AAY118 48	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No: 448.	193	100
1027	AAY359 56	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO.	193	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			205.	1:	Identity
1027	AAY360 98	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 483.	193	100
1028	AAM939 42	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4126.	1354	99
1028	ABB1142 2		HYSE- Human Zn finger protein homologue, SEQ ID NO:1792.	953	92
1028	gi646720 6	Homo sapiens	GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.	883	56
1029	gi128352 22	Mus musculus	putative	1562	82
1029	gi263665 4	Homo sapiens	Human myosin binding protein H (MyBP-H) gene, complete cds.	1206	66
1029	gi154681 3	Mus musculus	myosin binding protein H	1203	66
1030	AAY363 32	Homo sapiens	HUMA- Human secreted protein encoded by gene 109.	268	100
1030	gi100389 17	Buchnera sp. APS	hypothetical protein	76	42
1030	gi750051 8 (Unknown	hypothetical protein F35E2.7 - Caenorhabditis elegans >	63	38
1031	gi971940 9	Homo sapiens	candidate tumor suppressor protein mRNA, complete cds.	2030	99
1031	gi128565 14	Mus musculus	putative	922	86
1031	AAU220 41	Homo sapiens	HUMA- Human cardiovascular system antigen polypeptide SEQ ID No 815.	703	92
1032	AAR152 22	Homo sapiens	TEXA Chronic myelogenous leukaemia-derived myeloid-related protein.	635	100
1032	gi32402	Homo sapiens	Human mRNA for HP-1, a member of the corticostatin/defensin family.	493	100
1032	gi292363	Homo sapiens	Human neutrophil peptide-1 gene, complete cds.	493	100
1033	gi165525 02	Homo sapiens	cDNA FLJ32395 fis, clone SKMUS2000117, moderately similar to Homo sapiens MAGEF1 mRNA.	1599	100
1033	gi126591 42	Mus musculus	mage-g1	1178	76
1033	gi128571 18	Mus musculus	putative	1178	76
1034	AAB496 50	Homo sapiens	CURA- Human SEC2 protein sequence SEQ ID 4.	2615	100
1034	gi122265 32	Homo sapiens	unnamed protein product	2615	100
1034	gi147148 86	Mus musculus	Unknown (protein for IMAGE:3498778)	2343	89
	AAM237 21	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1246.	2889	100
1035	AAM792	Homo sapiens		2676	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	29		NO 1891.		
1035	AAB883 70	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0106.	1611	100
1036	AAY596 57	Homo sapiens	GEST Secreted protein 108-003-5-0-A8-FL.	689	100
1036	gi144956 99	Homo sapiens	clone MGC:15961 IMAGE:3538818, mRNA, complete cds.	689	100
1036	gi144245 22	Homo sapiens	clone MGC:14327 IMAGE:4298098, mRNA, complete cds.	689	100
1037	AAY276 26	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 60.	352	100
1038	AAD183 56 aal	Homo sapiens	INCY- Human lipid metabolism enzyme-5 (LME-5) cDNA.	1748	100
1038	AAB735 60	Homo sapiens	MILL- Human lipase 18892.	1748	100
1038	AAE1099	Homo sapiens	INCY- Human lipid metabolism enzyme-5 (LME-5) protein.	1748	100
1039	AAG034 75	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7556.	448	100
1039	AAY128 61	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:451.	448	100
1039	gi56760	Rattus norvegicus	neuronal nonacetlycholine binding subunit	75	23
1040	AAY530 49	Homo sapiens	GEMY Human secreted protein clone cj378_3 protein sequence SEQ ID NO:104.	463	100
1040	gi136036 74	Stellilabium pogonostalix	maturase	78	38
1040	gi136036	Telipogon parvulus	maturase	74	36
1041	AAY413 54	Homo sapiens	HUMA- Human secreted protein encoded by gene 47 clone HUFCJ30.	288	100
1041	gi152304	Arabidopsis thaliana	putative protein	63	43
1042	AAW747 77	Homo sapiens	HUMA- Human secreted protein encoded by gene 48 clone HFCA174.	245	100
1042	gi154889 20	Homo sapiens	Similar to RIKEN cDNA 2010107G23 gene, clone MGC:9596 IMAGE:3896656, mRNA, complete cds.	245	100
1042	gi128424 65	Mus musculus	putative	241	97
1043	gi152780 28	Homo sapiens	beta-galactose-3-O- sulfotransferase, 4, clone MGC:15045 IMAGE:3636329, mRNA, complete cds.	2568	100
1043	gi147945 24	Homo sapiens	Galbeta1-3GalNAc 3'- sulfotransferase mRNA, complete cds.	2564	99
1043	AAB938 92	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13832.	2556	99
1044	gi153215	Homo sapiens	empty spiracles-like protein	1341	100

SEC	Hit ID	Speicies	7		
ID		Speicles	Description	S score	Percent identity
1000	90		(EMX2) mRNA, complete cds.		Jacontity
1044	73		mRNA; cDNA DKFZp761M1614 (from clone DKFZp761M1614).	1341	100
1044	86		cDNA FLJ30479 fis, clone BRAWH1000168, highly similar to Homeotic protein emx2.	1336	99
1045	66		clone MGC:24447 IMAGE:4077762, mRNA, complete cds.	362	100
1045	59		clone MGC:24437 IMAGE:4075637, mRNA, complete cds.	362	100
1045	AAY949 59	Homo sapiens	GEMY Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	204	97
1046	gi239445	Caenorhabditis elegans	Hypothetical protein ZC178.2	406	30
1046	AAB875 75	Homo sapiens	GETH Human PRO1342.	384	38
1046	AAY994 08	Homo sapiens	GETH Human PRO1342 (UNQ697) amino acid sequence SEQ ID NO:243.	384	38
1047	gi120531 47	Homo sapiens	mRNA; cDNA DKFZp434F1726 (from clone DKFZp434F1726).	1484	98
1047	ABB1173 9	Homo sapiens	HYSE- Human IF-gamma receptor homologue, SEQ ID NO:2109.	1044	100
1047	AAR049 32	Homo sapiens	YEDA Interferon-gamma receptor segment from clone 39 responsiblefor binding the target.	829	98
1048	AAG739 89	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4753.	957	100
1048	AAB589 98	Homo sapiens	HUMA- Breast and ovarian cancer associated antigen protein sequence SEQ ID 706.	957	100
1048	AAM891 00	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:16693.	362	67
1049	gi100473 33	Homo sapiens	mRNA for KIAA1628 protein, partial cds.	5204	100
1049	gi 118629 39	Mus musculus	DDM36	4378	89
1049	gi118629 41	Mus musculus	DDM36E	4366	88
1050	gi190647	Homo sapiens	Human pregnancy-specific beta- 1 glycoprotein (PSG) mRNA, complete cds.	611	72
1050	gi984306	Homo sapiens	Human pregnancy-specific glycoprotein 13 (PSG13') mRNA, complete cds.	606	71
1050	gi190568	Homo sapiens	Human pregnancy-specific beta- 1-glycoprotein 11 (PSG11) mRNA, complete cds.	585	64
051	AAM436	Homo sapiens		588	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	55		SEQ ID NO 333.		
1051	AAM435 88	Homo sapiens	HUMA- Human polypeptide SEQ ID NO 266.	588	100
1051	AAW600 43	Homo sapiens	HUTC- Human MHC class I chain-related gene A (MICA) polypetide.	588	100
1052	gi487783	Rattus norvegicus	TRP2	524	74
1052	gi110956 41	Mus musculus	transient receptor potential channel 2-beta	521	73
1052	gi110956 39	Mus musculus	transient receptor potential channel 2-alpha	521	73
1053	AAB941 88	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14511.	1209	97
1053	gi104342 24	Homo sapiens	cDNA FLJ12623 fis, clone NT2RM4001746.	1209	97
1053	gi126527 97	Homo sapiens	clone MGC:5179 IMAGE:2900118, mRNA, complete cds.	1066	88
1054	AAY383 89	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 4.	152	90
1054	gi136246 35	Euglena viridis	maturase-like protein	63	42
1055	AAY275 82	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 16.	320	100
1055	gi134216 31	Caulobacter crescentus	conserved hypothetical protein	65	27
1055	gi161247 13	Caulobacter crescentus] > [Caulobacter crescentus]	conserved hypothetical protein	65	27
1056	AAO087 59	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22651.	613	100
1056	gi104375 69	Homo sapiens	cDNA: FLJ21463 fis, clone COL04765.	269	57
1056	AAY453 82	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 28.	266	58
1057	AAE0517 5	Homo sapiens	INCY- Human drug metabolising enzyme (DME-6) protein.	1830	99
1057	AAU122 25	Homo sapiens	GETH Human PRO4404 polypeptide sequence.	1830	99
1057	AAU183 63	Homo sapiens	HUMA- Human endocrine polypeptide SEQ ID No 318.	1092	95
1058	AAG812 74	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:66.	815	96
1058	gi140358 56	Homo sapiens	unnamed protein product	815	96
1058	AAG812 73	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:64.	652	99
1059	AAY359 80	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 229.	581	97
1059	ABB1196 0	Homo sapiens	HYSE- Human neuroendocrine- specific protein-like homologue, SEQ ID NO:2330.	246	100
1059	AAZ3831	Homo sapiens	PROT- Human transmembrane	240	97

SEQ	Hit ID	Constalan			
ID		Speicies	Description	S score	Percent identity
	9_aa1		protein cDNA clone HP02061.		Identity
1060	gi795932 5	Homo sapiens	mRNA for KIAA1529 protein, partial cds.	8481	100
1060	gi128363 54	Mus musculus	putative	511	63
1060	AAW036 26	Homo sapiens	UYNY Human thyrotropin GPR N-terminal sequence.	236	31
1061	AAY762 00	Homo sapiens	HUMA- Human secreted protein encoded by gene 77.	262	100
1061	gi159243 50	Staphylococcus aureus subsp. aureus Mu50	oxacillin resistance-related FmtC protein	64	31
1061	gi124836 31	Staphylococcus aureus	FmtC	64	31
1062	AAY362 70	Homo sapiens	HUMA- Human secreted protein encoded by gene 47.	359	100
1062	gi499607 9	Human herpesvirus 6	64% identical to U95 gene of strain U1102 of HHV-6~MCMV IE2 homolog, US22 gene family	68	37
1062	gi573357 6	Human herpesvirus 6B	U95	66	37
1063	gi526274 8	Rattus norvegicus	Proline rich synapse associated protein 2	3930	93
1063	gi738105 6	Rattus norvegicus	Shank postsynaptic density protein 3a	3895	92
1063	gi133591 73	Homo sapiens	mRNA for KIAA1650 protein, partial cds.	3085	100
1064	gi143367 49	Homo sapiens	16p13.3 sequence section 6 of 8.	974	99
1064	gi104400 21	Homo sapiens	cDNA: FLJ23360 fis, clone HEP15172.	974	99 .
1064	AAB941 88	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14511.	914	78
1065	AAB941 88	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14511.	1227	100
1065	gi104342 24	Homo sapiens	cDNA FLJ12623 fis, clone NT2RM4001746.	1227	100
1065	gi126527 97	Homo sapiens	clone MGC:5179 IMAGE:2900118, mRNA, complete cds.	1084	90
1066	AAY824 88	Homo sapiens	NISC- Human L-type amino acid transporter 1 protein sequence SEQ ID NO:2.	2438	94
1066	gi592673 2	Homo sapiens	mRNA for L-type amino acid transporter 1, complete cds.	2438	94
1066	gi442664 0	Homo sapiens	L-type amino acid transporter subunit LAT1 mRNA, complete cds.	2438	94
1067	AAG813 26	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:170.	1135	100
1067	gi140359 60	Homo sapiens	unnamed protein product	1135	100
1067	AAY788 05	Homo sapiens	PROT- Hydrophobic domain containing protein clone HP10508 protein sequence.	1053	99
1068	gi120529 83	Homo sapiens		2502	63

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			complete cds.		
1068	AAM797 60	Homo sapiens	HYSE- Human protein SEQ ID NO 3406.	2270	61
1068	AAB943 88	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14947.	2050	57
1069	gi126550 91	Homo sapiens	AD-003 protein, clone MGC:783 IMAGE:3050940, mRNA, complete cds.	546	53
1069	gi652379	Homo sapiens	adrenal gland protein AD-003 mRNA, complete cds.	536	53
1069	AAM518 24	Homo sapiens	BIOW- Human transcription regulator 13.	370	61
1070	gi143280 09	Homo sapiens	clone IMAGE:3942111, mRNA, partial cds.	2392	100
1070	gi145858 69	Homo sapiens	hypothetical protein SB146	2389	99
1070	gi160417 67	Homo sapiens	Similar to NADPH oxidase- related, C2 domain-containing protein, clone MGC:23187 IMAGE:4851468, mRNA, complete cds.	2384	99
1071	ABB1224 5	Homo sapiens	HYSE- Human CKSR-2 homologue, SEQ ID NO:2615.	256	50
1071	AAZ8823 9_aa1	Homo sapiens	INCY- Human cytokine signal regulator CKSR-2 encoding cDNA SEQ ID NO:4.	245	51
1071	AAB676 67	Homo sapiens	INCY- Amino acid sequence of human cytokine signal regulator 2.	245	51
1072	gi154189 97	Homo sapiens	capillary morphogenesis protein- 1 mRNA, complete cds.	3015	100
1072	AAB955 05	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18062.	2163	99
1072	gi104357 18	Homo sapiens	cDNA FLJ13645 fis, clone PLACE1011310, weakly similar to MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.	2163	99
1073	gi159850 82	Homo sapiens	unnamed protein product	3158	99
1073	AAU049 58	Homo sapiens	GETH Human Interleukin 17 receptor, IL-17RH4.	3148	97
1073	gi645355 2	Homo sapiens	mRNA; cDNA DKFZp434N1928 (from clone DKFZp434N1928).	3007	100
1074	AAB938 27	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13641.	884	99
1074	AAB236 06	Homo sapiens	ALPH- Human secreted protein SEQ ID NO: 12.	884	99
1074	gi104331 26	Homo sapiens	cDNA FLJ11790 fis, clone HEMBA1006091.	884	99
1075	gi157779 31	Homo sapiens	DGCRK3 gene for G-protein beta subunit like protein, complete cds.	1731	99
1075	gi150823 09	Homo sapiens	clone MGC:19898 IMAGE:4548339, mRNA, complete cds.	1731	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1075	gi133591 65		mRNA for KIAA1645 protein, partial cds.	1731	99
1076	gi166059 05	<u> </u>	unnamed protein product	100	32
1076	gi116111 88	Homo sapiens	Human DNA sequence from clone RP4-688G8 on chromosome 20q11.2-12. Contains the gene for a novel protein similar to ribosomal	94	32
			protein S2 (RPS2), a gene encoding a protein similar to basic protease inhibitor chelonianin, a novel gene, the 3' end of a novel gene, ESTs, STSs, GSSs and a CpG island, complete sequence.		
1076	AAY359 35	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 184.	83	29
1077	gi165542 29	Homo sapiens	cDNA FLJ25436 fis, clone TST08261.	1164	100
1077	gi150824 26	Homo sapiens	Similar to RIKEN cDNA 2810055F11 gene, clone MGC:20203 IMAGE:4684687, mRNA, complete cds.	1156	99
1077	gi128581 55	Mus musculus	putative	1054	89
1078	gi155592 90	Homo sapiens	clone MGC:20275 IMAGE:3842589, mRNA, complete cds.	1917	100
1078	gi156255 64	Homo sapiens	WD40- and FYVE-domain containing protein 2 (WDF2) mRNA, complete cds.	1893	99
1078	gi165542 04	Homo sapiens	cDNA FLJ25420 fis, clone TST03665.	1380	100
1079	AAB927 75	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11256.	3212	99
1079	gi140421 69	Homo sapiens	cDNA FLJ14564 fis, clone NT2RM4000229, weakly similar to Gallus gallus actin filament- associated protein (AFAP-110) mRNA.	3212	99
1079	gi156208 87	Homo sapiens	mRNA for KIAA1914 protein, partial cds.	1702	100
1080	AAG891 72	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 292.	591	100
1080	AAY125 32	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO: 197 from WO 9906553.	512	91
1080	AAB871 73	Homo sapiens	MILL- Human secreted protein TANGO 402 S22T variant, SEQ ID NO:215.	119	44
1081	gi996380 4	Homo sapiens	zinc finger protein ZNF286 (ZNF286) mRNA, complete cds.	574	94
1081	gi140179 65	Homo sapiens	mRNA for KIAA1874 protein, partial cds.	517	91
1081	AAU162 38	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1191.	362	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1082	AAG038 10	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7891.	841	99
1082	gi186800	Homo sapiens	Human ribosomal protein L12 mRNA, complete cds.	841	99
1082	gi141983 33	Homo sapiens	ribosomal protein L12, clone MGC:9760 IMAGE:3855674, mRNA, complete cds.	841	99
1083	AAY129 02	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:492.	134	100
1084	gi186774	Homo sapiens	Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.	3082	57
1084	gi273935	Homo sapiens	DNA from chromosome 19, BAC 33152, complete sequence.	2985	55
1084	AAM797 39	Homo sapiens	HYSE- Human protein SEQ ID NO 3385.	2612	53
1085	AAV481 25_aa1	Homo sapiens	HUMA- Nucleotide sequence encoding clone HMWGS46 of Prohibitin receptor family.	1354	93
1085	ABB1191 3	Homo sapiens	HYSE- Human B-cell receptor associated protein homologue, SEQ ID NO:2283.	1354	93
1085	AAY944 43	Homo sapiens	UNII Human repressor of estrogen repressor activity (REA) protein.	1354	93
1086	AAG723 70	Homo sapiens	YEDA Human OR-like polypeptide query sequence, SEQ ID NO: 2051.	333	100
1086	AAG714 53	Homo sapiens	YEDA Human olfactory receptor polypeptide, SEQ ID NO: 1134.	333	100
1086	AAE0455 6	Homo sapiens	INCY- Human G-protein coupled receptor-12 (GCREC- 12) protein.	315	100
1087	AAG813 23	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:164.	792	100
1087	gi140359 54	Homo sapiens	unnamed protein product	792	100
1087	gi128387 99	Mus musculus	putative	564	76
1088	AAE0969 1	Homo sapiens	HUMA- Human gene 2 encoding novel protein HCOKA10, SEQ ID NO:38.	96	55
1088	AAG761 25	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:6889.	96	55
1088	AAU169 44	Homo sapiens	HUMA- Human novel secreted protein, SEQ ID 185.	96	55
1089	AAY130 37	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 51.	187	100
1089	AAY363 95	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 5.	79	39
1089	gi130968 04	Mus musculus	Unknown (protein for IMAGE:3586067)	77	40
1090	gi151478	Mus musculus	Spred-2	2098	92

SEQ	Hit ID	Speicies	Description		
ID			Description	S score	Percent identity
1090	77	1			
L	75		Spred-1	1101	52
1090	AAU174	Homo sapiens	HUMA- Novel signal	1029	98
ĺ	15	· I	transduction pathway protein,	1	
1091	1 0:165517		Seq ID 980.		
1091	gi165517 62	Homo sapiens	cDNA FLJ31812 fis, clone	804	97
1	02	1	NT2RI2009406, moderately	1	
1		1	similar to Homo sapiens rec mRNA.		}
1091	gi668287	Homo sapiens	rec mRNA, complete cds.	453	55
	3		and the state of t	433	33
1091	gi723061	Rattus	small rec	451	56
1000	2	norvegicus			"
1092	gi122248	Homo sapiens	mRNA; cDNA DKFZp761I1011	241	94
1092	85 gi388056	Comment 1 1111	(from clone DKFZp761I1011).		
10,2	0.00000	Caenorhabditis elegans	Similarity to Yeast E1-E2	135	50
1	"	ciegaiis	ATPase (SW:YED1_YEAST), contains similarity to Pfam		
			domain: PF00122 (E1-E2	1 .	
			ATPase), Score=102.4, E-		
			value=2.7e-28, N=4~cDNA EST		
1			yk5f9.5 comes from this		
			gene~cDNA EST yk10d12.5		1 1
			comes from this gene~cDNA		
			EST yk5f9.3 comes from this		
			gene~cDNA EST yk10d12.3		
		.[comes from this gene~cDNA		1
			EST yk40h11.5 comes from this gene~cDNA EST yk131g11.3		
			comes from this gene~cDNA	j	
		'	EST ykl31g11.5 comes from]	1 1
			this gene~cDNA EST yk133d6.5	l	
			comes from this gene~cDNA		1
			EST yk318f2.3 comes from this		
			gene~cDNA EST yk318f2.5		1 1
			comes from this gene~cDNA		1
	ŀ	}	EST yk122a12.5 comes from		
		1	this gene~cDNA EST yk248h3.5 comes from this gene~cDNA		1 1
			EST yk260b8.5 comes from this		1
			gene~cDNA EST yk286h5.5		
			comes from this gene~cDNA		1
-			EST yk356g1.5 comes from this]
1000	*******		gene		
1092	gi165166 58	Homo sapiens	ORF for hypothetical protein.	129	52
1093	AAB409	Homo sapiens	CURA- Human ORFX ORF760	349	40
	96	•	polypeptide sequence SEQ ID	545	40
1005			NO:1520.		
1093	gi165166 58	Homo sapiens	ORF for hypothetical protein.	349	40
1093	gi104369 63	Homo sapiens	cDNA: FLJ20986 fis, clone	349	40
1094	gi169042	Homo sapiens	CAE01156.		
	08	rionio sapiens	very large G protein-coupled	1014	96
ł			receptor 1b (VLGR1) mRNA, complete cds.		
1094	gi169042	Mus musculus	very large G protein-coupled	808	78
			y a p. c.om vouprod	000	

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
11/	10		receptor 1		
1094	gi120444 71	Homo sapiens	mRNA; cDNA DKFZp761P0710 (from clone DKFZp761P0710); complete cds.	173	27
1095	gi124839 02	Rattus norvegicus	zinc finger protein HIT-10	1545	47
1095	AAB958 62	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18929.	1234	50
1095	gi104367 89	Homo sapiens	cDNA FLJ14345 fis, clone THYRO1001189, weakly similar to ZINC FINGER PROTEIN 91.	1234	50
1096	AAB509 63	Homo sapiens	GETH Human PRO1286 protein.	466	100
1096	AAU124 21	Homo sapiens	GETH Human PRO1286 polypeptide sequence.	466	100
1096	AAU091 79	Homo sapiens	GETH Human PRO1268 polypeptide.	466	100
1097	AAE1202 3	Homo sapiens	INCY- Human G-protein coupled receptor, GCREC-2.	2849	98
1097	AAG681 26	Homo sapiens	FARB Human 7TM-GPCR protein sequence SEQ ID NO:6.	2824	98
1097	gi 175125 39	Mus musculus	Unknown (protein for MGC:29266)	2183	73
1098	AAB941 08	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14340.	273	100
1098	AAU045 58	Homo sapiens	GETH Human Stra6 homologue, PRO19578.	273	100
1098	AAU045 57	Homo sapiens	GETH Human Stra6 homologue, PRO10282.	273	100
1099	AAU123 82	Homo sapiens	GETH Human PRO792 polypeptide sequence.	137	32
1099	AAB244 16	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:155.	137	32
1099	AAB240 55	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:31.	137	32
1100	gi633042 2	Homo sapiens	mRNA for KIAA1202 protein, partial cds.	4913	99
1100	gi123140 62	Homo sapiens	Human DNA sequence from clone RP11-119E20 on chromosome Xp11.21-11.23 Contains part of the gene for KIAA1202 protein, ESTs, STSs and GSSs, complete sequence.	4696	99
1100	gi154212 01	Homo sapiens	SHAP-A (SHAP) mRNA, partial cds, alternatively spliced.	3845	99
1101	gi 108346 07	Homo sapiens	cadherin 20 (CDH20) mRNA, complete cds.	4170	99
1101	gi410175	Mus musculus	cadherin 7 precursor	4032	96
1101	gi854635	Xenopus laevis	F-cadherin	3251	78
1102	AAY363 10	Homo sapiens	HUMA- Human secreted protein encoded by gene 87.	250	100
1103	gi165514 23	Homo sapiens	cDNA FLJ31547 fis, clone NT2RI2001010, weakly similar to FATTY ACYL-COA	853	98

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1100			HYDROLASE PRECURSOR, MEDIUM CHAIN (EC 3.1.2.14).		
1103	gi264198 6	auratus	carboxylesterase precursor	438	50
1103	AAD006 80_aa1		INCY- Human Hydrolase protein-5 (HYDRL-5) encoding cDNA.	428	52
1104	AAE0483 6		SUGE- Human SGP018 phosphatase polypeptide.	4915	95
1104	gi127188 35	Homo sapiens	unknown mRNA.	3350	99
1104	AAB409 19	Homo sapiens	CURA- Human ORFX ORF683 polypeptide sequence SEQ ID NO:1366.	718	79
1105	gi134926 50	Rattus norvegicus	potassium channel beta subunit KChIP4	1284	99
1105	gi115273 18	Mus musculus	calsenilin-like protein	1281	99
1105	gi140913 36	Homo sapiens	KCHIP4.1 (KCNIP4) mRNA, complete cds, alternatively spliced.	1278	99
1106	AAY131 26	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 140.	160	96
1107	gi412659 3	Cyprinus carpio	complement C3-S	156	29
1107	gi412658 9	Cyprinus carpio	complement C3-H1	148	26
1107	gi305335	Cavia porcellus	complement C3 protein (GPC3) precursor	146	50
1108	gi112448 73	Homo sapiens	PR-domain-containing protein 16 (PRDM16) mRNA, complete cds.	6646	99
1108	gi126978 95	Homo sapiens	mRNA for KIAA1675 protein, partial cds.	3570	99
1108	gi545408	human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]. [Homo sapiens	AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation}	3181	53
1109	gi107328 15	Homo sapiens	concentrative Na+-nucleoside cotransporter hCNT3 (CNT3) mRNA, complete cds.	3609	100
1109	gi107328 17	Mus musculus	concentrative Na+-nucleoside cotransporter mCNT3	2872	78
1109	gi154893 79	Mus musculus	solute carrier family 28 (sodium- coupled nucleoside transporter), member 3	2859	77
1110	gi178651 50	Plasmodium berghei	cysteine repeat modular protein 3 PbCRM3	97	30
1110	gi665071 1	Giardia intestinalis	variant-specific surface protein VSP1267-2	96	29
110	gi861294	Caenorhabditis elegans	F35D2.4 gene product	94	31
111	gi795917 7	Homo sapiens	mRNA for KIAA1458 protein, partial cds.	2993	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1111	AAB947 91	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15907.	1037	100
1111	AAU011 01	Homo sapiens	HUMA- Gene 38 Human secreted protein homologous amino acid sequence.	842	99
1112	gi173907 60	Mus musculus	RIKEN cDNA 2610205H19 gene	664	99
1112	gi128482 92	Mus musculus	putative	664	99
1112	gi203072	Rattus sp.	0-44 protein	661	98
1113	gi142503 19	Homo sapiens	clone IMAGE:3448367, mRNA, partial cds.	2143	93
1113	gi145827 73	Homo sapiens	sumo/sentrin-specific protease	2138	93
1113	gi170260 32	Macaca fascicularis	hypothetical protein	2068	89
1114	AAB937 77	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13502.	1064	99
1114	AAM413 87	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6318.	1064	99
1114	AAM396 01	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2746.	1064	99
1115	gi152772 40	Homo sapiens	genomic DNA, chromosome 6p21.3, HLA Class I region, section 17/20.	2256	100
1115	gi118754 05	Homo sapiens	HZFw1 protein mRNA, complete cds.	2251	99
1115	gi118754 07	Homo sapiens	HZFw2 protein mRNA, complete cds.	1733	99
1116	AAB957 26	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18602.	1644	99
1116	AAB951 09	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17089.	1644	99
1116	gi140420 78	Homo sapiens	cDNA FLJ14510 fis, clone NT2RM1000623, weakly similar to RIBONUCLEASE INHIBITOR.	1644	99
1117	gi140093 46	Homo sapiens	nGAP-like protein (AF9q34) mRNA, complete cds.	5475	98
1117	gi152775 25	Rattus norvegicus	DOC2/DAB2 interactive protein	5006	96
1117	gi126980 31	Homo sapiens	mRNA for KIAA 1743 protein, partial cds.	3024	98
1118	AAB652 11	Homo sapiens	GETH Human PRO1152 (UNQ582) protein sequence SEQ ID NO:216.	1937	99
1118	AAB688 83	Homo sapiens	INCY- Human RECAP polypeptide, SEQ ID NO: 13.	1937	99
1118	AAU281 83	Homo sapiens	HYSE- Novel human secretory protein, Seq ID No 352.	1937	99
1119	AAG021 97	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6278.	522	99
1119	AAU172 24	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 789.	485	100
1119	AAU175 97	Homo sapiens	HUMA- Novel signal transduction pathway protein,	449	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			Seq ID 1162.		Identity
1120	gi179636		cytoplasmic phosphotyrosyl protein phosphatase (clone type 1) complete cds.	717	88
1120	gi114781 2	Homo sapiens	Human red cell-type low molecular weight acid phosphatase (ACP1) gene, exon 6 and 7, complete cds.	717	88
1120	gi575913 1	Rattus norvegicus	low molecular weight protein tyrosine phosphatase isoform A	647	76
1121	gi767046 6	Mus musculus	unnamed protein product	255	61
1121	gi341381 0	Mus musculus	Bassoon	105	25
1121	gi50715	Mus musculus	myosin heavy chain	103	26
1122	gi104403 35	Homo sapiens	cDNA: FLJ23594 fis, clone LNG14867.	1513	100
1122	gi146028 89	Homo sapiens	clone MGC:13119 IMAGE:4100726, mRNA, complete cds.	702	53
1122	gi142498 27	Homo sapiens	clone MGC:10992 IMAGE:3637387, mRNA, complete cds.	702	53
1123	ABB1120 0	Homo sapiens	HYSE- Human Kupffer cell receptor homologue, SEQ ID NO:1570.	1838	99
1123	gi154890 66	Mus musculus	Kupffer cell c-type lectin receptor	1000	45
1123	gi166936 0	Mus musculus	Kupffer cell receptor	1000	45
1124	AAY308 47	Homo sapiens	HUMA- Human secreted protein encoded from gene 37.	239	100
1124	gi145960 27	Arabidopsis thaliana	Unknown protein	70	45
1124	gi975895 7	Arabidopsis thaliana	contains similarity to unknown protein~gb AAF64546.1~gene_i d:MRB17.15	70	45
1125	AAY013 90	Homo sapiens	HUMA- Secreted protein encoded by gene 8 clone HTXDJ88.	301	100
1125	gi156399 42	Treponema pallidum] > [Treponema pallidum	dicarboxylate transporter (dctM)	63	38
1126	AAG681 89	Homo sapiens	GENO- Cytosolic thyroid hormone-binding protein SEQ ID NO:105.	152	78
1126	gi35505	Homo sapiens	H.sapiens M gene for M1-type and M2-type pyruvate kinase.	152	78
1126	gi338827	Homo sapiens	Human TCB gene encoding cytosolic thyroid hormone-binding protein, complete cds.	152	78
	gi426168 9	Homo sapiens	complement factor B mRNA, complete cds.	3976	97
	gi297569	Homo sapiens	H.sapiens mRNA for complement factor B.	3976	97
127	AAX041	Homo sapiens	UNIW Human Factor B	3972	97

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	25 aa1		encoding cDNA.		
1128	AAB500 12	Homo sapiens	PHAA Wild-type human alpha7 ligand gated ion channel.	1794	100
1128	AAB826 90	Homo sapiens	TEWE- Nicotinic acetylcholine receptor alpha7.	1794	100
1128	AAB240 88	Homo sapiens	GETH Human PRO2145 protein sequence SEQ ID NO:77.	1794	100
1129	gi537329	Homo sapiens	Human (clone pHAIV2-12) alpha-2 collagen type IV (COL4A2) mRNA, 3' end.	3756	99
1129	gi102232 3	Mus musculus	collagen alpha-2(IV) chain	3480	87
1129	gi556299	Mus musculus	alpha-2 type IV collagen	3477	87
1130	gi150114 89	Tetrahymena thermophila	heme maturase	68	29
1131	AAB509 64	Homo sapiens	GETH Human PRO1313 protein.	926	100
1131	AAB472 90	Homo sapiens	GETH PRO1313 polypeptide.	926	100
1131	AAB244 31	Homo sapiens	GETH Human PRO1313 protein sequence SEQ ID NO:216.	926	100
1132	gi128553 07	Mus musculus	putative	2919	89
1132	gi155595 25	Homo sapiens	Similar to RIKEN cDNA 4932416D09 gene, clone IMAGE:4578228, mRNA, partial cds.	2523	99
1132	AAY540 52	Homo sapiens	PHAA An angiogenesis- associated protein which binds plasminogen.	1435	62
1133	AAY130 84	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 98.	127	62
1133	gi104404 68	Homo sapiens	mRNA for FLJ00070 protein, partial cds.	75	41
1133	gi455864 0	Homo sapiens	chromosome 19, cosmid R27516, complete sequence.	74	44
1134	AAM802 75	Homo sapiens	HYSE- Human protein SEQ ID NO 3921.	1510	99
1134	91	Homo sapiens	HYSE- Human protein SEQ ID NO 1953.	1500	99
1134	gi168774 49	Homo sapiens	hypothetical protein MGC20781, clone MGC:21670 IMAGE:3885455, mRNA, complete cds.	1367	100
1135	gi771086 9	Homo sapiens	Human DNA sequence from clone RP11-31M2 on chromosome 9p23-24.3. Contains (part of) the gene for a novel protein similar to the GLI family of zinc finger proteins, STSs, GSSs and two putative CpG islands, complete sequence.	1629	100
1135	AAM254 73	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:988.	861	98
1135	gi144860 69	Drosophila melanogaster	Zn finger transcription factor lame duck	699	63

SEC	Hit ID	Speicles	Description	S score	Percent
ID				S score	identity
1136	62		DANA- Laminin -binding protein encoded by insert from J9 lambda gt10 phage.	1327	94
1136			Human colin carcinoma laminin- binding protein mRNA, complete cds.	1327	94
1136	02		laminin receptor 1 (67kD, ribosomal protein SA), clone MGC:17122 IMAGE:3446816, mRNA, complete cds.	1327	94
1137	84	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1329.	734	98
1137	gi179281	Homo sapiens	ATP synthase beta subunit precursor (ATPSB) gene, complete cds.	734	98
1137	gi167413 73	Homo sapiens	Similar to ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:5231 IMAGE:2900336, mRNA, complete cds.	734	98
1138	AAG014 68	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5549.	282	98
1138	AAG014 67	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5548.	206	100
1138	AAB438 84	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1329.	206	100
1139	gi179279	Homo sapiens	Human ATP synthase beta subunit gene, exons 8-10.	757	69
1139	gi128456 67	Mus musculus	putative	744	68
1139	gi28940	Homo sapiens	Human mRNA for F1-ATPase beta subunit (F-1 beta).	742	69
1140	AAB438 84	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1329.	1124	89
1140	gi179281	Homo sapiens	ATP synthase beta subunit precursor (ATPSB) gene, complete cds.	1124	89
1140	gi167413 73	Homo sapiens	Similar to ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:5231 IMAGE:2900336, mRNA, complete cds.	1124	89
1141	AAW540 79	Homo sapiens	TEXA Homo sapiens BARD1 sequence.	4101	100
1141	gi171017 5	Homo sapiens	Human BRCA1-associated RING domain protein (BARD1) mRNA, complete cds.	4101	100
1141	AAW540 81	Homo sapiens	TEXA Homo sapiens BARD1 P553 sequence.	4097	99
1142	AAW540 89	Homo sapiens	TEXA Homo sapiens BARD1 MR658C sequence.	394	100
1142	AAW540 88	Homo sapiens	CONTRACT CONTRACTOR	394	100
1142	AAW540	Homo sapiens	TEXA Homo sapiens BARD1	394	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	87		MQ564H sequence.		
1143	gi174322 41	Homo sapiens	MSTP027 (MST027) mRNA, complete cds.	730	100
1143	gi160416 88	Homo sapiens	hypothetical protein FLJ21661, clone MGC:16816 IMAGE:3922036, mRNA, complete cds.	730	100
1143	gi140398 31	Homo sapiens	elongation factor G2 (EFG2) mRNA, complete cds; nuclear gene for mitochondrial product.	730	100
1144	AAM407 29	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5660.	271	98
1144	AAM389 43	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2088.	271	98
1144	AAY123 25	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:356.	271	98
1145	gi173903 20	Homo sapiens	clone MGC:9678 IMAGE:3846678, mRNA, complete cds.	872	100
1145	gi120020 02	Homo sapiens	clone 022f05 My030 protein mRNA, complete cds.	872	100
1145	AAY360 68	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 453.	844	97
1146	gi173903 20	Homo sapiens	clone MGC:9678 IMAGE:3846678, mRNA, complete cds.	504	95
1146	gi120020 02	Homo sapiens	clone 022f05 My030 protein mRNA, complete cds.	504	95
1146	AAY360 68	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 453.	495	94
1147	AAB616 17	Homo sapiens	PROT- Human protein HP10688.	1488	100
1147	gi125784	Homo sapiens	unnamed protein product	1488	100
1147	AAY027 81	Homo sapiens	HUMA- Human secreted protein.	1146	77
1148	gi165400 2	Homo sapiens	H.sapiens mRNA for Sop2p-like protein.	572	99
1148	gi128050 63	Mus musculus	actin related protein 2/3 complex, subunit 1A (41 kDa)	567	97
1148	gi126672 58	Rattus norvegicus	suppressor of profilin/p41 of actin-related complex 2/3	567	97
1149	AAB952 58	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17435.	3560	100
1149	gi104347 40	Homo sapiens	cDNA FLJ12957 fis, clone NT2RP2005531, weakly similar to PROTEIN 4.1.	3560	100
1149	gi100471 61	Homo sapiens	mRNA for KIAA1548 protein, partial cds.	2487	100
1150	AAR998 44	Homo sapiens	SUME Human natural killer cell, cell surface mol. NKG7.	552	71
1150	AAQ863 84 aa1	Homo sapiens	ASAN/ G-CSF stimulated human myelocytic cell cDNA.	307	65
1150	AAQ985 51_aa1	Homo sapiens	ASAN/ Granulocyte colony stimulating factor (G-CSF)-	307	65

SEQ ID	Hit ID	Speicies	Description	S score	Percent
			inducible myelocyte gene.		identity
1151	AAM237	Homo sapiens	HYSE- Human EST encoded	620	89
i .	81		protein SEQ ID NO: 1306.	020	0.5
1151	AAM238	Homo sapiens	HYSE- Human EST encoded	481	100
	37		protein SEQ ID NO: 1362.	401	100
1151	AAY647	Homo sapiens	GEST Human 5' EST related	471	98
<u> </u>	47	1	polypeptide SEQ ID NO:908.	1 4/1	1 20
1152	AAB652	Homo sapiens	GETH Human PRO1187	656	100
ļ	77		(UNQ601) protein sequence	050	100
			SEQ ID NO:399.		İ
1152	AAY667	Homo sapiens	GETH Membrane-bound protein	656	100
	54		PRO1187.	050	100
1152	AAB240	Homo sapiens	GETH Human PRO1187 protein	656	100
	77	•	sequence SEQ ID NO:55.	030	100
1153	gi833175	Homo sapiens	X28 region near ALD locus	1747	92
İ	7	•	containing dual specificity	1,4,	32
			phosphatase 9 (DUSP9),		İ
1]		ribosomal protein L18a	1	
Ī	1		(RPL18a), Ca2+/Calmodulin-	ļ	
		İ	dependent protein kinase I		
ļ	1		(CAMKI), creatine transporter	.[
ŀ	1		(CRTR), CDM protein (CDM),		1
	ŀ		adrenoleukodystrophy protein		1
	ł		(ALD), plexin-related protein		1
	ŀ		(PLXB3), muscle-specific serine		
			kinase (MSSK), NAD-isocitrate		ļ
İ	1		dehydrogenase (IDH),	1	
			translocon-associated protein		
	1		delta (TRAP), and LU1 protein		
			(LU1) genes, complete cds; and		1
Ì]		CCp pseudogene, complete		1
11.5			sequence.		1
1153	AAW884	Homo sapiens	INCY- Disease associated	1667	88
11.55	36		protein kinase DAPK-5.		
1153	gi313519	Rattus	Ca2+/calmodulin-dependent	1661	87
	7	norvegicus	protein kinase I beta 2		
1154	AAG675	Homo sapiens	LEXI- Amino acid sequence of a	413	98
4 1 2 1	48		human transporter protein.		
1154	gi165886	Homo sapiens	anion transporter/exchanger-8	413	98
	84		(SLC26A8) mRNA, complete		
11.51			cds.		
1154	gi153415	Homo sapiens	putative anion transporter	413	98
ì	54		(SLC26A8) mRNA, complete		
44.00			cds.		
1155	AAB649	Homo sapiens	ROSE/ Human secreted protein	995	98
1	53		sequence encoded by gene 12		
			SEQ ID NO:131.		
1155	gi128543	Mus musculus	pulative	781	65
	24				
1155	gi152170	Homo sapiens	glioma pathogenesis-related	443	40
İ	75		protein (RTVP1) mRNA,		
			complete cds.		
1156	AAB262	Homo sapiens	UNLO Wild-type human Rac1	508	100
	56		protein.	y -	
1156	gi857403	Homo sapiens	rac1 gene.	508	100
	8	-			
1156	gi232620	Homo sapiens	Rac3 (RAC3) mRNA, complete	508	100
	6		cds.		
			140		

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
157	gi104398 53	Homo sapiens	cDNA: FLJ23235 fis, clone CAS04980.	1536	100
157	AAW855 96	Homo sapiens	MERI Human GABA-A receptor theta subunit.	73	35
157	gi159782 47	Yersinia pestis	putative membrane protein	73	27
1158	gi104398 53	Homo sapiens	cDNA: FLJ23235 fis, clone CAS04980.	1347	90
1158	AAW855 96	Homo sapiens	MERI Human GABA-A receptor theta subunit.	73	35
1158	gi159782 47	Yersinia pestis	putative membrane protein	73	27
1159	gi119331 49	Homo sapiens	mRNA for 6-phosphofructo-2- kinase heart isoform, complete cds.	2452	100
1159	gi309041 9	Homo sapiens	pfkfb2 gene, exons 1 to 15.	2329	99
1159	gi309042	Homo sapiens	mRNA for 6-phosphofructo-2-kinase.	2319 .	98
1160	gi617778 5	Homo sapiens	mRNA for HKR1, partial cds.	3083	99
1160	gi133254 27	Homo sapiens	cione IMAGE:3928207, mRNA, partial cds.	2388	99
1160	gi487783	Homo sapiens	Human zinc finger protein ZNF133.	1592	54
1161	gi145858 59	Homo sapiens	hypothetical protein SB138	1558	98
1161	AAB946 41	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15526.	1543	100
1161	AAG644 03	Homo sapiens	SHAN- Human paneth cell enhanced expression-like protein.	1543	. 100
1162	AAY536 41	Homo sapiens	CHIR A bone marrow secreted protein designated BMS42.	2182	99
1162	gi966315 3	Homo sapiens	partial mRNA for transport- secretion protein 2.2, (TTS-2.2 gene).	2179	98
1162	gi966315	Homo sapiens	partial mRNA for transport- secretion protein 2.1 (TTS-2.1 gene).	2179	98
1163	AAM933 60	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2919.	3300	100
1163	gi168782 06	Homo sapiens	hypothetical protein DKFZp434J037, clone MGC:29812 IMAGE:5088037, mRNA, complete cds.	3300	100
1163	gi120532 81	Homo sapiens	mRNA; cDNA DKFZp434J037 (from clone DKFZp434J037); complete cds.	3300	100
1164	AAG812 82	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:82.	3032	100
1164	AAU171 02	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 667.	3032	100
1164	gi175299 89	Homo sapiens	oxysterol-binding protein-like protein OSBPL9 (OSBPL9) mRNA, complete cds.	3032	100

SEQ ID		Speicies	Description	S score	Percent identity
1165	gi146271 21	Homo sapiens	Human DNA sequence from clone RP5-824F16 on chromosome 20 Contains the 5' end of the ANGPT4 gene for	230	64
			angiopoietin 4, part of the gene for a novel protein similar to mouse thrombospondin type 1 domain protein R-spondin, ESTs, STSs, GSSs and a CpG island, complete sequence.		
1165	gi166053 78	Mus musculus	unnamed protein product	226	42
1165	gi128506 80	Mus musculus	putative	226	42
1166	AAF8417 l_aa1	Homo sapiens	CHUG- Human OATP-B coding sequence.	3573	97
1166	AAZ9240 3_aa1		SCHE cDNA encoding human DC-PGT.	3573	97
1166	AAC618 83_aa1	Homo sapiens	CHIR cDNA encoding a human secreted protein.	3573	97
1167	gi30224	Homo sapiens	H.sapiens CRP mRNA for C-reactive protein.	327	100
1167	gi30213	Homo sapiens	H.sapiens mRNA for C-reactive protein.	327	100
1167	gi181068	Homo sapiens	Human C-reactive protein gene, complete cds.	327	100
1168	AAH761 94_aa1	Homo sapiens	MILL- Human seven- transmembrane protein 31945 coding sequence.	3429	99
1168	AAB857 67	Homo sapiens	MILL- Human seven- transmembrane protein 31945 sequence.	3429	99
1168	gi165519 33	Homo sapiens	cDNA FLJ31951 fis, clone NT2RP7007177, weakly similar to Homo sapiens multiple membrane spanning receptor TRC8 mRNA.	3429	99
1169	AAB602 99	Homo sapiens	MILL- Human aminopeptidase 17867.	5048	99
1169	AAE0487 9	Homo sapiens	INCY- Human protease protein- 6 (PRTS-6).	5048	99
1169	gi110659 00	Homo sapiens	aminopeptidase mRNA, complete cds.	5048	99
1170	gi128441 36	Mus musculus	putative	700	52
	AAA999 05_aa1	Homo sapiens	GETH cDNA encoding human protein PRO846.	662	94
	AAB653 00	Homo sapiens	GETH Human PRO846 protein sequence SEQ ID NO:517.	662	94
	gi126539 43	Homo sapiens	clone MGC:2742 IMAGE:2822914, mRNA, complete cds.	3104	100
	36	Homo sapiens	SEQ ID NO: 5317.	522	94
		Saccharomyces cerevisiae var. diastaticus	glucoamylase	196	22

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1172	gi134304 08	Homo sapiens	BTBD2 protein mRNA, complete cds.	2705	99
1172	gi170260 62	Mus musculus	glucose signal repressing protein	1946	77
1172	gi134304 06	Homo sapiens	BTBD1 protein mRNA, complete cds.	1937	76
1173	gi172261 21	Homo sapiens	F-box protein (FBG4) mRNA, complete cds.	1503	100
1173	gi165539 18	Homo sapiens	cDNA FLJ25205 fis, clone REC05844, highly similar to Mus musculus F-box protein FBX17 mRNA.	1503	100
1173	gi152145 27	Homo sapiens	Similar to f-box only protein 17, clone MGC:9379 IMAGE:3864760, mRNA, complete cds.	1503	100
1174	AAB883 73	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0109.	2158	100
1174	AAB932 15	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12194.	2158	100
1174	AAB931 42	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12045.	2158	100
1175	AAB883 73	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0109.	3646	95
1175	AAB932 15	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12194.	3646	95
1175	gi140425 71	Homo sapiens	cDNA FLJ14791 fis, clone NT2RP4001064, weakly similar to SYNAPTONEMAL COMPLEX PROTEIN SC65.	3646	95
1176	AAB363 92	Homo sapiens	CHUG- Human tumour suppressor Gros 1-S protein SEQ ID NO:4.	3861	99
1176	gil11276 38	Homo sapiens	GROS1-L protein mRNA, complete cds.	3861	99
1176	AAB883 73	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0109.	3847	99
1177	gi104385	Homo sapiens	cDNA: FLJ22233 fis, clone HRC02016.	2015	100
1177	AAE0489 2	Homo sapiens	INCY- Human transporter and ion channel-5 (TRICH-5) protein.	2009	99
1177	gi139256 61	Mus musculus	sodium/calcium exchanger protein	1708	84
1178	AAB651 92	Homo sapiens	GETH Human PRO839 (UNQ472) protein sequence SEQ ID NO:167.	366	100
1178	AAG814 32	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:382.	366	100
1178	AAY666 69	Homo sapiens	GETH Membrane-bound protein PRO839.	366	100
1179	gi599683	Bos taurus	Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit	4034	98

SEQ	Hit ID	Speicies	Description	S score	Percent
1179	gi154890 17	Mus musculus	cleavage and polyadenylation specific factor 2, 100kD subunit	3993	identity 97
1179	gi233103 6	Mus musculus	cleavage and polyadenylation specificity factor	3993	97
1180	AAZ3464 8_aa1		ZYMO Human growth factor zalpha5 cDNA.	2182	91
1180	AAZ4585 2_aa1		COMP- Human liver angiopoietin-like growth factor DNA sequence.	2182	91
1180	AAA497 16_aa1	Homo sapiens	GETH Human PRO179 cDNA clone DNA16451-1078.	2182	91
1181	AAH231 83_aa1	Homo sapiens	ISIS- Human macrophage migration inhibitory factor encoding DNA.	564	94
1181	AAB603 25	Homo sapiens	KIRI Human wild-type glycosylation-inhibiting factor (GIF).	564	94
1181	AAB853 43	Homo sapiens	ISIS- Human macrophage migration inhibitory factor.	564	94
1182	gi726393 8	Homo sapiens	mRNA for sodium-glucose cotransporter (SGLT2 gene).	3408	100
	gi567946 4	Homo sapiens	Human DNA sequence from clone RP1-90G24 on chromosome 22 Contains the RFPL2 gene for RET finger protein-like 2, a Immunoglobulin Lambda Light Chain C region (IGLC) pseudogene, the gene for SAAT1 (low affinity sodium glucosecotransporter (sodium:solute symporter family)) and a Cleavage and Polyadenylation Specific Factor CPSF 160 kD subunit pseudogene. Contains ESTs, GSSs and three putative CpG islands, complete sequence.	3408	100
1182	AAY312 21	Homo sapiens	KOEP/ Human SAAT1 protein.	3390	99
1183	gi136233 01	Homo sapiens	Similar to Zink transporter 2, clone MGC:11303 IMAGE:3948165, mRNA, complete cds.	1659	100
1183	gi125637 8	Rattus norvegicus	zinc transporter ZnT-2	1186	67
1183	gi176337 4	Mus musculus	ZnT-3	721	44
1184	AAB926 36	Homo sapiens	HELI- Human protein sequence SEQ ID NO:10951.	1480	81
1184	gi702218 5	Homo sapiens	cDNA FLJ10260 fis, clone HEMBB1000973, moderately similar to Mus musculus schlafen3 mRNA.	1480	81
1184	AAM403 57	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3502.	1479	81
1185	AAB953 51	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17641.	3148	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
185	gi104350 75	Homo sapiens	cDNA FLJ13170 fis, clone NT2RP3003809, weakly similar	3148	99
1185	gi126543	Homo sapiens	to SAV PROTEIN. clone MGC:5347 IMAGE:2985725, mRNA,	3106	99
			complete cds.		100
1186	gi105675 90	Homo sapiens	sodium bicarbonate cotransporter-like protein mRNA, partial cds.	5645	100
1186	gi134477 47	Homo sapiens	sodium bicarbonate cotransporter NBC4a (NBC4) mRNA, complete cds.	5486	99
1186	gi154195 75	Homo sapiens	sodium bicarbonate cotransporter NBC4c (NBC4) mRNA, complete cds, alternatively spliced.	5382	98
1187	gi101858 24	Homo sapiens	SEBOX (SEBOX) gene, complete cds.	1209	100
1187	gi100921 60	Mus musculus	SEBOX	581	63
1187	gi101858 26	Rattus norvegicus	SEBOX	565	63
1188	AAM435 40	Homo sapiens	HUMA- Human polypeptide SEQ ID NO 218.	246	94
1188	AAM404 68	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5399.	246	94
1188	AAM386 82	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 1827.	246	94
1189	gi104381 35	Homo sapiens	cDNA: FLJ21924 fis, clone HEP04086.	3703	99
1189	AAM680 38	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28344.	700	100
1189	AAM556 56	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 27761.	700	100
1190	gi143885	Macaca fascicularis	hypothetical protein	1240	96
1190	AAG932 58	Homo sapiens	NISC- Human protein HP10582.	979	100
1190	gi128548 23	Mus musculus	putative	882	72
1191	AAB945 45	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15296.	2344	99
1191	gi104352 28	Homo sapiens	cDNA FLJ13273 fis, clone OVARC1001010.	2344	99
1191	gi128604 75	Mus musculus	putative	1811	83
1192	gi104404 42	Homo sapiens	mRNA for FLJ00057 protein, partial cds.	3033	99
1192	gi120823 03	Mus musculus	DNA helicase B	1697	61
1192	gi263521	Bacillus subtilis	similar to conjugation transfer protein	114	22
1193	AAE1044 5	Homo sapiens	BIOJ Human transmembrane protein (TMP).	2286	100
1193	AAY862	Homo sapiens	HUMA- Human secreted protein	1889	85

SEC ID		Speicies	Description	S score	1 10
1193				5 50010	Percent identity
1193	30		HKFBC53, SEQ ID NO:145.		
1104	02		HUMA- Fragment of human secreted protein encoded by gene 69.	798	96
1194	29	•	hypothetical protein FLJ12598, clone MGC:31807 IMAGE:4552964, mRNA, complete cds.	1180	100
1194	62	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14456.	1173	99
1194	83	Homo sapiens	cDNA FLJ12598 fis, clone NT2RM4001384.	1173	99
1195	gi724306 9	Homo sapiens	mRNA for KIAA1344 protein, partial cds.	4137	100
1195	AAB940 73	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14262.	1839	99
1195	gi104340 25	Homo sapiens	cDNA FLJ12501 fis, clone NT2RM2001681.	1839	99
1196	AAB088 94	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 4 SEQ ID NO:51.	235	67
1196	gi335913	Vesicular stomatitis virus	glycoprotein	71	30
1196	gi296009 3	Mycobacterium tuberculosis H37Rv	hypothetical protein Rv3669	71	30
1197	AAM943 12	Homo sapiens	HUMA- Human reproductive system related antigen SEQ ID NO: 2970.	1211	98
1197	gi843939 6	HERV-H/env62	envelope protein	763	36
1197	gi495938 2	Homo sapiens	human endogenous retrovirus HERV-H19 pol protein (pol) gene, partial cds; env protein (env) gene, complete cds; and 3' LTR, complete sequence.	757	36
1198	gi140173 81	Homo sapiens	tumor endothelial marker 8 precursor (TEM8) mRNA, complete cds.	1512	100
1198	gi104379 39	Homo sapiens	cDNA: FLJ21776 fis, clone HEP00171.	1512	100
1198	gi159875 05	Mus musculus	tumor endothelial marker 8 precursor	1484	97
1199	AAB652 70	Homo sapiens	GETH Human PRO1158 (UNQ588) protein sequence SEQ ID NO:375.	609	100
1199	AAB875 59	Homo sapiens	GETH Human PRO1158.	609	100
199	AAY667 47	Homo sapiens	GETH Membrane-bound protein PRO1158.	609	100
200	AAM413 80	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6311.	844	87
200	AAY017 85	Homo sapiens	INCY- Human ubiquitin- conjugating enzyme HUBI-1.	818	87
200	41	Homo sapiens	PROS- Human NCE-2 protein.	818	87
201	AAW748	Homo sapiens	HUMA- Human secreted protein	197	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	99		encoded by gene 172 clone HODCW06.		
1201	gi137944 93	Guillardia theta	hypothetical protein	67	36
1202	AAS0794 0_aa1	Homo sapiens	AREN- Human cDNA encoding G-protein coupled receptor, hRUP13.	2087	92
1202	AAS1258 3_aa1	Homo sapiens	FARB DNA encoding human serotonin-like G protein-coupled receptor (5-HT-GPCR).	2087	92
1202	AAD195 79_aa1	Homo sapiens	INCY- Human G-protein coupled receptor, GCREC-3 cDNA.	2087	92
1203	AAS0794 0_aa1	Homo sapiens	AREN- Human cDNA encoding G-protein coupled receptor, hRUP13.	2318	100
1203	AAS1258 3_aa1	Homo sapiens	FARB DNA encoding human serotonin-like G protein-coupled receptor (5-HT-GPCR).	2318	100
1203	AAD195 79_aa1	Homo sapiens	INCY- Human G-protein coupled receptor, GCREC-3 cDNA.	2318	100
1204	AAM936 12	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3436.	3475	100
1204	gi140431 11	Homo sapiens	Similar to ubiquitin associated and SH3 domain containing, A, clone MGC:15437 IMAGE:2958242, mRNA, complete cds.	3412	100
1204	gi163041 76	Homo sapiens	nm23-phosphorylated unknown substrate mRNA, complete cds.	2759	100
1205	AAB014 24	Homo sapiens	MILL- Human TANGO 213.	1264	100
1205	AAM257 35	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1250.	1066	100
1205	AAY762 67	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 11.	1066	100
1206	AAW749 39	Homo sapiens	HUMA- Human secreted protein encoded by gene 49 clone HAGBI17.	211	100
1207	gi151265 59	Mus musculus	Similar to Cd63 antigen	504	99
1207	gi141980 88	Mus musculus	Cd63 antigen	504	99
1207	gi541060 5	Mus musculus	tetraspanin membrane protein CD63	504	99
1208	AAB951 48	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17173.	3590	99
1208	gi119905 93	Homo sapiens	organic anion transporter polypeptide-related protein 4 (OATPRP4) mRNA, complete cds.	3515	99
1208	AAB491 47	Homo sapiens	BRIM Human organic anion transport protein RP4 protein.	3503	99
1209	AAB733 81	Homo sapiens	NANF- Human gas vesicle protein homologue hGvpT-b.	1866	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent
1209	gi120055 09	Homo sapiens	HT025 mRNA, complete cds.	1866	identity 100
1209	gi104402 36	Homo sapiens	cDNA: FLJ23518 fis, clone LNG04878.	1600	100
1210	gi120530 21	Homo sapiens	mRNA; cDNA DKFZp434L0714 (from clone DKFZp434L0714); complete cds.	4230	99
1210	AAG643 76	Homo sapiens	BIOD- Human II aminoacyl- tRNA synthetase 75.	3517	99
1210	gi104399 91	Homo sapiens	cDNA: FLJ23339 fis, clone HEP13401.	3010	99
1211	AAB589 41	Homo sapiens	HUMA- Breast and ovarian cancer associated antigen protein sequence SEQ ID 649.	1188	99
1211	gi120059 18	Homo sapiens	CDA016 mRNA, complete cds.	1176	98
1211	AAB366 15	Homo sapiens	INCY- Human FLEXHT-37 protein sequence SEQ ID NO:37.	862	98
1212	gi104371 94	Homo sapiens	cDNA: FLJ21148 fis, clone CAS09413.	2238	96
1212	gi128456 48	Mus musculus	putative	1808	80
1212	gi122603 3	Saccharomyces cerevisiae	unknown	259	25
1213	gi104371 94	Homo sapiens	cDNA: FLJ21148 fis, clone CAS09413.	2203	91
1213	gi128456 48	Mus musculus	putative	1774	76
1213	gi122603 3	Saccharomyces cerevisiae	unknown	249	25
1214	gi663099 2	Danio rerio	NCC receptor protein 1	418	42
1214	gi127116 29	Oreochromis niloticus	nonspecific cytotoxic cell receptor protein	389	41
1214	gi663099 8	Ictalurus punctatus	NCC receptor protein 1	361	40
1215	AAC843 82_aa1	Homo sapiens	MILL- Human TANGO 209 polypeptide coding sequence.	2430	100
1215	AAS1457 6_aa1	Homo sapiens	ELIL Human cDNA encoding cysteine-rich secreted protein hCRSP1.	2430	100
1215	AAB481 07	Homo sapiens	MILL- Human TANGO 209 polypeptide.	2430	100
1216	ABB1188 0	Homo sapiens	HYSE- Human lipocortin homologue, SEQ ID NO:2250.	1091	99
1216	AAB434 43	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:888.	1071	99
1216	AAR224 02	Homo sapiens	BIOS Human lipocortin.	1050	99
1217	ABB1188 0	Homo sapiens	HYSE- Human lipocortin homologue, SEQ ID NO:2250.	1511	100
1217	AAB434 43	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:888.	1511	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1217	AAY084 12	Homo sapiens	UYMC- Human p-40/annexin I protein.	1511	100
1218	ABB1188	Homo sapiens	HYSE- Human lipocortin homologue, SEQ ID NO:2250.	967	100
1218	AAB434 43	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:888.	967 -	100
1218	AAY084 12	Homo sapiens	UYMC- Human p-40/annexin I protein.	967	100
1219	gi410698 4	Homo sapiens	Human DNA from chromosome 19-specific cosmid R30923, genomic sequence, complete sequence.	2992	100
1219	AAB427 92	Homo sapiens	CURA- Human ORFX ORF2556 polypeptide sequence SEQ ID NO:5112.	2967	99
1219	gi146031 76	Homo sapiens	Similar to RIKEN cDNA 2410153K17 gene, clone MGC:19595 IMAGE:3840843, mRNA, complete cds.	2432	100
1220	AAG814 43	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:404.	492	100
1220	gi150802 20	Homo sapiens	Similar to hypothetical protein, MGC:7764, clone MGC:20548 IMAGE:3607345, mRNA, complete cds.	492	100
1220	gi140361 94	Homo sapiens	unnamed protein product	492	100
1221	AAE0518 3	Homo sapiens	INCY- Human drug metabolising enzyme (DME-14) protein.	2258	100
1221	AAY913 48	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 3 SEQ ID NO:69.	2258	100
1221	gi118545 2	Homo sapiens	Human cytochrome P450 monooxygenase CYP2J2 mRNA, complete cds.	932	44
1222	AAE0518 3	Homo sapiens	INCY- Human drug metabolising enzyme (DME-14) protein.	1344	100
1222	AAY913 48	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 3 SEQ ID NO:69.	1344	100
1222	gi118545 2	Homo sapiens	Human cytochrome P450 monooxygenase CYP2J2 mRNA, complete cds.	548	44
1223	AAW346 18	Homo sapiens	IMUT- Human C3 protein mutant DV-7N.	597	34
1223	AAW346 17	Homo sapiens	IMUT- Human C3 protein mutant DV-6.	597	34
1223	AAW346 16	Homo sapiens	IMUT- Human C3 protein mutant CV-5.	597	34
1224	gi173900 00	Homo sapiens	Similar to RIKEN cDNA 5730455013 gene, clone MGC:24718 IMAGE:4278022, mRNA, complete cds.	1693	100
1224	AAB417	Homo sapiens	CURA- Human ORFX	1166	100

SEC		Speicies	Description	S score	Percent
	53		ORF1517 polypeptide sequence SEQ ID NO:3034.		identity
1224	19		putative	1036	87
1225	03		GEST Human secreted protein, SEQ ID NO: 4984.	294	100
1225			thymosin beta-10 gene, 3'end.	169	97
1225			Human thymosin beta-10 mRNA, complete cds.	169	97
1226	86	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 41 SEQ ID NO:107.	558	100
1226	gi999289 3	Homo sapiens	phosphoinositol 3-phosphate binding protein-1 (PEPP1) mRNA, complete cds.	75	40
1226	gi101907 44	Homo sapiens] > [Homo sapiens	pleckstrin homology domain- containing, family A (phosphoinositide binding specific) member 4; phosphoinositol 3-phosphate binding protein-1	75	40
1227	AAY600 08	Homo sapiens	META- Human endometrium tumour EST encoded protein 68.	2286	100
1227	AAW747 97	Homo sapiens	HUMA- Human secreted protein encoded by gene 68 clone HKIXR69.	2286	100
1227	gi576230 5	Mus musculus	COP1 protein	2268	99
1228	AAG892 92	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 412.	119	71
1228	AAM937 24	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3677.	119	71
1228	gi128036 69	Homo sapiens	CDK4-binding protein p34SEI1, clone MGC:3465 IMAGE:3613213, mRNA, complete cds.	119	71
1229	AAY913 70	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 25 SEQ ID NO:91.	293	100
1230	gi120045 83	Mus musculus	unknown	2566	81
1230	gi128365 62	Mus musculus	putative	2541	80
1230	AAB418 60	Homo sapiens	CURA- Human ORFX ORF1624 polypeptide sequence SEQ ID NO:3248.	1401	100
1231	AAG760 80	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:6844.	300	84
1231	AAG013 47	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5428.	300	84
1231	AAG013 46	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5427.	300	84
1232	ABB1165 5	Homo sapiens	homologue, SEQ ID NO:2025.	2233	99
1232	gi159297 48	Mus musculus	Unknown (protein for IMAGE:4222865)	1826	81

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1232	gi128527	Mus musculus	putative	1815	81
1233	AAB279 77	Homo sapiens	HUMA- Human secreted protein BLAST search protein SEQ ID NO: 131.	290	96
1233	AAY134 58	Homo sapiens	UYRQ Amino acid sequence of human Fe65.	290	96
1233	gi392493 6	Homo sapiens	Fe65 protein gene, exons 3 through 14 and partial cds.	290	96
1234	AAO077 68	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 21660.	294	100
1234	75	Homo sapiens	HUMA- Human secreted protein encoded by gene 12 clone HFTCU19.	288	98
1234	gi729722 6	Drosophila melanogaster	CG4497 gene product	67	42
1235	AAB942 20	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14581.	3191	99
1235	gi104342 88	Homo sapiens	cDNA FLJ12661 fis, clone NT2RM4002189, weakly similar to GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3).	3191	99
1235	gi140183 79	Schizosaccharom yces pombe	hypothetical protein; sequence orphan; low similarity to glycoamylases and other cell surface proteins; contains ~250-270 copies of a 13 AA repeat, NSSTPITSSSIL	355	26
1236	AAU035 93	Homo sapiens	INCY- Human DNA modification protein, DNAMP- 8.	4977	98
1236	gi606313	Mus musculus	F-box protein FBX18	4406	92
1236	AAB942 00	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14538.	4039	99
1237	AAB013 95	Homo sapiens	INCY- Neuron-associated protein.	1507	95
1237	AAU205 29	Homo sapiens	HUMA- Human secreted protein, Seq ID No 521.	1156	86
1237	gi128430 76	Mus musculus	putative	644	95
1238	gi165508 22	Homo sapiens	cDNA FLJ31400 fis, clone NT2NE1000185, weakly similar to UDP-N- ACETYLGLUCOSAMINE PEPTIDE N- ACETYLGLUCOSAMINYLTR ANSFERASE 110 KDA SUBUNIT (EC 2.4.1).	1999	96
1238	gi136041 67	Homo sapiens	ARG99 mRNA, complete cds.	781	100
1238	gi672116	Arabidopsis thaliana	putative O-linked GlcNAc transferase	372	27
1239	AAY734 14	Homo sapiens	GEMY Human secreted protein clone yb101_1 protein sequence SEQ ID NO:50.	472	100
1239	gi719065	Chlamydia '	conserved hypothetical protein	70	28

SEQ ID	Hit ID	Speicies	Description	S score	Percent
10	6	muridarum	<u> </u>		identity
1239	gi332875		hypothetical protein		
	9	trachomatis	hypothetical protein	68	28
1240	AAW886		HUMA- Secreted protein	525	97
	15	1	encoded by gene 82 clone	323) 97
			HNGBT31.		·
1240	AAY840	Homo sapiens	USGO Amino acid sequence of	71	30
1	40	1	cancer associated polypeptide	1	
1240	gi148609	human	CH1-9a11-2.		
1240	75	herpesvirus 2	DNA polymerase	70	36
1241	gi111214	Homo sapiens	mRNA for calsyntenin-2 (CS2	+	
	83	Tromo supiciis	gene).	5080	100
1241	gi111215	Mus musculus	calsyntenin-2	4733	
	06			4/33	94
1241	gi115582	Gallus gallus	calsyntenin-1 protein	2962	57
1010	48				137
1242	AAM933	Homo sapiens	HELI- Human polypeptide, SEQ	1034	100
1242	76 AAW781	17	ID NO: 2951.		
1242	51	Homo sapiens	HUMA- Human secreted protein	1034	100
	"		encoded by gene 26 clone HT3BE24.		
1242	AAY298	Homo sapiens	GEMY Human secreted protein	1034	100
	65		clone pe213_1.	1034	100
1243	gi104395	Homo sapiens	cDNA: FLJ23033 fis, clone	2982	99
1010	94		LNG02005.		1"
1243	AAB413 96	Homo sapiens	CURA- Human ORFX	2486	100
ļ	90		ORF1160 polypeptide sequence		1
1243	gi128530	Mus musculus	SEQ ID NO:2320.	0000	
	18	I TAND III GOOGLES	putative	2002	88
1244	AAY122	Homo sapiens	GEST Human 5' EST secreted	321	92
<u> </u>	52		protein SEQ ID NO: 565.] "
1244	AAU163	Homo sapiens	HUMA- Human novel secreted	320	92
1244	32 AAU158	77	protein, Seq ID 1285.		
1244	73	Homo sapiens	HUMA- Human novel secreted	320	92
1245	AAE0487	Homo sapiens	protein, Seq ID 826.	1.510	
	8	Tiomo supiciis	INCY- Human protease protein- 5 (PRTS-5).	1542	100
1245	gi135436	Homo sapiens	clone MGC:14793	1524	99
	81	•	IMAGE:4047601, mRNA,	1324	99
			complete cds.		1 . 1
1245	AAB475	Homo sapiens	MILL- Ubiquitin hydrolase-like	1499	100
1246	27 gi140435	TYama	protein - long form.		
1240	23	Homo sapiens	clone IMAGE:4098694,	1991	97
1246	gi120608	Homo sapiens	mRNA, partial cds. serologically defined breast	1001	
l	22	Tromo oupromo	cancer antigen NY-BR-16	1991	97
			mRNA, complete cds.		
1246	gi129638	Mus musculus	gene trap ankyrin repeat	1980	96
1045	69		containing protein	- -	-
1247	AAB543	Homo sapiens	HUMA- Human pancreatic	301	100
	57		cancer antigen protein sequence		
1247	AAY486	Homo sapiens	SEQ ID NO:809.		
1	00	Tromo sabiciis	META- Human breast tumour- associated protein 61.	285	98
	gi156129	Bacillus	BH0396~unknown conserved	63	22
			,	O.J.	32

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
, L	59	halodurans] > [Bacillus halodurans	protein		
248	AAM405 66	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 5497.	379	46
248	AAM387 80	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 1925.	379	46
248	gi653960 6	Homo sapiens	metastasis suppressor protein mRNA, complete cds.	379	46
249	gi139925 24	Homo sapiens	mRNA for type II alpha phosphatidylinositol 4-kinase gene.	2546	100
249	gi131119 89	Homo sapiens	Similar to hypothetical protein FLJ11105, clone MGC:4395 IMAGE:2905670, mRNA, complete cds.	2546	100
249	gi136607	Rattus norvegicus	55 kDa type II phosphatidylinositol 4-kinase	2409	94
1250	AAB954 25	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17833.	4871	100
1250	gi104354 87	Homo sapiens	cDNA FLJ13465 fis, clone PLACE1003493, weakly similar to ENDOTHELIAL CELL MULTIMERIN PRECURSOR.	4871	100
1250	AAY363 00	Homo sapiens	HUMA- Human secreted protein encoded by gene 77.	2472	98
1251	gi644932	Mus musculus	retinoic acid-responsive protein HA1R-62	83	68
1251	gi647869	Soybean mosaic virus	P1 protease	67	33
1252	gi124078 29	Homo sapiens	netrin 4 precursor (NTN4) mRNA, complete cds.	3361	99
1252	AAG664 49	Homo sapiens	GEHO Human beta-netrin.	3347	99
1252	gi111200 48	Homo sapiens	beta-netrin mRNA, complete cds.	3347	99
1253	gi168780 83	Homo sapiens	enolase 3, (beta, muscle), clone MGC:29581 IMAGE:4902149, mRNA, complete cds.	558	94
1253	gi34789	Homo sapiens	H.sapiens mRNA for muscle specific enclase (MSE) (EC 4.2.1.11).	555	94
1253	gi31170	Homo sapiens	Human ENO3 mRNA for beta- enolase (EC 4.2.1.11).	551	93
1254	AAY078 95	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 44.	537	100
1254	gi171320 82	Nostoc sp. PCC 7120	ORF_ID:alr2988~hypothetical protein	69	38
1255	AAB937 52	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13419.	1000	99
1255	gi104327 85	Homo sapiens	cDNA FLJ11515 fis, clone HEMBA1002241, weakly similar to PROLIFERATING- CELL NUCLEOLAR ANTIGEN P120.	1000	99
1255	gi156801 85	Homo sapiens	Similar to RIKEN cDNA 2810405F18 gene, clone	875	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
ļ			MGC:22960 IMAGE:4865283, mRNA, complete cds.		333337
1256	gi141608 80		PKCI-1-related HIT protein mRNA, complete cds.	827	100
1256	gi136501 28		HIT-17kDa mRNA, complete cds.	827	100
1256	AAM257 39		HYSE- Human protein sequence SEQ ID NO:1254.	806	94
1257	gi128492 77	Mus musculus	putative	793	93
1257	gi642529 5	elegans	predicted using Genefinder-contains similarity to Pfam domain: PF00023 (Ank repeat), Score=71.3, E- value=6.5e-18, N=2	200	40
1257	gi433575 6	Arabidopsis thaliana	putative ankyrin	195	44
1258	AAB876 09	Homo sapiens	GETH Human PRO1890.	1307	99
1258	AAB733 09	Homo sapiens	UROG- Human C-type lectin transmembrane antigen PC-LECTIN, SEQ ID NO:2.	1307	99
1258	AAU124 41	Homo sapiens	GETH Human PRO1890 polypeptide sequence.	1307	99
1259	AAY053 68	Homo sapiens	UYPR- Human HCMV inducible gene protein, SEQ ID NO 4.	1682	97
1259	AAY070 36	Homo sapiens	LUDW- Breast cancer associated antigen precursor sequence.	1682	97
1259	gi995603 5	Homo sapiens	clone CDABP0047 mRNA sequence.	1682	97
1260	AAB189 68	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	1132	100
1260	gi155303 13	Homo sapiens	clone MGC:2853 IMAGE:2987806, mRNA, complete cds.	1132	100
1260	gi139375 95	Homo sapiens	Similar to RIKEN cDNA 1810017F10 gene, clone MGC:2583 IMAGE:3140820, mRNA, complete cds.	1132	100
1261	AAB189 68	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	926	85
1261	gi155303 13	Homo sapiens	clone MGC:2853 IMAGE:2987806, mRNA, complete cds.	926	85
1261	gi139375 95	Homo sapiens	Similar to RIKEN cDNA 1810017F10 gene, clone MGC:2583 IMAGE:3140820, mRNA, complete cds.	926	85
	AAB944 34	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15054.	1629	100
	gi175121 03	Homo sapiens		1629	100
262	gi104348	Homo sapiens		1629	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	74	·	NT2RP3001355, weakly similar to TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR.		
1263	gi178640	Homo sapiens	Human angiotensinogen mRNA, complete CDS.	2366	96
1263	gil 19749 7	Homo sapiens	H.sapiens angiotensinogen gene exon 2 (and joined CDS).	2366	96
1263	AAB673 50	Homo sapiens	UTAH Human angiotensinogen protein.	2363	96
1264	gi240126	Homo sapiens	HLA-C gene (HLA-Cw*0701 allele), complete cds.	1099	98
1264	gi152772 17	Homo sapiens	genomic DNA, chromosome 6p21.3, HLA Class I region, section 7/20.	1099	98
1264	gi147819	Homo sapiens	H.sapiens mRNA for human leukocyte antigen C alpha chain.	1099	98
1265	gi386775	Homo sapiens	Human MHC class I HLA-B8 chain gene (A1,2; B5,8), complete cds.	1033	92
1265	gi240125	Homo sapiens	HLA-B gene (HLA-B*0801 allele), complete cds.	1033	92
1265	gi152772 16	Homo sapiens	genomic DNA, chromosome 6p21.3, HLA Class I region, section 6/20.	1033	92
1266	AAM237 60	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1285.	937	100
1266	gi458664	Homo sapiens	Human MHC class I antigen HLA-B (HLA-B-0704 allele) mRNA, complete cds.	937	100
1266	gi307221	Homo sapiens	Human MHC HLA protein (allele B7) complete cds.	937	100
1267	gi32181	Homo sapiens	H.sapiens HLA-Bw57 gene.	977	88
1267	gi307222	Homo sapiens	Human MHC HLA protein, allele B57, complete cds.	977	88
1267	gi674637 1	Homo sapiens	HLA class I histocompatibility antigen B-57 (HLA-B57) mRNA, complete cds.	971	88
1268	gi149705 74	Homo sapiens	HLA-A gene for MHC class I antigen, allele HLA-A*68011, exons 1-8.	1801	94
1268	gi172403 4	Homo sapiens	Human HLA class I A locus antigen A*68new mRNA, complete cds.	1796	93
1268	gi613877	Homo sapiens	HLA-A gene for MHC Class I antigen, A*68 allele, exons 1-8.	1792	93
1269	gi307225	Homo sapiens	Human MHC HLA protein, allele A25, complete cds.	1160	96
1269	gi142503 59	Homo sapiens	clone MGC:17191 IMAGE:4157200, mRNA, complete cds.	1160	96
1269	gi152697	Homo sapiens	H.sapiens mRNA for human leucocyte antigen, HLA-A25.	1152	96
1270	gi645336 5	Homo sapiens	mRNA for human leucocyte antigen B (HLA-B gene, B*1501102N allele).	314	88
1270	AAY647	Homo sapiens	GEST Human 5' EST related	148	81

SEQ ID	Hit ID	Speicies	Description	S score	Percent
	49		polypeptide SEQ ID NO:910.	+	identity
1270	AAP7015		BEHW Sequence encoded by genomic DNA encoding human histocompatibilityantigen HLA-B 27.	138	62
1271	gi825674		H.sapiens gene encoding HLA- Cw6, exons 1-3.	1120	99
1271	gi297097		H.sapiens mRNA for HLA-Cw*0602.	1120	99
1271	gi194448 0	Homo sapiens	mRNA for HLA-Cw*0602, partial cds.	1120	99
1272	gi222589 0	Homo sapiens	Human HLA-A26null allele, complete cds.	977	85
1272	gi487909	Homo sapiens	mRNA for HLA-A11 antigen A11.1, complete cds.	847	94
1272	gi446825 6	Homo sapiens	mRNA for MHC class I antigen, allele A*1103.	847	94
1273	gi860968	Homo sapiens	Human HLA-A1 gene.	1122	100
1273	gi825024 5	Homo sapiens	HLA-A*0101 gene for MHC class I antigen, exons 1-8.	1122	100
1273	gi386893	Homo sapiens	Human MHC class I HLA-A1 chain gene (A1,2; B8,5), complete cds.	1122	100
1274	AAB944 86	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15170.	2982	100
1274	AAM940 18	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 106.	2982	100
1274	gi140424 96	Homo sapiens	cDNA FLJ14750 fis, clone NT2RP3002948, weakly similar to RING CANAL PROTEIN.	2982	100
1275	gi120532 77	Homo sapiens	mRNA; cDNA DKFZp434B227 (from clone DKFZp434B227); complete cds.	2242	99
1275	gi104403 05	Homo sapiens	cDNA: FLJ23571 fis, clone LNG12303.	2124	94
1275	gil16116 03	Macaca fascicularis	hypothetical protein	2064	90
1276	gi891893 2	Mus musculus	unnamed protein product	2826	95
1276	gi632981 2	Homo sapiens	mRNA for KIAA1130 protein, partial cds.	2716	100
1276	AAS1459 5_aa1	Homo sapiens	MILL- Human cDNA encoding a novel glycosyltransferase 33877.	1606	58
1277	AAB906 76	Homo sapiens	GEMY Human BV141_2 protein sequence SEQ ID 28.	400	98
1277	AAW589 85	Homo sapiens	GEMY Homo sapiens adult brain clone BV141_2 encoded protein.	201	100
277	gi295048 1	Schizosaccharom yces pombe	hypothetical protein	71	34
1278	AAY144 55	Homo sapiens	HUMA- Human secreted protein encoded by gene 45 clone HCFBJ91.	284	100
,	AAB858 85	Homo sapiens	HELI- Human adenylate kinase 3 (AK3)-like protein.	135	78

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1279	AAB934 87	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12786.	135	78
1279	AAB930 66	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11883.	135	78
1280	AAB652 42	Homo sapiens	GETH Human PRO1291 (UNQ659) protein sequence SEQ ID NO:291.	1378	100
1280	AAB875 55	Homo sapiens	GETH Human PRO1291.	1378	100
1280	AAY667 19	Homo sapiens	GETH Membrane-bound protein PRO1291.	1378	100
1281	AAB956 82	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18481.	1675	96
1281	gi140419 89	Homo sapiens	cDNA FLJ14456 fis, clone HEMBB1001915, moderately similar to UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15).	1675	96
1281	gi729543	Drosophila melanogaster	Ubp64E gene product	892	71
1282	AAW678 41	Homo sapiens	HUMA- Human secreted protein encoded by gene 35 clone HOABG65.	500	100
1282	AAY122 38	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO: 551.	423	100
1282	AAY119 53	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No: 553.	276	94
1283	AAM259 58	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1473.	484	78
1283	AAW678 69	Homo sapiens	HUMA- Human secreted protein encoded by gene 63 clone HHGDB72.	484	78
1283	AAY022 85	Homo sapiens	GEMY Secreted protein clone k232 2x polypeptide sequence.	467	78
1284	gi29963	Homo sapiens	Human gene for creatine kinase B (EC 2.7.3.2).	162	71
1284	gi180570	Homo sapiens	Human creatine kinase isozyme CK-B gene, exon 8.	162	71
1284	gi180555	Homo sapiens	Human creatine kinase-B mRNA, complete cds.	162	71
1285	gi128498 20	Mus musculus	putative	1170	71
1285	AAM253 89	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:904.	790	98
1285	AAY249 17	Homo sapiens	INCY- Human phosphatase HPA-2.	550	39
1286	gi128498 20	Mus musculus	putative	1456	85
1286	AAY249 17	Homo sapiens	INCY- Human phosphatase HPA-2.	798	48
1286	gi897982 5	Homo sapiens	Human DNA sequence from clone RP4-776F14 on chromosome 20p12.2-13. Contains the 5' end of the FKBP1A gene for FK506-binding protein 1A (12kD), the	798	40

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			gene for P47 protein, part of a novel member of the PTPNS (protein tyrosine phosphatase, non-receptor type substrate 1) gene family, ESTs, STSs, GSSs and two CpG islands, complete sequence.		- Idounty
1287	gi317190 8	Homo sapiens	mRNA for DnaJ protein.	659	100
1287	gi160418 37	Homo sapiens	DnaJ (Hsp40) homolog, subfamily A, member 2, clone MGC:9488 IMAGE:3922477, mRNA, complete cds.	659	100
1287	gi152783 95	Homo sapiens	Similar to DnaJ (Hsp40) homolog, subfamily A, member 2, clone MGC:819 IMAGE:3505399, mRNA, complete cds.	659	100
1288	gi157412 21	Homo sapiens	gene overexpressed in astrocytoma mRNA, complete cds.	3391	99
1288	gi135440 35	Homo sapiens	clone IMAGE:3535476, mRNA, partial cds.	2095	100
1288	gi168781 87	Homo sapiens	Similar to gene overexpressed in astrocytoma, clone MGC:29809 IMAGE:5017710, mRNA, complete cds.	2079	100
1289	AAY927 19	Homo sapiens	GENZ Human polycistin.	20114	99
1289	gi904223	Homo sapiens	polycystic kidney disease i protein (PKD1) mRNA, complete cds.	20114	99
1289	AAW238 30	Homo sapiens	DEKR- Human PKD1 protein.	20111	99
1290	AAY559 65	Homo sapiens	SUGE- Full length human ZC4 protein.	1906	100
1290	AAY559 34	Homo sapiens	SUGE- Human ZC4 protein.	1808	100
1290	gi278017 3	Homo sapiens	Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.	1588	95
1291	gi104380 63	Homo sapiens	cDNA: FLJ21868 fis, clone HEP02432.	1605	99
1291	gi152774 43	Mus musculus	Unknown (protein for MGC:19083)	1379	84
1291	AAB429 53	Homo sapiens	CURA- Human ORFX ORF2717 polypeptide sequence SEQ ID NO:5434.	522	100
1292	gi795926 3	Homo sapiens	mRNA for KIAA1501 protein, partial cds.	1824	100
1292	ABB1748 8	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 6145.	984	100
1292	AAB979	Homo sapiens	SHAN- Human G-protein	965	57

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	11		activating protein 129 SEQ ID NO:2.		
1293	gi104430 48	Homo sapiens	Human DNA sequence from clone RP11-465L10 on chromosome 20. Contains 10	3567	90
			CpG islands, ESTs, STSs and GSSs. Contains the gene for a novel protein similar to		
			Drosophila CG11399, the gene for a novel C2H2 type zinc finger protein similar to chicken		
			FZF-1, a Ferritin light polypeptide (FTL) pseudogene, the MMP9 gene for matrix metalloproteinase 9 (gelatinase		
			B, 92kD gelatinase, 92kD type IV collagenase) (CLG4B), a novel gene, the SLC12A5 gene		
		·	for solute carrier family 12, (potassium-chloride transporter) member 5 (KIAA1176) and the 3' end of gene KIAA1637,		
1293	AAH282 26 aa1	Homo sapiens	complete sequence. PFIZ Nucleotide sequence of matrix metalloproteinase-9.	3556	90
1293	AAB204 91	Homo sapiens	SMIK Human matrix metalloproteinase-9 (MMP-9).	3556	90
1294	AAH282 26 aal	Homo sapiens	PFIZ Nucleotide sequence of matrix metalloproteinase-9.	2375	100
1294	AAB204 91	Homo sapiens	SMIK Human matrix metalloproteinase-9 (MMP-9).	2375	100
1294	AAB846	Homo sapiens	PFIZ Amino acid sequence of matrix metalloproteinase-9.	2375	100
1295	AAG040 88	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 8169.	601	91
1295	gi897761	Homo sapiens	H.sapiens mRNA for protein phosphatase 5.	450	92
1295	gi455863 8	Homo sapiens	chromosome 19, BAC 82621 (CIT-B-139a18), complete sequence.	450	.92
1296	AAY647 86	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:947.	200	100
1296	gi162640 94	Sinorhizobium meliloti] > [Sinorhizobium meliloti	HYPOTHETICAL PROTEIN	63	35
1297	gi126980	Homo sapiens	mRNA for KIAA1734 protein, partial cds.	3889	100
1297	gi104386	Homo sapiens	cDNA: FLJ22346 fis, clone HRC06158.	3877	99
1297	AAB943 54	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14875.	2421	99
1298	gi145756	Homo sapiens	hemicentin mRNA, complete cds.	10314	89
1298	gi165519 93	Homo sapiens	cDNA FLJ31995 fis, clone NT2RP7009236, weakly similar to BASEMENT MEMBRANE- SPECIFIC HEPARAN	4274	91

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SEQ ID	Hit ID	Speicles	Description	S score	Percent identity
			SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR.		dentity
1298	gi 138728 13	Homo sapiens	partial mRNA for fibulin-6 (FIBL-6 gene).	2907	99
1299	gi548084	Rattus norvegicus	olfactory cyclic nucleotide-gated	2811	93
1299	gi538129	Rattus norvegicus	cyclic nucleotide gated cation channel	2811	93
1299	gi908824	Bos taurus	alpha subunit of CNG-channel expressed in bovine testis and retinal cone	1576	53
1300	AAB419 63	Homo sapiens	CURA- Human ORFX ORF1727 polypeptide sequence SEQ ID NO:3454.	514	100
1300	gi155297 03	Homo sapiens	importin 9 mRNA, complete cds.	514	100
1300	gi151867 58	Mus musculus	RANBP9 isoform 2	514	100
1301	gi105053 49	Homo sapiens	regulator of G-protein signaling (RGS8) mRNA, complete cds.	926	100
1301	gi173820 46	Homo sapiens	unnamed protein product	926	100
1301	gi266205 7	Rattus norvegicus	RGS8	921	98
1302	AAB953 02	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17538.	1242	100
1302	gi104349 69	Homo sapiens	cDNA FLJ13105 fis, clone NT2RP3002351, weakly similar to Human mRNA for NAD- dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).	1242	100
1302	gi128347 26	Mus musculus	putative	873	94
1303	gi546603	human, tumorous liver, mRNA Partial, 2631 nt]. [Homo sapiens	glutamine synthetase	1787	100
1303	gi175120 38	Homo sapiens	clone MGC:20095 IMAGE:3352740, mRNA, complete cds.	1787	100
1303	gi150801 57	Homo sapiens	glutamate-ammonia ligase (glutamine synthase), clone MGC:20322 IMAGE:4137547, mRNA, complete cds.	1787	100
1304	gi546603	human, tumorous liver, mRNA Partial, 2631 nt]. [Homo sapiens	glutamine synthetase	432	89
1304	gi31833	Homo sapiens	Human mRNA for glutamine synthetase (E.C. 6.3.1.2).	432	89
1304	gi31831	Homo sapiens	Human rearranged mRNA for glutamine synthase.	432	89
1305	gi165517 55	Homo sapiens	cDNA FLJ31807 fis, clone NT2RI2009215, moderately similar to ZINC FINGER	492	54

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			PROTEIN 165.		
1305	AAM416 49	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6580.	462	51
1305	AAM939 17	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 4075.	462	51
1306	AAU162 46	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1199.	1010	96
1306	gi128328 45	Mus musculus	putative	585	83
1306	AAU162 40	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1193.	342	95
1307	gi979845	Homo sapiens	mRNA for putative capacitative calcium channel (trp7 gene).	4470	100
1307	gi532685	Mus musculus	receptor-activated calcium channel	4392	98
1307	gi229590 3	Homo sapiens	Human putative calcium influx channel (htrp3) mRNA, complete cds.	3529	81
1308	gi611460	Homo sapiens	mRNA for stromal antigen 3 (STAG3 gene).	281	74
1308	gi309042	Mus musculus	stag3	203	49
1308	gi131951 63	Rattus norvegicus	stromal antigen 3	199	47
1309	gi611460	Homo sapiens	mRNA for stromal antigen 3 (STAG3 gene).	295	82
1309	gi309042	Mus musculus	stag3	200	55
1309	gi131951 63	Rattus norvegicus	stromal antigen 3	198	54
1310	gi985856 2	Homo sapiens	Rh type B glycoprotein (RHBG) mRNA, complete cds.	2176	99
1310	gi157184 71	Homo sapiens	Rh type B glycoprotein (RHBG) gene, exons 9, and 10 and complete cds.	2176	99
1310	gi143460 06	Pan troglodytes	Rh type B glycoprotein	2161	99
1311	gi724314	Homo sapiens	mRNA for KIAA1384 protein, partial cds.	3377	100
1311	gi128576 73	Mus musculus	putative	2817	98
1311	gi724297	Homo sapiens	mRNA for KIAA1309 protein, partial cds.	913	33
1312	AAY862 97	Homo sapiens	HUMA- Human secreted protein HLDCE79, SEQ ID NO:212.	530	100
1312	AAY216 23	Homo sapiens	REGC Ligand binding domain of nuclear receptor hGR.	74	32
1312	AAP8091 9	Homo sapiens	SALK Sequence of the primary protein sequence of human glucocorticoidreceptor (hGR).	74	32
1313	gil10226 90	Homo sapiens	ifp1 mRNA for interferon- responsive finger protein 1 long form, complete cds.	4302	99
1313	AAB955 86	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18252.	2612	100
1313	gi140428 69	Homo sapiens	cDNA FLJ14970 fis, clone THYRO1000501, weakly	2612	100

SEQ	Hit ID	Speicies	Description	S score	Percent identity
		<u> </u>	similar to 52 KD RO PROTEIN.	 	испину
1314	gi178613 72	Homo sapiens	lysyl oxidase-like 4 mRNA, complete cds.	984	93
1314	gi166601 31	Homo sapiens	lysyl oxidase-like 4 (LOXL4) mRNA, complete cds.	984	93
1314	gi146694 71	Homo sapiens	lysyl oxidase-related protein C (LOXC) mRNA, complete cds.	984	93
1315	gi165494 49	Homo sapiens	cDNA FLJ30273 fis, clone BRACE2002685, moderately similar to Homo sapiens androgen-regulated short-chain dehydrogenase/reductase 1 (ARSDR1) mRNA.	1612	98
1315	gi128616 68	Mus musculus	putative	1374	84
1315	gi167406 49	Mus musculus	Similar to RIKEN cDNA A930033N07 gene	1315	81
1316	gi142862 86	Homo sapiens	Similar to hypothetical protein FLJ20515, clone MGC:2696 IMAGE:2820596, mRNA, complete cds.	1006	100
1316	AAY530 23	Homo sapiens	GEMY Human secreted protein clone qf662_3 protein sequence SEQ ID NO:52.	990	99
1316	AAE0483 5	Homo sapiens	SUGE- Human SGP001 phosphatase polypeptide.	931	95
1317	AAN500 69_aa1	Homo sapiens	MITU DNA encoding cardiodilatin in plasmid pHANF48.	771	100
1317	AAW981 93	Homo sapiens	CURA- Human atrial natriuretic peptide prohormone.	771	100
1317	AAP5124 1	Homo sapiens	BIOT- Sequence of pre-pro- atrial natriuretic/vasodilatorpolypeptid e (ANVP).	771	100
1318	AAE0618 3	Homo sapiens	HUMA- Human gene 57 encoded secreted protein fragment, SEQ ID NO:245.	3182	89
1318	AAY872 06	Homo sapiens	HUMA- Human secreted protein sequence SEQ ID NO:245.	3182	89
1318	7	Homo sapiens	HUMA- Human gene 57 encoded secreted protein HRACD80, SEQ ID NO:159.	2906	88
1319	AAU089 95	Homo sapiens	MILL- Human G protein- coupled receptor, GPCR, 45449.	410	96
1319	gi122142 87	Homo sapiens	Human DNA sequence from clone RP3-402H5 on chromosome 6p12.3-21.1 Contains ESTs, STSs and GSSs. Contains the 3' part of a gene for a novel 7 transmembrane receptor of the rhodopsin family and a novel gene, complete sequence.	410	96
1319	gi157973 18	Homo sapiens	unnamed protein product	410	96
1320	gi897761	Homo sapiens	H.sapiens mRNA for protein	387	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			phosphatase 5.		<u> </u>
1320	gi455863 8	Homo sapiens	chromosome 19, BAC 82621 (CIT-B-139a18), complete sequence.	387	100
1320	gi128050 33	Homo sapiens	protein phosphatase 5, catalytic subunit, clone MGC:5260 IMAGE:3459309, mRNA, complete cds.	387	100
1321	AAB566 13	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1191.	1174	100
1321	gi182644	Homo sapiens	Human FK506-binding protein 25 (FKBP25) mRNA, complete cds.	1169	100
1321	gi182626	Homo sapiens	Human rapamycin binding protein (FK506) mRNA, complete cds.	1169	100
1322	gi150426	Homo sapiens	sorting nexin 18 (SNX18) mRNA, complete cds.	2895	100
1322	gi155590 64	Mus musculus	SNAG1	2440	86
1322	AAW990 23	Homo sapiens	MOUN 17G2 peptide sequence.	1605	95
1323	gi128048 03	Homo sapiens	clone MGC:4499 IMAGE:2964565, mRNA, complete cds.	1266	100
1323	gi 126545 15	Homo sapiens	clone MGC:2827 IMAGE:2964565, mRNA, complete cds.	1266	100
1323	AAB543 74	Homo sapiens	HUMA- Human pancreatic cancer antigen protein sequence SEQ ID NO:826.	1261	99
1324	gi119075	Homo sapiens	protein kinase HIPK2 mRNA, complete cds.	6242	99
1324	AAB656 61	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 188.	6086	97
1324	gi172253 77	Homo sapiens	homeodomain interacting protein kinase 2 (HIPK2) mRNA, complete cds.	6083	97
1325	AAB656 61	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 188.	6124	99
1325	gi172253 77	Homo sapiens	homeodomain interacting protein kinase 2 (HIPK2) mRNA, complete cds.	6121	99
1325	gi119075	Homo sapiens	protein kinase HIPK2 mRNA, complete cds.	6072	97
1326	gi165522 98	Homo sapiens	cDNA FLJ32230 fis, clone PLACE6004464, weakly similar to Human placenta (Diff48) mRNA.	3064	99
1326	gi 132742 02	Homo sapiens	Human DNA sequence from clone RP4-530115 on chromosome 20 Contains the 3' end of the PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 (EC 3.1.3.48), the gene for a novel	2261	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			protein similar to placental protein DIFF40, an RPL36 (60S ribosomal protein L36)		
			pseudogene, a novel gene, two putative novel genes, ESTs, STSs and GSSs, complete sequence.		
1326	gi222471 3	Homo sapiens	Human mRNA for KIAA0386 gene, complete cds.	963	34
1327	AAU121 77	Homo sapiens	GETH Human PRO305 polypeptide sequence.	1472	82
1327	AAY814 87	Homo sapiens	FUJY Human cathepsin L2.	1472	82
1327	AAY023 58	Homo sapiens	ONOY Polypeptide identified by the signal sequence trap method.	1472	82
1328	AAU121 77	Homo sapiens	GETH Human PRO305 polypeptide sequence.	1698	84
1328	AAY814 87	Homo sapiens	FUJY Human cathepsin L2.	1698	84
1328	AAY023 58	Homo sapiens	ONOY Polypeptide identified by the signal sequence trap method.	1698	84
1329	AAY873 29	Homo sapiens	INCY- Human signal peptide containing protein HSPP-106 SEQ ID NO:106.	692	94
1329	gi151454 28	Caenorhabditis elegans	Hypothetical protein Y22D7AL.14	74	23
1329	gi361801 6	Human immunodeficienc y virus type 1	nef	73	35
1330	AAB823 15	Homo sapiens	UYCO Human immunoglobulin receptor isoform IRTA2c.	1120	99
1330	AAB823 14	Homo sapiens	UYCO Human immunoglobulin receptor isoform IRTA2b.	1120	99
1330	AAB823 13	Homo sapiens	UYCO Human immunoglobulin receptor isoform IRTA2a.	1120	99
1331	gi143367 57	Homo sapiens	16p13.3 sequence section 6 of 8.	1178	100
1331	gi134362 69	Homo sapiens	hypothetical protein FLJ20898, clone MGC:10688 IMAGE:3622114, mRNA, complete cds.	1178	100
1331	AAG814 30	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:378.	954	100
1332	gi568955 7	Homo sapiens	mRNA for KIAA1110 protein, partial cds.	3820	99
1332	ABB1171 3	Homo sapiens	HYSE- Human KIAA1110 protein homologue, SEQ ID NO:2083.	3809	99
1332	gi388224 7	Homo sapiens	mRNA for KIAA0763 protein, complete cds.	1587	44
1333	gi133662 77	Homo sapiens	Human DNA sequence from clone RP5-998H6 on chromosome 20q13.1. Contains the gene for the ortholog of rat PB-Cadherin, ESTs, STSs, GSS, two CpG islands and genomic marker D20S17, complete	4283	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			sequence.		
1333	gi476057	Mus musculus	PB-Cadherin	3918	92
1333	gi139890	Rattus norvegicus	long type PB-cadherin	3907	92
1334	gi302304	Enterococcus faecalis	orfC	302	45
1334	gi496520	Streptococcus pyogenes	orf iota	271	39
1334	gi129570	Enterococcus faecalis	hypothetical protein	251	38
1335	gi128384 81	Mus musculus	putative	491	71
1335	gi207249	Mus musculus	perforatorial protein PERF 15	481	68
1335	gi151952	Rattus norvegicus	PERF15 protein	477	68
1336	gi104384	Homo sapiens	cDNA: FLJ22171 fis, clone HRC00654.	3750	100
1336	gi104381	Homo sapiens	cDNA: FLJ21935 fis, clone HEP04373.	3734	99
1336	gi135295 54	Mus musculus	Similar to hypothetical protein FLJ21935	3203	85
1337	gi128034 45	Homo sapiens	clone MGC:2217 IMAGE:3139026, mRNA, complete cds.	463	100
1337	gi729634	Drosophila melanogaster	CG4186 gene product	201	47
1337	gi529133	Saccharomyces cerevisiae	Yhrl 16wp	113	41
1338	gi104343 52	Homo sapiens	cDNA FLJ12697 fis, clone NT2RP1000522, weakly similar to UBIQUITIN CARBOXYL- TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15).	6400	99
1338	AAB951 46	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17169.	6396	99
1338	AAB746	Homo sapiens	INCY- Human protease and protease inhibitor PPIM-4.	4021	99
1339	gi108016 26	Macaca fascicularis	hypothetical protein	1668	98
1339	gi128367	Mus musculus	putative	1439	84
1339	gi104383	Homo sapiens	cDNA: FLJ22054 fis, clone HEP09634.	1351	99
1340	gi175120 67	Homo sapiens	hypothetical protein DKFZp434D0421, clone MGC:20807 IMAGE:4330507, mRNA, complete cds.	1903	100
1340	gi140437 17	Homo sapiens	hypothetical protein DKFZp434D0421, clone MGC:14446 IMAGE:4304040, mRNA, complete cds.	1903	100
1340	gi120531 19	Homo sapiens	mRNA; cDNA DKFZp434D0421 (from clone DKFZp434D0421); complete cds.	1903	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1341	AAB087 65	Homo sapiens	INCY- A human leukocyte and blood related protein (LBAP).	716	93
1341	AAM409 91		HYSE- Human polypeptide SEQ ID NO 5922.	508	93
1341	AAB747 18	Homo sapiens	INCY- Human membrane associated protein MEMAP-24.	456	96
1342	AAB955 63	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18202.	3214	99
1342	gi104359 04	Homo sapiens	cDNA FLJ13782 fis, clone PLACE4000489, weakly similar to PROTEIN GRAINY-HEAD.	3214	99
1342	gi128327 62	Mus musculus	putative	2094	94
1343	AAG893 36	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 456.	801	100
1343	AAG813 52	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:222.	801	100
1343	AAY914 23	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 11 SEQ ID NO:144.	801	100
1344	AAY949 78	Homo sapiens	GEMY Human secreted protein clone pw337_6 2nd protein sequence SEQ ID NO:238.	444	. 100
1344	gi759453 4	Arabidopsis thaliana	putative protein	79	31
1345	gi430989 4	Homo sapiens	PAC clone RP4-555L14 from 7q34-q36, complete sequence.	818	100
1345	gi176464 48	Mus musculus	gammaN-crystallin	724 .	83
1345	gi176464 46	Homo sapiens	gammaN-crystallin variant (CRYGN) mRNA, complete cds.	600	100
1346	AAY762 16	Homo sapiens	HUMA- Human secreted protein encoded by gene 93.	225	97
1347	AAY114 47	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No 269.	210	97
1347	gi761976 9	Streptomyces coelicolor A3(2)	probable LacI-family transcriptional regulatory protein.	66	53
1347	gi755580	Streptomyces lividans	ORF-RDR; LacI homolog, similar to E. coli Lac repressor, Swiss-Prot Accession Number P03023	66	53
1348	gi173910 52	Homo sapiens	clone MGC:9915 IMAGE:3871205, mRNA, complete cds.	2220	100
1348	AAG741 53	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4917.	1072	98
1348	gi525318	Haematobia irritans	putative ATPase	937	44
1349	gi173910 52	Homo sapiens	clone MGC:9915 IMAGE:3871205, mRNA, complete cds.	1919	88
1349	AAG741 53	Homo sapiens		782	76
1349	gi525318	Haematobia		749	39

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
		irritans			
1350	AAB433 15	Homo sapiens	CURA- Human ORFX ORF3079 polypeptide sequence SEQ ID NO:6158.	1463	99
1350	gi668259 0	Homo sapiens	chromosome 14 clones RP11- 111016 and RP11-61F4 containing genes for nuclear receptor coactivator NCoA-62 (nuclear receptor coactivator NCoA-62) gene, complete cds; and unknown gene, complete sequence.	1463	99
1350	AAW820 03	Homo sapiens	GEMY Human foetal brain secreted protein fh3_6 (alternative sequence).	1249	99
1351	gi128411 45	Mus musculus	putative	1153	93
1351	gi135292 12	Homo sapiens	Similar to RIKEN cDNA 1810018M11 gene, clone MGC:12485 IMAGE:3932127, mRNA, complete cds.	1136	99
1351	AAY962 02	Homo sapiens	UYNY IkappaB kinase (IKK) binding protein, Y2H56.	1126	98
1352	gi151267 88	Mus musculus	Similar to ferritin heavy chain	947	100
1352	gi50954	Mus musculus	ferrerin H subunit	947	100
1352	gi50952	Mus musculus	ferritin heavy subunit (AA 1 - 182)	947	100
1353	AAB705 38	Homo sapiens	CURA- Human PRO8 protein sequence SEQ ID NO:16.	2777	98
1353	AAB705 37	Homo sapiens	CURA- Human PRO7 protein sequence SEQ ID NO:14.	2777	98
1353	gi131857 25	Homo sapiens	n 1755 can be A, G, C, or T.	2777	98
1354	AAB535 41	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:1081.	110	73
1354	AAR729 86	Homo sapiens	GENZ Creatine-kinase subunit B.	110	73
1354	gi29963	Homo sapiens	Human gene for creatine kinase B (EC 2.7.3.2).	110	73
1355	gi124074 05	Homo sapiens	tripartite motif protein TRIM9 isoform beta (TRIM9) mRNA, complete cds; alternatively spliced.	2831	100
1355	gi167555 24	Rattus norvegicus	Spring	2783	97
1355	gi166580 3	Homo sapiens	Human mRNA for KIAA0282 gene, partial cds.	2575	99
1356	AAY536 41	Homo sapiens	CHIR A bone marrow secreted protein designated BMS42.	346	98
1356	gi966315 3	Homo sapiens	partial mRNA for transport- secretion protein 2.2, (TTS-2.2 gene).	346	98
1356	gi966315 1	Homo sapiens	partial mRNA for transport- secretion protein 2.1 (TTS-2.1 gene).	346	98

SEQ	Hit ID	Speicles	Description	S score	Percent
1357	gi108011 97	Homo sapiens	heparanase-like protein HPA2b mRNA, complete cds.	2785	identity 100
1357	gi151326 69	Homo sapiens	unnamed protein product	2785	100
1357	AAA910 97_aa1	Homo sapiens	INSI- Human heparanase, hnhp1, coding sequence.	2626	88
1358	gi633035 8	Homo sapiens	mRNA for KIAA1193 protein, partial cds.	2885	100
1358	AAU162 16	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1169.	1216	88
1358	AAY158 35	Homo sapiens	PATE/ A human er1 protein.	751	43
1359	AAB749 45	Homo sapiens	YAMA Human ADAM type metal protease MDTS2 protein SEQ ID NO:10.	6065	99
1359	gi114935 89	Homo sapiens	zinc metalloendopeptidase (ADAMTS10) mRNA, partial cds.	5940	99
1359	AAB723 00	Homo sapiens	HIRO/ Human ADAMTS-10 alternative amino acid sequence.	5484	97
1360	gi173842 56	Homo sapiens	partial MUC5AC gene for mucin 5, clone A.	1291	80
1360	gi563375	Homo sapiens	H.sapiens (JER47) MUC5AC mRNA for mucin (partial).	978	91
1360	gi173842 54	Homo sapiens	partial mRNA for mucin 5 (MUC5AC gene).	905	75
1361	AAM243 95	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1920.	634	100
1361	AAY761 79	Homo sapiens	HUMA- Human secreted protein encoded by gene 56.	634	100
1361	AAB473 27	Homo sapiens	CURA- FCTR4.	74	27
1362	gi150802 64	Homo sapiens	clone MGC:20279 IMAGE:3949150, mRNA, complete cds.	1043	100
1362	gi104390 83	Homo sapiens	cDNA: FLJ22623 fis, clone HSI05687.	1043	100
1362	gi173894 37	Homo sapiens	hypothetical protein FLJ22623, clone MGC:22173 IMAGE:4274089, mRNA, complete cds.	1031	99
1363	AAH787 30_aa1	Homo sapiens	HUMA- Human HIBCJ89 serine/threonine phosphatase cDNA sequence.	1635	99
1363	AAU205 55	Homo sapiens	HUMA- Human secreted protein, Seq ID No 547.	1635	99
1363	AAU206 63	Homo sapiens	HUMA- Human secreted protein, Seq ID No 655.	1635	99
1364	AAB957 00	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18526.	752	100
1364	gi153418 46	Homo sapiens	hypothetical protein FLJ14107, clone MGC:21030 IMAGE:4389733, mRNA, complete cds.	752	100
1364	gi104364 85	Homo sapiens	cDNA FLJ14107 fis, clone MAMMA 1001252.	752	100
1365	AAY673	Homo sapiens		367	100

SEQ	Hit ID	Speicies	Description	S score	Percent identity
	16		BL341_4 amino acid sequence.		
1365	AAY086 25	Homo sapiens	GEMY Human secreted protein BL341_4.	367	100
1365	AAW420 18	Homo sapiens	JACO/ Clone BL341_4 protein.	363	98
1366	AAU197 15	Homo sapiens	HUMA- Human novel extracellular matrix protein, Seq ID No 365.	2225	99
1366	gi613679 8	Mus musculus	synaptotagmin VIdeltaTM2	2150	96
1366	gi613679	Mus musculus	synaptotagmin VIdeltaTM1	2150	96
1367	AAU197 15	Homo sapiens	HUMA- Human novel extracellular matrix protein, Seq ID No 365.	2173	97
1367	gi613679	Mus musculus	synaptotagmin VIdeltaTM2	2098	94
1367	gi613679	Mus musculus	synaptotagmin VIdeltaTM1	2098	94
1368	AAE0517 5	Homo sapiens	INCY- Human drug metabolising enzyme (DME-6) protein.	2614	97
1368	AAU122 25	Homo sapiens	GETH Human PRO4404 polypeptide sequence.	2614	97
1368	gil 19330 56	Sus scrofa	cytochrome P450	1305	50
1369	AAW781 35	Homo sapiens	HUMA- Human secreted protein encoded by gene 10 clone HPMGQ80.	385	100
1369	AAO023 10	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 16202.	76	39
1369	AAO087 72	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22664.	74	35
1370	gi100473	Homo sapiens	mRNA for KIAA1613 protein, partial cds.	3532	100
1370	AAB361 71	Homo sapiens	LEXI- Novel human transporter protein SEQ ID NO: 28.	3412	100
1370	AAB361 70	Homo sapiens	LEXI- Novel human transporter protein SEQ ID NO: 26.	3408	99
1371	AAB416 73	Homo sapiens	CURA- Human ORFX ORF1437 polypeptide sequence SEQ ID NO:2874.	1221	96
1371	AAB616 11	Homo sapiens	PROT- Human protein HP03377.	1220	100
1371	AAE0365 6	Homo sapiens	INCY- Human extracellular matrix and cell adhesion molecule-20 (XMAD-20).	1220	100
1372	gi529588	Mus musculus	kinesin like protein 9	3618	88
1372	AAB947 68	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15849.	3257	99
1372	gi104359 68	Homo sapiens	cDNA FLJ13832 fis, clone THYRO1000666, highly similar to Mus musculus mRNA for kinesin like protein 9.	3257	99
1373	AAH255 68_aa1	Homo sapiens	CURA- Nucleotide sequence of an interferon omega-1 like	3294	100

SEQ ID	Hit ID	Speicles	Description	S score	Percent identity
1000	<u> </u>		protein NOV2.		
1373	AAG675 23	Homo sapiens	SMIK Amino acid sequence of a human secreted polypeptide.	3294	100
1373	AAB844 69	Homo sapiens	CURA- Amino acid sequence of an interferon omega-1 like protein NOV2.	3294	100
1374	gi592399 2 gi142457	Homo sapiens Giardia	Human DNA sequence from clone RP5-1043E3 on chromosome 6p21.1-21.2 Contains part of a novel gene, an transcription factor E2F4 pseudogene, ESTs, STSs and GSSs, complete sequence.	945	99
	13	intestinalis	kinesin-like protein 9	543	44
1374	gi150223 94	Leishmania major	possible kinesin-like protein	531	42
1375	AAG747 79	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5543.	1405	99
1375	gi798126 1	Homo sapiens	Human DNA sequence from clone RP1-50O24 on chromosome 1p35.1-35.3. Contains the 3' end of the gene for a novel protein similar to C. elegans K07B1.7 (Tr:O01886), the gene for a novel protein (translation of cDNA NT2RM2001100 (Em:AK001211)), the SFN gene for stratifin (14-3-3 protein sigma), the gene for a novel protein with DHHC zinc finger domain, the gene for a novel protein (translation of cDNA KAT07271 (Em:AK000484)) and the gene for B120 (C10rf4) (ARID DNA binding domain containing protein). Contains ESTs, STSs, GSSs and six putative CpG islands, complete sequence.	1122	67
1375	AAG812 54	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:26.	1118	72
1376	gi805223 7	Homo sapiens	ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene.	5605	100
1376	gi805232 0	Mus musculus	Cegp1 protein	5054	89
1376	AAG675 29	Homo sapiens	SMIK Amino acid sequence of a human secreted polypeptide.	3226	61
1377	gi104370 45	Homo sapiens	cDNA: FLJ21044 fis, clone CAE11659.	1663	100
1377	gi420638 6	Mus musculus	rig-1 protein	1543	72
1377	AAB570 88	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ	1518	98

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			ID NO:1666.		
1378	AAY026 97	Homo sapiens	HUMA- Human secreted protein encoded by gene 48 clone HTNBR95.	165	100
1379	AAY733 86	Homo sapiens	INCY- HTRM clone 3279329 protein sequence.	529	.100
1379	AAB631 62	Homo sapiens	ROSE/ Human secreted protein sequence encoded by gene 29 SEQ ID NO:88.	363	100
1379	AAB951 24	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17122.	83	32
1380	gi101981 15	Homo sapiens	2P domain potassium channel TREK2 (KCNK10) mRNA, complete cds.	2760	100
1380	gi845290 0	Rattus norvegicus	potassium channel TREK-2	2555	95
1380	gi458479	Mus musculus	TREK-1 K+ channel subunit	1238	64
1381	gi132766 55	Homo sapiens	mRNA; cDNA DKFZp761M0423 (from clone DKFZp761M0423); complete cds.	2626	99
1381	AAE0436	Homo sapiens	INCY- Human kinase (PKIN)-2.	2588	97
1381	gi183616 1	Rattus sp.	Ca2+/calmodulin-dependent protein kinase IV kinase isoform; CaM-kinase kinase alpha	2468	93
1382	gi123827 81	Homo sapiens	OSBP-related protein 4 mRNA, complete cds.	1124	100
1382	gi133592 01	Homo sapiens	mRNA for KIAA1664 protein, partial cds.	1036	100
1382	gi142098 40	Homo sapiens	oxysterol binding protein 2 (OSBP2) gene, complete cds.	919	100
1383	gi128055 53	Mus musculus	Unknown (protein for MGC:7583)	792	99
1383	gi128586 56	Mus musculus	putative	787	98
1383	AAM238 65	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1390.	672	83
1384	gi300292 5	Homo sapiens	T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds.	679	73
1384	gi298250 8	Homo sapiens	mRNA for TCR beta chain, specific for Mage 3/HLA-A2.	667	71
1384	AAM240 51	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1576.	655	100
1385	gi138792 62	Mus musculus	RIKEN cDNA 0610011E17 gene	710	97
1385	gi128503 53	Mus musculus	putative	710	97
1385	AAB429 05	Homo sapiens	CURA- Human ORFX ORF2669 polypeptide sequence SEQ ID NO:5338.	582	79
1386	AAB950 62	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16896.	741	99
1386	AAM241	Homo sapiens	HYSE- Human EST encoded	681	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	27		protein SEQ ID NO: 1652.		Identity
1386	AAY873 28	Homo sapiens	INCY- Human signal peptide containing protein HSPP-105 SEQ ID NO:105.	681	100
1387	AAM235 76		HYSE- Human EST encoded protein SEQ ID NO: 1101.	691	100
1387	AAB718 99	Homo sapiens	ZYMO Human zaipha48.	306	68
1387	AAE0658 0	Homo sapiens	SAGA Human protein having hydrophobic domain, HP10786.	306	68
1388	AAB718 63	Homo sapiens	MILL- Human h15571 GPCR.	6511	97
1388	gi159874 91	Homo sapiens	tumor endothelial marker 5 precursor (TEM5) mRNA, complete cds.	6511	97
1388	gi159874 99	Mus musculus	tumor endothelial marker 5	5693	85
1389	AAE0135 4	Homo sapiens	HUMA- Human gene 3 encoded secreted protein HOHBL42, SEQ ID NO:76.	3747	99
1389	gi431420	Mus musculus	MPS1 protein	2714	77
1389	gi505204 8	Rattus norvegicus	Mpg-1 protein	2672	75
1390	AAM242 00	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1725.	329	100
1390	AAY195 88	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	329	100
1391	AAG742 49	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5013.	888	98
1391	gi128351 18	Mus musculus	putative	884	95
1391	gi730176 3	Drosophila melanogaster	CGI 1900 gene product	497	59
1392	gi128032 69	Homo sapiens	Similar to CG10641 gene product, clone MGC:3052 IMAGE:3343900, mRNA, complete cds.	701	100
1392	gi104419 42	Homo sapiens	clone PP3051 unknown mRNA.	701	100
1392	AAB954 96	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18039.	698	99
1393	AAY125 12	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:543.	320	98
1394	AAB948 33	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15998.	2735	100
1394	gi104362 42	Homo sapiens	cDNA FLJ13941 fis, clone Y79AA1000850.	2735	100
1394	AAB428 18	Homo sapiens	CURA- Human ORFX ORF2582 polypeptide sequence SEQ ID NO:5164.	1115	99
1395	AAB948 33	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15998.	2713	97
	gi104362 42	Homo sapiens	cDNA FLJ13941 fis, clone Y79AA1000850.	2713	97
1	AAB428 18	Homo sapiens	CURA- Human ORFX ORF2582 polypeptide sequence	1093	94

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			SEQ ID NO:5164.		
1396	gi726392 8	Homo sapiens	Human DNA sequence from clone RPI-61A9 on	5326	99
			chromosome 1p35.2-36.13		1
			Contains part of the EPHB2		
			gene for tyrosine-protein kinase,		i
			the gene KIAA0478 for a C2H2	}	
			type zinc finger gene, ESTs,		
			STSs, GSSs and three putative		1
			CpG Islands, complete sequence.	<u> </u>	
1396	AAE0436 2	Homo sapiens	INCY- Human kinase (PKIN)-3.	5308	99
1396	AAU006 91	Homo sapiens	CURA- Ephrin type-A receptor 8-like protein.	5259	99
1397	gi104376	Homo sapiens	cDNA: FLJ21511 fis, clone	3713	99
	26	•	COL05748.		
1397	gi167414	Mus musculus	Similar to hypothetical protein	3125	82
	00		FLJ21511		
1397	gi145889	Saccharomyces cerevisiae	hypothetical protein	690	29
1398	AAB947 13	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15714.	2869	100
1398	gi 104357	Homo sapiens	cDNA FLJ13664 fis, clone	2869	100
1370	45	110mo sapiens	PLACE1011649.	2007	1 200
1398	gi168772	Homo sapiens	Similar to hypothetical protein	2843	99
1330	91	1101110 Sapicits	24432, clone MGC:21034	20.5	
			IMAGE:4400396, mRNA,		
			complete cds.		
1399	AAB829	Homo sapiens	UYNY Human androgen	1429	100
1399	40	Tromo saprens	receptor trapped protein 5		
	""		(ART5).		
1399	AAB560	Homo sapiens	HUMA- Human secreted protein	1429	100
	85		sequence encoded by gene 9	ŀ	1
	33		SEQ ID NO:179.		
1399	gi104392	Homo sapiens	cDNA: FLJ22709 fis, clone	1429	100
	04		HSI13338.		
1400	gi104396	Homo sapiens	cDNA: FLJ23056 fis, clone	1190	100
	25		LNG03287.		
1400	gi729573	Drosophila	ft gene product	185	27
	2	melanogaster			
1400	gi157409	Drosophila	fat protein	185	27
	•	melanogaster			
1401	gi139362	Mus musculus	TRH4	1332	61
	85				
1401	gi128455	Mus musculus	putative	1330	61
	40		·		
1401	AAU007	Homo sapiens	INCY- Human apoptosis	1092	65
	82	<u></u>	protein, APOP-2.		
1402	AAU004	Homo sapiens	MILL- Human INTERCEPT	4272	97
	75		394 alternative form protein.		
1402	AAU004	Homo sapiens	MILL- Human INTERCEPT	4089	99
	73	1	394 protein.		
1402	gi104384	Homo sapiens	cDNA: FLJ22169 fis, clone	3505	99
	50		HRC00632.		
1403	gi107988	Homo sapiens	HCMOGT-1 mRNA for sperm	3737	98
-	04		antigen, complete cds.		
1403	ABB1229	Homo sapiens	HYSE- Human secreted protein	2811	100

SEQ	Hit ID	Speicies	Description	S score	Percent
	7	<u> </u>	homologue, SEQ ID NO:2667.		identity
1403	AAM252 55	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:770.	2778	98
1404	AAB954 25	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17833.	4871	100
1404	gi104354 67	Homo sapiens	cDNA FLJ13465 fis, clone FLACE1003493, weakly similar to ENDOTHELIAL CELL MULTIMERIN PRECURSOR.	4871	100
1404	AAY363 00	Homo sapiens	HUMA- Human secreted protein encoded by gene 77.	2472	98
1405	gi100472 11	Homo sapiens	mRNA for KIAA 1573 protein, partial cds.	6270	100
1405	gi143883 34	Macaca fascicularis	hypothetical protein	5174	99
1405	AAB958 83	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18994.	3679	100
1406	gi147146 04	Homo sapiens	clone MGC:17248 IMAGE:4215164, mRNA, complete cds.	3291	96
1406	AAW803 18	Homo sapiens	SMIK Neurodegenerative polypeptide HHPDZ65var.	2893	100
1406	gi834683 4	Homo sapiens	mRNA for putative acid-sensing ion channel (ASIC4 gene).	2893	100
1407	AAB656 97	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 225.	1647	100
1407	gi140439 28	Homo sapiens	clone IMAGE:4139786, mRNA, partial cds.	1117	100
1407	AAG024 79	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6560.	442	100
1408	AAR499 43	Homo sapiens	YAMA/ Human hippocampal cholinergic neurotrophic peptide precursor.	881	89
1408	gi704465	Homo sapiens	H.sapiens mRNA for phosphatidylethanolamine binding protein.	881	89
1408	gi435638	Homo sapiens	Human mRNA for human homologue of rat phosphatidylethanolamine binding protein, complete cds.	881	89
1409	AAB955 17	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18089.	4520	99
1409	gi 104357 76	Homo sapiens	cDNA FLJ13687 fis, clone PLACE2000061.	4520	99
1409	gi726465 3	Mus musculus	Kiaa0575	1867	48
1410	gi170283 41	Homo sapiens	hypothetical protein FLJ21820, clone MGC:14932 IMAGE:3611020, mRNA, complete cds.	1732	100
	gi 104379 97	Homo sapiens	cDNA: FLJ21820 fis, clone HEP01232.	1732	100
	gi167697 18	Drosophila melanogaster	LP01162p	437	33
	gi150797 29	Homo sapiens	hypothetical protein FLJ21125, clone MGC:14948 IMAGE:4303449, mRNA,	1530	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			complete cds.		
1411	gi104371 58	Homo sapiens	cDNA: FLJ21125 fis, clone CAS06077.	1530	99
1411	AAY946 74	Homo sapiens	ZYMO Human zsig83 mature protein sequence.	142	34
1412	gi104381 26	Homo sapiens	cDNA: FLJ21918 fis, clone HEP04006.	3799	100
1412	AAY844 40	Homo sapiens	INCY- Amino acid sequence of a human RNA-associated protein.	2085	59
1412	gi702009	Homo sapiens	cDNA FLJ20171 fis, clone COL09761.	1246	66
1413	gi140310 72	Homo sapiens	Human DNA sequence from clone RP3-331H24 on chromosome 6 Contains a putative novel gene, part of the gene for hypothetical protein FLJ21079, similar to opioid growth factor receptor, ESTs, STSs, GSSs and a CpG island, complete sequence.	1307	99
1413	gi104370 94	Homo sapiens	cDNA: FLJ21079 fis, clone CAS02253.	1307	99
1413	gi128434 68	Mus musculus	putative	922	73
1414	AAB943 98	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14968.	3638	100
1414	gi104347 85	Homo sapiens	cDNA FLJ12987 fis, clone NT2RP3000068, weakly similar to SON OF SEVENLESS PROTEIN HOMOLOG 1.	3638	100
1414	AAB956 39	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18376.	3001	100
1415	gi136234 91	Homo sapiens	clone MGC:13125 IMAGE:4111572, mRNA, complete cds.	3054	100
1415	gi165537	Homo sapiens	cDNA FLJ25103 fis, clone CBR01405.	1586	74
1415	AAM662 79	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26585.	1301	100
1416	ABB1167	Homo sapiens	HYSE- Human secreted protein homologue, SEQ ID NO:2045.	1238	99
1416	gi159289 21	Homo sapiens	hypothetical protein FLJ14393, clone MGC:17935 IMAGE:3916148, mRNA, complete cds.	1238	99
1416	AAY452 72	Homo sapiens	HUMA- Human secreted protein encoded from gene 16.	1236	99
1417	gi136232 49	Homo sapiens	Similar to RIKEN cDNA 3110082I17 gene, clone MGC:11257 IMAGE:3941780, mRNA, complete cds.	945	95
1417	gi128520 07	Mus musculus	putative	466	61
1417	AAW679 36	Homo sapiens	HUMA- Fragment of human secreted protein encoded by	329	98

SEQ	Hit ID	Speicies	Description	S score	Percent
ID					identity
1418	gi139382		gene 57.		
	74		clone MGC:15548 IMAGE:3051320, mRNA, complete cds.	3136	99
1418	73	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1326.	963	100
1418	22	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 875.	963	100
1419	81	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11914.	1812	98
1419	gi140424 19	Homo sapiens	cDNA FLJ14712 fis, clone NT2RP3000825, weakly similar to NEUROGENIC LOCUS NOTCH 3 PROTEIN.	1812	98
1419	AAY727 13	Homo sapiens	HUMA- HWAAQ40 clone human attractin-like protein.	1212	99
1420	AAU124 18	Homo sapiens	GETH Human PRO1275 polypeptide sequence.	643	98
1420	AAY993 79	Homo sapiens	GETH Human PRO1275 (UNQ645) amino acid sequence SEQ ID NO:136.	643	98
1420	AAB256 83	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 19 SEQ ID NO:72.	643	98
1421	gi104387 12	Homo sapiens	cDNA: FLJ22358 fis, clone HRC06415.	3025	100
1421	gi142111 39	Homo sapiens	NADPH oxidase 5 gamma mRNA, complete cds.	3019	99
1421	gi142111 37	Homo sapiens	NADPH oxidase 5 alpha mRNA, complete cds.	3019	99
1422	gi126583 05	Homo sapiens	kappa B and V(D)J recombination signal sequences binding protein (KRC) mRNA, complete cds.	8934	99
1422	gi100471 75	Homo sapiens	mRNA for KIAA1555 protein, partial cds.	8588	99
1422	gi137788 6	Mus musculus	DNA binding protein Rc	6216	76
1423	gi173892 08	Homo sapiens	clone MGC:16889 IMAGE:3883022, mRNA, complete cds.	2465	100
1423	gi152781 67	Homo sapiens	differentiation-related DIF14 long form (DIF14) mRNA, complete cds, alternatively spliced.	2448	99
1423	gi965122 0	Mus musculus	LMBR1 long form	2391	96
1424	gi104370 78	Homo sapiens	cDNA: FLJ21069 fis, clone CAS01594.	2523	99
1424	gi159297 78	Homo sapiens	hypothetical protein FLJ21069, clone MGC:21026 IMAGE:4431888, mRNA, complete cds.	2517	99
424	gi128597 74	Mus musculus	putative	2182	86
425	AAM937 35	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3701.	1364	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1425	gi128553 79	Mus musculus	putative	1332	87
1425	gi163593 63	Mus musculus	Similar to hypothetical protein MGC12921	652	53
1426	gi165536 18	Homo sapiens	cDNA FLJ33140 fis, clone UTERU1000160, moderately similar to ZINC FINGER PROTEIN 191.	2173	99
1426	gi104400 85	Homo sapiens	cDNA: FLJ23407 fis, clone HEP19601.	1146	100
1426	gi142501 46	Homo sapiens	hypothetical protein FLJ23407, clone MGC:14819 IMAGE:4248596, mRNA, complete cds.	1143	99
1427	gi127341 04	Homo sapiens	Human DNA sequence from clone RP11-371L19 on chromosome 20. Contains two novel genes, the gene for a novel protein similar to 40S ribosomal protein S10 (RPS10), ESTs, STSs, GSSs and five CpG islands, complete sequence.	2452	100
1427	gi155241 16	Homo sapiens	unnamed protein product	2431	98
1427	gi146024 88	Homo sapiens	clone MGC:10698 IMAGE:3689286, mRNA, complete cds.	2395	98
1428	AAG675 09	Homo sapiens	SMIK Amino acid sequence of a human secreted polypeptide.	4286	100
1428	gi156208 67	Homo sapiens	mRNA for KIAA1904 protein, partial cds.	4272	99
1428	gi319197 5	Homo sapiens	Human DNA sequence from clone RP1-63G5 on chromosome 22q12.3-13.1 Contains the 3' part of the PSCD4 gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, a novel gene and the gene coding for a Leucine rich protein. Contains ESTs, STSs, GSSs and three putative CpG islands, complete sequence.	953	100
1429	AAG023 49	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6430.	468	100
1429	gi177046 2	Homo sapiens	H.sapiens mRNA for M-phase phosphoprotein, mpp6.	468	100
1429	gi150296 28	Homo sapiens	Similar to M-phase phosphoprotein 6, clone MGC:13538 IMAGE:4287267, mRNA, complete cds.	468	100
1430	AAB883 77	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0113.	239	100
1430	AAB089 04	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 14 SEQ ID NO:61.	239	100
1430	gi142726	Homo sapiens	unnamed protein product	239	100

SEQ	Hit ID	Speicies	Description	S score	Percent
ID	08	•		<u> </u>	identity
1431	gi999289	Homo sapiens	phorphoinosital 2 phorphoi	2006	
1131	3	Homo sapiens	phosphoinositol 3-phosphate binding protein-1 (PEPP1) mRNA, complete cds.	3906	95
1431	AAB420 86	Homo sapiens	CURA- Human ORFX ORF1850 polypeptide sequence SEQ ID NO:3700.	427	71
1431	gi458958 2	Homo sapiens	mRNA for KIAA0969 protein, complete cds.	256	31
1432	gi999289 3	Homo sapiens	phosphoinositol 3-phosphate binding protein-1 (PEPP1) mRNA, complete cds.	4152	99
1432	AAB420 86	Homo sapiens	CURA- Human ORFX ORF1850 polypeptide sequence SEQ ID NO:3700.	672	99
1432	AAO125 92	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 26484.	475	100
1433	AAY949 47	Homo sapiens	GEMY Human secreted protein clone cw1292_8 protein sequence SEQ ID NO:100.	408	100
1433	AAB651 95	Homo sapiens	GETH Human PRO830 (UNQ470) protein sequence SEQ ID NO:175.	215	64
1433	AAY666 72	Homo sapiens	GETH Membrane-bound protein PRO830.	215	64
1434	gi165538 18	Homo sapiens	cDNA FLJ25124 fis, clone CBR06414.	1573	100
1434	AAG021 37	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6218.	554	98
1434	AAH755 22_aa1	Homo sapiens	SHAN- Human myosin heavy chain 74 encoding cDNA.	275	22
1435	AAF8417 1_aa1	Homo sapiens	CHUG- Human OATP-B coding sequence.	188	92
1435	AAZ9240 3_aa1	Homo sapiens	SCHE cDNA encoding human DC-PGT.	188	92
1435	AAC618 83_aa1	Homo sapiens	CHIR cDNA encoding a human secreted protein.	188	92
1436	gi112304 87	Rattus norvegicus	NTPDase6	501	96
1436	AAB722 42	Homo sapiens	HYSE- Mature human CD39 like protein CD39-L2 amino acid sequence.	414	80
1436	AAB722 41	Homo sapiens	HYSE- Human CD39 like protein CD39-L2 amino acid sequence.	414	80
1437	gi724322 9	Homo sapiens	mRNA for KIAA1424 protein, partial cds.	6604	99
1437	AAB979 11	Homo sapiens	SHAN- Human G-protein activating protein 129 SEQ ID NO:2.	6021	99
1437	AAB416 60	Homo sapiens	CURA- Human ORFX ORF1424 polypeptide sequence SEQ ID NO:2848.	4377	99
1438	AAB088 94	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 4 SEQ ID NO:51.	211	69
1438	gi156262	Buffalopox virus	p8 protein homologue	69	31

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	57				
1438	gi583067 8	variola minor virus	A14L protein	68	27
1439	AAG017 13	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5794.	670	99
1439	gi120019 70	Homo sapiens	clone 015h12 My015 protein mRNA, complete cds.	495	96
1439	gi996391	Xenopus laevis	Churchill protein	495	71
1440	gi140178	Homo sapiens	mRNA for KIAA1807 protein, partial cds.	1751	100
1440	gi104388 85	Homo sapiens	cDNA: FLJ22479 fis, clone HRC10831.	1524	100
1440	gi144245 58	Homo sapiens	KIAA0239 protein, clone IMAGE:4301096, mRNA, partial cds.	157	28
1441	AAB436 17	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1062.	1481	93
1441	AAP9191	Homo sapiens	BEHW Anticoagulative PP4X.	1481	93
1441	gi189617	Homo sapiens	Human protein PP4-X mRNA, complete cds.	1481	93
1442	AAE0379 0	Homo sapiens	HUMA- Human gene 9 encoded secreted protein fragment, SEQ ID NO:60.	391	100
1442	AAE0378 5	Homo sapiens	HUMA- Human gene 9 encoded secreted protein HMWDW68, SEQ ID NO:55.	391	100
1442	AAY734 25	Homo sapiens	GEMY Human secreted protein clone yj3_1 protein sequence SEQ ID NO:72.	391	100
1443	gi388232	Homo sapiens	mRNA for KIAA0804 protein, partial cds.	6282	100
1443	AAB943 56	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14879.	4093	99
1443	gi104346 28	Homo sapiens	cDNA FLJ12883 fis, clone NT2RP2003981, weakly similar to VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.	4093	99
1444	gi125396	Homo sapiens	AKAP-associated sperm protein (ASP) mRNA, complete cds.	1215	99
1444	gi157790 77	Homo sapiens	AKAP-associated sperm protein, clone MGC:26950 IMAGE:4820798, mRNA, complete cds.	1212	99
1444	gi118782 18	Mus musculus	cAMP-dependent protein kinase regulatory subunit	937	78
1445	AAB435 99	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1044.	1283	100
1445	gi141249 28	Homo sapiens	clone MGC:3644 IMAGE:2966331, mRNA, complete cds.	1219	100
1.445	gi140438 53	Homo sapiens	thymidine kinase 1, soluble, clone MGC:14441	1219	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			IMAGE:4303880, mRNA, complete cds.		add at the state of the state o
1446	AAE0040 4		ZYMO Human phosphodiesterase zcytor13 protein.	2733	100
1446	gi139223	Homo sapiens	unnamed protein product	2733	100
1446	AAM255 48	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1063.	2584	100
1447	gi376644 3	Homo sapiens	QDPR gene, exon 1 and joined CDS.	1069	87
1447	gi30819	Homo sapiens	Human mRNA for dihydropteridine reductase (hDHPR).	1069	87
1447	gi181553	Homo sapiens	Human dihydropteridine reductase (hDHPR) mRNA, complete cds.	1069	87
1448	gi132766 31	Homo sapiens	mRNA; cDNA DKFZp761F241 (from clone DKFZp761F241); complete cds.	747	100
1448	gi128448 72	Mus musculus	putative	650	87
1448	AAY597 95	Homo sapiens	META- Human normal ovarian tissue derived protein 72.	554	100
1449	AAB429 06	Homo sapiens	CURA- Human ORFX ORF2670 polypeptide sequence SEQ ID NO:5340.	834	100
1449	gi131951 51	Homo sapiens	transcription factor TZP (TZP) mRNA, complete cds.	534	54
1449	gi102414 61	Homo sapiens	Human DNA sequence from clone RP5-1121G12 on chromosome 20 Contains the 3' end of a gene encoding the hepatocellular carcinoma-associated antigen 58 (HCA58), the SCAND1 gene encoding the domain-containing 1 protein, a novel gene, 2 CpG islands, ESTs, STSs and GSSs, complete sequence.	534	54
1450	AAY120 21	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO: 334.	265	97
1450	gi962621 8	Beet curly top virus	ORF20.1 > [Beet curly top	63	27
1451	AAG018 78	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5959.	348	92
1451	AAB541 58	Homo sapiens	HUMA- Human pancreatic cancer antigen protein sequence SEQ ID NO:610.	225	91
1452	AAO083 54	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22246.	1451	89
1452	AAY733 84	Homo sapiens	INCY- HTRM clone 2284580 protein sequence.	1451	89
1452	02	Homo sapiens	mRNA for nucleolar phosphoprotein Nopp34, complete cds.	1451	89
453	gi142499	Homo sapiens		2387	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	53		FLJ22376, clone MGC:16044 IMAGE:3610443, mRNA, complete cds.		
1453	gi167405 59	Homo sapiens	clone MGC:13247 IMAGE:4040497, mRNA, complete cds.	1067	100
1453	gi165517 33	Homo sapiens	cDNA FLJ31791 fis, clone NT2R12008749, weakly similar to SPLICEOSOME ASSOCIATED PROTEIN 49.	1023	53
1454	AAM663 21	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26627.	883	50
1454	AAM539 33	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 26038.	883	50
1454	gi449038	Felis silvestris	polyprotein	672	44
1455	AAB948 15	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15961.	719	100
1455	gi104362 05	Homo sapiens	cDNA FLJ13920 fis, clone Y79AA1000420.	719	100
1455	gi128475 56	Mus musculus	putative	169	46
1456	gi33044	Homo sapiens	Human mRNA for insulin-like growth factor II (clone P21).	742	97
1456	gi182528	Homo sapiens	Human preproinsulin-like growth factor II (IGF-II) variant mRNA, complete cds.	717	78
1456	AAY703 64	Homo sapiens	UYLO- Insulin-like growth factor II.	714	78
1457	AAY993 51	Homo sapiens	GETH Human PRO1481 (UNQ750) amino acid sequence SEQ ID NO:41.	1725	100
1457	AAB102 59	Homo sapiens	GEMY Human fetal placenta protein fragment BA176_1i.	1631	88
1457	AAB102 51	Homo sapiens	GEMY Human adult testes protein fragment AJ142_1i.	761	97
1458	AAB436 07	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1052.	664	88
1458	gi695360	Homo sapiens	nuclear-encoded mitochondrial cytochrome c oxidase Va subunit mRNA, complete cds.	658	87
1458	gi128585 80	Mus musculus	putative	544	73
1459	gi754922	Mus musculus	PALS1	3386	96
1459	AAB941 80	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14494.	2590	99
1459	gi104342 10	Homo sapiens	cDNA FLJ12615 fis, clone NT2RM4001629, weakly similar to MAGUK P55 SUBFAMILY MEMBER 3.	2590	99
1460	gi126979 87	Homo sapiens	mRNA for KIAA1721 protein, partial cds.	3859	99
1460	AAB944	Homo sapiens	HELI- Human protein sequence	3853	99

SEQ	Hit ID	Speicies	Description	S score	Percent
ID	125				identity
1460	35 gi104348	IIomi	SEQ ID NO:15056.		
	78	Homo sapiens	cDNA FLJ13046 fis, clone NT2RP3001374.	3853	99
1461	gi152144 23	Homo sapiens	clone IMAGE:4563921, mRNA, partial cds.	2603	100
1461	gi179017 49	Homo sapiens	unnamed protein product	2603	100
1461	gi167407 25	Mus musculus	Similar to hexokinase 1	2411	91
1462	AAG755 79	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:6343.	714	85
1462	AAB435 66	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1011.	714	85
1462	gi239865 7	Homo sapiens	H.sapiens mRNA translocon- associated protein delta subunit precursor.	714	85
1463	AAG891 28	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 248.	2076	100
1463	gi163068 50	Homo sapiens	hypothetical protein FLJ22637, clone MGC:2443 IMAGE:2821972, mRNA, complete cds.	2076	100
1463	gi104391 04	Homo sapiens	cDNA: FLJ22637 fis, clone HSI06677.	2076	100
1464	AAW642 62	Homo sapiens	BGHM Human neutrophil elastase.	1326	96
1464	AAP8033 5	Homo sapiens	TORA) TORAY IND INC (AOKI/ Sequence of serine protease (SP) of human myeloid cellorigin and leader peptide.	1326	96
1464	gi386981	Homo sapiens	Human neutrophil elastase gene, exon 5.	1326	96
1465	AAY113 85	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No 207.	220	100
1465	AAB677 83	Homo sapiens	INRM Amino acid sequence of a human thyroid NADPH-oxidase.	75	33
1465	AAM245 05	Homo sapiens	CORI- Colon tumour related amino acid sequence for C799P.	75	33
1466	gi289575 8	Bos taurus	phosphatidic acid-preferring phospholipase A1	4245	91
1466	gi126979 55	Homo sapiens	mRNA for KIAA1705 protein, partial cds.	2582	99
1466	gi165541 84	Homo sapiens	cDNA FLJ25408 fis, clone TST02965, highly similar to Bos taurus phosphatidic acid- preferring phospholipase A1 mRNA.	2378	100
1467	gi147900 25	Homo sapiens	clone MGC:9168 IMAGE:3876839, mRNA, complete cds.	1488	100
1467	gi167686 82	Drosophila melanogaster	HL02815p	1155	49
1467	gi107269 44	Drosophila melanogaster	CG11306 gene product	1155	49
468	AAB747	Homo sapiens	HUMA- Human secreted protein	902	91

SEQ ID	Hit ID	Speicics	Description	S score	Percent identity
	60		sequence encoded by gene 18 SEQ ID NO:69.		
1468	AAB747 59	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 18 SEQ ID NO:68.	902	91
1468	AAB747 50	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 18 SEQ ID NO:59.	902	91
1469	AAB747 60	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 18 SEQ ID NO:69.	1006	96
1469	AAB747 59	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 18 SEQ ID NO:68.	1006	96
1469	AAB747 50	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 18 SEQ ID NO:59.	1006	96
1470	AAW131 08	Homo sapiens	ONYX- Human 14-3-3 beta or HS1 1054.	1225	95
1470	gi279155 2	Homo sapiens	Human DNA sequence from clone RP1-148E22 on chromosome 20q12-13.12 Contains the YWHAB gene encoding tyrosine 3-monooxygenase/ntryptophan 5-monooxygenase activation protein, beta polypeptide, a novel gene similar to PABPC1	1225	95
1470		Name and in	(poly (A)-binding protein, cytoplasmic 1), 2 CpG islands, ESTs, STSs and GSSs, complete sequence. H.sapiens mRNA for HS1	1225	95
1470	gi23114	Homo sapiens	protein.		
1471	AAB948 34	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16000.	2638	100
1471	gi104362 44	Homo sapiens	cDNA FLJ13942 fis, clone Y79AA1000962, weakly similar to MYOSIN HEAVY CHAIN, NON-MUSCLE.	2638	100
1471	gi142905 66	Homo sapiens	hypothetical protein FLJ13942, clone MGC:9884 IMAGE:3867690, mRNA, complete cds.	1501	100
1472	AAB105 50	Homo sapiens	HOFM/ Human aspartate protease psl 4 protein.	1925	100
1472	AAB088 60	Homo sapiens	INCY- Amino acid sequence of a human secretory protein.	1925	100
1472	AAB089 71	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 25 SEQ ID NO:128.	1920	99
1473	AAG892 62	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 382.	231	100
1473	AAY307 21	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	231	100
1473	AAB236 15	Homo sapiens	ALPH- Human secreted protein SEQ ID NO: 30.	222	97
1474	gi702033	Homo sapiens	cDNA FLJ20318 fis, clone	2962	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	6		HEP08704.		Identity
1474	AAM406 51		HYSE- Human polypeptide SEQ ID NO 5582.	1804	47
1474	AAM388 65	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2010.	1804	47
1475	gi144956 2i	Homo sapiens	hypothetical protein FLJ22578, cione MGC:14892 IMAGE:3506508, mRNA, complete cds.	816	100
1475	gi104390 14	Homo sapiens	cDNA: FLJ22578 fis, clone HSI02546.	802	100
1475	AAM728 25	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 33131.	616	100
1476	gi222469 7	Homo sapiens	Human mRNA for KIAA0378 gene, partial cds.	4017	100
1476	gi668158 3	Homo sapiens	ELKS mRNA, complete cds.	3463	72
1476	gi134457 84	Mus musculus	Rab6-interacting protein 2 isoform A	3423	70
1477	gi155303 23	Homo sapiens	clone MGC:4131 IMAGE:2961417, mRNA, complete cds.	3200	99
1477	gi163075 02	Mus musculus	Unknown (protein for MGC:11530)	3076	95
1477	gi152772 34	Homo sapiens	genomic DNA, chromosome 6p21.3, HLA Class I region, section 12/20.	2227	99
1478	AAY117 94	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No: 394.	375	100
1478	AAB949 77	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16558.	68	35
1478	gi104331 41	Homo sapiens	cDNA FLJ11800 fis, clone HEMBA1006252.	68	35
1479	AAB087 32	Homo sapiens	UYCO Amino acid sequence of a human OLD-35 polypeptide.	3498	98
1479	gi128358 17	Mus musculus	putative	2439	89
1479	AAB926 84	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11065.	2369	99
1480	gi144245 68	Homo sapiens	Mov10 (Moloney leukemia virus 10, mouse) homolog, clone MGC:15000 IMAGE:4109453, mRNA, complete cds.	4983	100
1480	gi128034 47	Homo sapiens	Similar to Moloney leukemia virus 10, clone MGC:2948 IMAGE:3138543, mRNA, complete cds.	4983	100
1480	gi100473 39	Homo sapiens	mRNA for KIAA1631 protein, partial cds.	4983	100
1481	AAU055 84	Homo sapiens	OXFO- Human breast cancer membrane protein 81, BCMP- 81.	718	100
1481	AAU257 27	Homo sapiens	OXFO- Breast cancer-associated membrane protein (BCMP) 81.	718	100
1481	AAW857 38	Homo sapiens	SAGA Polypeptide with transmembrane domain.	718	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1482	gi140179 57	Homo sapiens	mRNA for KIAA1870 protein, partial cds.	1496	94
1482	AAB420 00	Homo sapiens	CURA- Human ORFX ORF1764 polypeptide sequence SEQ ID NO:3528.	1302	93
1482	AAB938 66	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13743.	860	100
1483	gi140179 57	Homo sapiens	mRNA for KIAA1870 protein, partial cds.	1608	100
1483	AAB420 00	Homo sapiens	CURA- Human ORFX ORF 1764 polypeptide sequence SEQ ID NO:3528.	1414	100
1483	AAB938 66	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13743.	860	100
1484	gi499184	Felis catus	neuronal protein	617	96
1484	AAB950 41	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16804.	507	77
1484	gi795925 1	Homo sapiens	mRNA for KIAA1495 protein, partial cds.	507	77
1485	AAB604 57	Homo sapiens	INCY- Human cell cycle and proliferation protein CCYPR-5, SEQ ID NO:5.	928	100
1485	gi150805 50	Homo sapiens	hypothetical protein FLJ23467, clone MGC:21000 IMAGE:4509736, mRNA, complete cds.	928	100
1485	gi104401 66	Homo sapiens	cDNA: FLJ23467 fis, clone HSI11213.	925	99
1486	AAB933 01	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12369.	4341	99
1486	gi140426 07	Homo sapiens	cDNA FLJ14812 fis, clone NT2RP4002081, weakly similar to TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS.	4341	99
1486	gi100471	Homo sapiens	mRNA for KIAA1557 protein, partial cds.	4168	99
1487	AAB948 04	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15939.	2050	100
1487	gi150825 06	Homo sapiens	hypothetical protein FLJ13910, clone MGC:20406 IMAGE:4636136, mRNA, complete cds.	2050	100
1487	gi104361 89	Homo sapiens	cDNA FLJ13910 fis, clone Y79AA1000131.	2050	100
1488	gi128460 13	Mus musculus	putative	1876	97
1488	gi783955 9	Homo sapiens	PAD mRNA, complete cds.	1789	98
1488	gi136041 69	Homo sapiens	ARG147 mRNA, complete cds.	1575	99
1489	gi126979 35	Homo sapiens	mRNA for KIAA1695 protein, partial cds.	2124	100
1489	gi104386 24	Homo sapiens	cDNA: FLJ22297 fis, clone HRC04521.	2124	100
1489	AAB424 21	Homo sapiens	CURA- Human ORFX ORF2185 polypeptide sequence	1571	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			SEQ ID NO:4370.		исицу
1490	AAB475 62	Homo sapiens	INCY- Protease PRTS-4.	4321	99
1490	AAM937 85	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3804.	4317	99
1490	gi128363 32	Mus musculus	putative	4152	95
1491	gi165538 16	Homo sapiens	cDNA FLJ25123 fis, clone CBR06154.	1752	93
1491	AAO118 34	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 25726.	1347	98
1491	AAM257 94	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1309.	919	99
1492	gi140433 13	Homo sapiens	clone IMAGE:3609599, mRNA, partial cds.	780	100
1492	AAY122 25	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO: 538.	511	97
1492	AAG005 45	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4626.	500	97
1493	AAM934 50	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3100.	2693	99
1493	AAY077 54	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 11.	1723	100
1493	AAW790 94	Homo sapiens	GEMY Human secreted protein do568_11.	1699	98
1494	AAG648 94	Homo sapiens	BIOD- Human phosphoenol pyruvate carboxylase 81.	3851	100
1494	AAB952 50	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17415.	1589	100
1494	gi132766 65	Homo sapiens	mRNA; cDNA DKFZp761K1524 (from clone DKFZp761K1524); complete cds.	1493	100
1495	AAB437 37	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1182.	817	89
1495	AAR592 88	Homo sapiens	SHIO Human reg protein.	817	89
1495	gi576455 5	Homo sapiens	lithostathine (REG1A) mRNA, complete cds.	817	89
1496	gi126525 61	Homo sapiens	Similar to cytochrome b-561, clone MGC:3308 IMAGE:3509626, mRNA, complete cds.	1129	96
1496	gi128042 35	Homo sapiens	Similar to cytochrome b-561, clone MGC:2190 IMAGE:3535771, mRNA, complete cds.	1126	95
1496	gi939707	Homo sapiens	Human cytochrome b561 gene, exon 5 and complete cds.	1124	95
1497	gi104370 90	Homo sapiens	cDNA: FLJ21077 fis, clone CAS02152.	2182	99
1497	gi104372 11	Homo sapiens	cDNA: FLJ21159 fis, clone CAS09969.	1885	100
1497	AAB639 60	Homo sapiens	LUDW- Human prostate cancer associated antigen protein sequence SEQ ID NO:1322.	904	96

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1498	AAB409 96	Homo sapiens	CURA- Human ORFX ORF760 polypeptide sequence SEQ ID NO:1520.	3391	95
1498	gi104369 63	Homo sapiens	cDNA: FLJ20986 fis, clone CAE01156.	3137	99
1498	AAM935 25	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3259.	2627	99
1499	AAB998 91	Homo sapiens	CHUG- Human RNA helicase gene helicain B protein sequence SEQ ID NO:4.	3818	100
1499	gi165665 50	Homo sapiens	DEAD/DEXH helicase DDX31 mRNA, complete cds.	3817	99
1499	gi152152 73	Homo sapiens	hypothetical protein FLJ13633, clone MGC:14872 IMAGE:3941452, mRNA, complete cds.	3455	100
1500	gi120055 11	Homo sapiens	HT027 mRNA, complete cds.	744	100
1500	gi104368 44	Homo sapiens	cDNA: FLJ20886 fis, clone ADKA03257.	739	99
1500	gi110369 73	Homo sapiens	HSP22-like protein interacting protein 17 mRNA, complete cds.	459	100
1501	AAB952 61	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17444.	906	100
1501	gi104347 55	Homo sapiens	cDNA FLJ12967 fis, clone NT2RP2005806.	906	100
1501	AAB942 67	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14682.	587	95
1502	gi165534 61	Homo sapiens	cDNA FLJ33132 fis, clone UMVEN2000133, weakly similar to RABPHILIN-3A.	2594	99
1502	gi104386 90	Homo sapiens	cDNA: FLJ22344 fis, clone HRC06080.	1661	99
1502	AAB935 62	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12957.	1289	55
1503	gi165493 30	Homo sapiens	cDNA FLJ30165 fis, clone BRACE2000698, weakly similar to ANKYRIN 2.	2280	98
1503	gi126527 41	Homo sapiens	clone MGC:3130 IMAGE:3352851, mRNA, complete cds.	2267	78
1503	AAO018 50	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 15742.	1975	89
1504	AAB662 95	Homo sapiens	ICOS- Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.	6088	99
1504	AAB662 94	Homo sapiens	ICOS- Human tankyrase2 TANK2-LONG SEQ ID NO: 133.	6088	99
1504	AAB662 90	Homo sapiens	ICOS- Human tankyrase2 clone consensus protein SEQ ID NO: 107.	6088	99
1505	gi568942 7	Homo sapiens	mRNA for KIAA1045 protein, partial cds.	2087	99
1505	gi133586 52	Macaca fascicularis	hypothetical protein	1205	96

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	6		related polypeptide SEQ ID NO 5463.		Additiv
1506	gi568942 7	Homo sapiens	mRNA for KIAA1045 protein, partial cds.	2052	94
1506	gi133586 52	Macaca fascicularis	hypothetical protein	1205	96
1506	ABB1680 6	•	HUMA- Human nervous system related polypeptide SEQ ID NO 5463.	370	100
1507	gi104390 66	Homo sapiens	cDNA: FLJ22612 fis, clone HSI04965.	2767	100
1507	gi145298 86	Mus musculus	bM145O4.1 (novel protein)	2276	78
1507	gi128553 00	Mus musculus	putative	2276	78
1508	gil14933 65	Homo sapiens	Human DNA sequence from clone RP5-1009E24 on chromosome 20 Contains the SN gene encoding sialoadhesin, a novel gene similar to KIAA0417, the CENPB gene for centromere protein B, the CDC25B gene for Cell division cycle protein 25B, three novel genes, the 5' end of gene KIAA1271, nine CpG islands, ESTs, STSs and GSSs, complete sequence.	6334	99
1508	gi126561 30	Homo sapiens	sialoadhesin mRNA, complete cds.	6330	99
1508	gi104404 38	Homo sapiens	mRNA for FLJ00055 protein, partial cds.	5046	99
1509	AAY765 39	Homo sapiens	META- Human ovarian tumor EST fragment encoded protein 35.	261	98
1510	AAE0488 4	Homo sapiens	INCY- Human protease protein- 11 (PRTS-11).	424	100
1510	AAB732 63	Homo sapiens	UYAL- Human triacylglycerol hydrolase, TGH.	209	51
1510	gi180950	Homo sapiens	Human carboxylesterase mRNA, complete cds.	209	51
1511	AAB944 05	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14983.	4412	100
1511	gi104347 98	Homo sapiens	cDNA FLJ12994 fis, clone NT2RP3000207, weakly similar to GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3).	4412	100
1511	gi104371 27	Homo sapiens	cDNA: FLJ21104 fis, clone CAS04958.	978	100
1512	AAB621 75	Homo sapiens	PLAC Human pl10FYVE protein.	4028	99
1512	AAF5740 3_aa1	Homo sapiens	PLAC Human pl10FYVE protein encoding DNA.	4027	99
1512	gi113449 51	Homo sapiens	FYVE-finger-containing Rab5 effector protein Rabenosyn-5 mRNA, complete cds.	4027	99
1513	gi795926	Homo sapiens	mRNA for KIAA1500 protein,	4061	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	1		partial cds.		
1513	gi983742 7	Lytechinus variegatus	embryonic blastocoelar extracellular matrix protein precursor	1085	34
1513	AAG733 54	Homo sapiens	HUMA- Human gene 9-encoded secreted protein HETAM53, SEQ ID NO:125.	517	100
1514	gi165501 08	Homo sapiens	cDNA FLJ30829 fis, clone FEBRA2001790, highly similar to Xenopus laevis RRM- containing protein SEB-4 mRNA.	914	100
1514	gi136244 61	Homo sapiens	Human DNA sequence from clone RP1-259A10 on chromosome 6p22.1-23 Contains the gene for an ssDNA binding protein (SEB4D), ESTs, STSs, GSSs and a CpG island, complete sequence.	914	100
1514	gi889569	Xenopus laevis	RRM-containing protein SEB-4	790	88
1515	gi165515 80	Homo sapiens	cDNA FLJ31673 fis, clone NT2RI2005061.	3158	99
1515	AAB949 29	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16399.	2275	100
1515	gi104328 47	Homo sapiens	cDNA FLJ11565 fis, clone HEMBA1003229.	2275	100
1516	gi394768	Homo sapiens	mRNA for Sec24 protein (Sec24A isoform), partial.	5355	98
1516	AAM791	Homo sapiens	HYSE- Human protein SEQ ID NO 1773.	3090	55
1516	gi394769	Homo sapiens	mRNA for Sec24 protein (Sec24B isoform).	3090	55
1517	AAY120 49	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO: 362.	253	92
1517	gi415506	Helicobacter pylori J99	putative	75	29
1517	gi573852	Schizosaccharom yces pombe	putative pre-mrna splicing factor atp-dependent ma helicase	69	33
1518	AAB203 49	Homo sapiens	UYRQ Human vomeronasal-like receptor hVLR1 (long form).	1859	99
1518	AAG642 95	Homo sapiens	HELI- Human GTP-binding protein-coupled receptor GPRv31.	1859	99
1518	gi998858 5	Homo sapiens	putative pheromone receptor V1RL1 long form (V1RL1) mRNA, complete cds.	1859	99
1519	gi142499 09	Homo sapiens	clone IMAGE:3506174, mRNA, partial cds.	2759	90
1519	gi142499 07	Homo sapiens	clone IMAGE:3506145, mRNA, partial cds.	2759	90
1519	AAY993 55	Homo sapiens	GETH Human PRO1295 (UNQ664) amino acid sequence SEQ ID NO:54.	1265	100
1520	gi160416 86	Homo sapiens	hypothetical protein FLJ22393, clone MGC:16798 IMAGE:3916157, mRNA,	1470	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			complete cds.		
1520	gi104387 63	Homo sapiens	cDNA: FLJ22393 fis, clone HRC07880.	1463	99
1520	gi128534 19	Mus musculus	putative	1446	98
1521	AAR350 72	Homo sapiens	UYPR- Human t-complex associated testes expressed protein 1.	2576	97
1521	gi201910	Mus musculus	Tcte-1 peptide	1883	74
1521	gi730028 5	Drosophila melanogaster	CG14325 gene product	348	27
1522	gi128517 62	Mus musculus	putative	689	88
1522	AAG022 98	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6379.	382	100
1522	gi167690 34	Drosophila melanogaster	LD15209p	294	38
1523	AAQ905 26_aa1	Homo sapiens	OKLA- Human SIII 15 kDa subunit cDNA.	426	100
1523	AAW138 50	Homo sapiens	OKLA- Human RNA polymerase transcription factor elongin 15 kDa subunit.	426	100
1523	AAR750 87	Homo sapiens	OKLA- Human SIII 15 kDa subunit.	426	100
1524	gi128556 72	Mus musculus	putative	2165	85
1524	AAU174 29	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 994.	987	98
1524	AAG040 81	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 8162.	507	99
1525	AAW130 85	Homo sapiens	SAGA Human E2 ubiquinone binding enzyme.	667	88
1525	gi130971 95	Homo sapiens	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13), clone MGC:5063 IMAGE:2900313, mRNA, complete cds.	667	88
1525	gi126532 55	Homo sapiens	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13), clone MGC:8489 IMAGE:2822013, mRNA, complete cds.	667	88
1526	AAY872 71	Homo sapiens	INCY- Human signal peptide containing protein HSPP-48 SEQ ID NO:48.	471	86
1526	gi 171280 86	Corynebacterium glutamicum	cdsA	70	27
1526	gi125442 26	Corynebacterium glutamicum	RXA01894	70	27
1527	gi 133589 42	Macaca fascicularis	hypothetical protein	2660	97
1527	AAB875 87	Homo sapiens	GETH Human PRO1693.	2647	100
1527	AAU124 39	Homo sapiens	GETH Human PRO1693 polypeptide sequence.	2647	100
1528	AAB425	Homo sapiens	CURA- Human ORFX	2137	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	73		ORF2337 polypeptide sequence SEQ ID NO:4674.		
1528	gi128458 23	Mus musculus	putative	1792	95
1528	gi449506 3	Homo sapiens	Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.	1468	99
1529	gi158236 36	Homo sapiens	ALS2 mRNA, complete cds, long form.	8660	99
1529	gi160768 12	Homo sapiens	alsin mRNA, complete cds.	8646	99
1529	gi158236 40	Mus musculus	Als2	8005	91
1530	AAG641 71	Homo sapiens	TAKE Human profilin IIL.	750	100
1530	gi128042 13	Homo sapiens	profilin 2, clone MGC:1684 IMAGE:3533907, mRNA, complete cds.	750	100
1530	gi109525 20	Homo sapiens	profilin IIa (PFN2) mRNA, complete cds, alternatively spliced.	750	100
1531	AAG641 71	Homo sapiens	TAKE Human profilin IIL.	636	87
1531	gi128042 13	Homo sapiens	profilin 2, clone MGC:1684 IMAGE:3533907, mRNA, complete cds.	636	87
1531	gi109525 20	Homo sapiens	profilin IIa (PFN2) mRNA, complete cds, alternatively spliced.	636	87
1532	AAB949 52	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16482.	1830	99
1532	gi179077 91	Homo sapiens	TAIP-2 mRNA for TGF-beta induced apotosis protein 2, complete cds.	1830	99
1532	gi104330 16	Homo sapiens	cDNA FLJ11703 fis, clone HEMBA1005075.	1830	99
1533	gi141332 23	Homo sapiens	mRNA for KIAA0876 protein, partial cds.	4559	100
1533	gi691056 3	Homo sapiens	chromosome 19, BC335474 (CIT-HSPC_482H14), complete sequence.	4370	99
1533	gi139380 56	Mus musculus	Similar to KIAA0677 gene product	3313	73
1534	gi724319 1	Homo sapiens	mRNA for KIAA1405 protein, partial cds.	3986	99
1534	gi123136 47	Mus musculus	MmKIF17	3319	77
1534	gi410218 4	Homo sapiens	KIF3-related motor protein (KIF3X) mRNA, partial cds.	1084	90
1535	gi120533 11	Homo sapiens	mRNA; cDNA DKFZp434K229 (from clone DKFZp434K229); complete cds.	1600	100

SEQ ID		Speicies	Description	S score	Percent identity
1535	gi104389 86		cDNA: FLJ22557 fis, clone HSI01483.	1405	100
1535	gi152145 57		RIKEN cDNA 2410042D21 gene	1369	86
1536	gi122749 33	Homo sapiens	mRNA for alanine:glyoxylate aminotransferase 2 homolog 1, spilee form 1 (AGXT2L1 gene).	2018	100
1536	gi128367 24	Mus musculus	putative	1689	83
1536	gi158596 90	Homo sapiens	unnamed protein product	1189	66
1537	gi140178 47	Homo sapiens	mRNA for KIAA1815 protein, partial cds.	2117	100
1537	gi123141 59	Homo sapiens	Human DNA sequence from clone RP11-207C16 on chromosome 9p23-24.3. Contains the 3' end of the gene for a novel protein similar to C. elegans R06F6.8 (Sw:Q09417) (contains KIAA1432), the 3' end of the gene for a novel protein similar to predicted yeast, plant and worm proteins, ESTs, STSs and GSSs, complete sequence.	2117	100
1537	gi104399 48	Homo sapiens	cDNA: FLJ23309 fis, clone HEP11618.	1725	99
1538	gi104371 87	Homo sapiens	cDNA: FLJ21144 fis, clone CAS07955.	1919	99
1538	AAB953 60	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17664.	1912	99
1538	gi128518 10	Mus musculus	putative	1672	84
1539	gi332703 6	Homo sapiens	mRNA for KIAA0611 protein, partial cds.	4702	100
1539	gi139053 02	Mus musculus	Similar to ATPase, class II, type 9A	3961	98
1539	gi643496 8	Mus musculus	putative E1-E2 ATPase	3942	98
1540	AAB939 76	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14051.	2580	100
1540	gi104338 68	Homo sapiens	cDNA FLJ12401 fis, clone MAMMA1002796.	2580	100
1540	AAM698 00	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 30106.	1108	100
1541	AAB949 01	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16290.	1317	99
1541	gi104327 16	Homo sapiens	cDNA FLJ11457 fis, clone HEMBA1001522.	1317	99
1541	gi128531 91	Mus musculus	putative	887	62
1542	AAB735 07	Homo sapiens	INCY- Human transferase HTFS-14, SEQ ID NO:14.	1698	99
1542	gi165524 96	Homo sapiens	cDNA FLJ32390 fis, clone SKMUS1000177, weakly similar to PROTEIN-L- ISOASPARTATE O-	1698	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			METHYLTRANSFERASE (EC 2.1.1.77).		
1542	gi113231 92	Homo sapiens	Human DNA sequence from clone RP5-1022E24 on chromosome 20 Contains the 3' end of the OPRL1 gene encoding Opiate receptor-like 1 protein, the GPR8 gene encoding a G protein-coupled receptor, the KIAA0835 gene encoding a protein similar to the myelin transcription factor 1 (MYT1), a novel gene, 7 CpG islands, ESTs, STSs and GSSs, complete	1156	69
1543	AAB946 44	Homo sapiens	sequence. HELI- Human protein sequence SEQ ID NO:15536.	1941	100
1543	gi146258 75	Homo sapiens	mRNA for putative autophagy- related cysteine endopeptidase (AUTL1 gene).	1941	100
1543	gi140426 98	Homo sapiens	cDNA FLJ14867 fis, clone PLACE1002319.	1941	100
1544	gi996720 4	Macaca fascicularis	hypothetical protein	2621	100
1544	AAB883 51	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0076.	2616	99
1544	gi142725 56	Homo sapiens	unnamed protein product	2616	99
1545	gi120054 29	Homo sapiens	homeobox-containing transcripton factor HOXD1 (HOXD1) mRNA, complete cds.	1726	100
1545	gil10956	Homo sapiens	HOX D1 protein (HOXD1) gene, complete cds.	1726	100
1545	gi156802 45	Homo sapiens	homeo box D1, clone MGC:23144 IMAGE:4869019, mRNA, complete cds.	1718	99
1546	AAB953 66	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17677.	2511	100
1546	gi140425 38	Homo sapiens	cDNA FLJ14773 fis, clone NT2RP3004566, weakly similar to ZINC FINGER PROTEIN 84.	2511	100
1546	gi104386 30	Homo sapiens	cDNA: FLJ22301 fis, clone HRC04777.	2511	100
1547	gi155596 28	Homo sapiens	mitochondrial ribosomal protein S5, clone MGC:20735 IMAGE:4561399, mRNA, complete cds.	2262	99
1547	gi136208 81	Homo sapiens	MRPS5 mRNA for mitochondrial ribosomal protein S5, complete cds.	2262	99
1547	gi136208 83	Mus musculus	mitochondrial ribosomal protein S5	1821	79
1548	gi126979 11	Homo sapiens	mRNA for KIAA1683 protein, partial cds.	1772	72
1548	gi120532 39	Homo sapiens	mRNA; cDNA DKFZp434O194 (from clone DKFZp434O194); complete cds.	1690	49

SEQ		Speicies	Description	S score	Percent identity
1548	84		HUMA- Novel signal transduction pathway protein, Seq ID 1049.	1659	100
1549	gi104381 66		cDNA: FLJ21945 fis, clone HEP04702.	3738	99
1549	gi104419 56	Homo sapiens	clone PP384 unknown mRNA.	1196	99
1549	AAU222 52	Homo sapiens	HUMA- Human cardiovascular system antigen polypeptide SEQ ID No 1026.	480	98
1550	gi128524 81	Mus musculus	putative	1049	56
1550	AAB189 66	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	922	89
1550	AAB427 81	Homo sapiens	CURA- Human ORFX ORF2545 polypeptide sequence SEQ ID NO:5090.	513	100
1551	gi633040 1	Homo sapiens	mRNA for KIAA1199 protein, partial cds.	2521	97
1551	AAY257 93	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 12.	1919	96
1551	gi851818 8	Homo sapiens	mRNA full length insert cDNA clone EUROIMAGE 2155535.	1352	95
1552	AAB944 17	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15016.	1027	99
1552	gi104348 35	Homo sapiens	cDNA FLJ13018 fis, clone NT2RP3000685.	1027	99
1552	gi128375 67	Mus musculus	putative	972	92
1553	gil59294 11	Homo sapiens	clone IMAGE:4040789, mRNA, partial cds.	1369	100
1553	AAG034 90	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7571.	450	96
1553	gi128458 28	Mus musculus	putative	376	68
1554	gi998895 8	Homo sapiens	F-box protein FBX30 mRNA, complete cds.	1211	100
1554	gi140437 44	Homo sapiens	Similar to F-box only protein 6, clone MGC:14140 IMAGE:4054414, mRNA, complete cds.	1211	100
1554	AAB429 89	Homo sapiens	CURA- Human ORFX ORF2753 polypeptide sequence SEQ ID NO:5506.	675	99
1555	gi938026	Homo sapiens	Human mRNA for RanBP1 (Ran-binding protein 1), complete cds.	916	100
1555	AAB566 19	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1197.	904	99
1555	gi620083	Homo sapiens		904	99
1556	gi 133832 65	Homo sapiens	mRNA for actin related protein, complete cds.	1962	100
1556	gi165500 55	Homo sapiens	cDNA FLJ30784 fis, clone FEBRA2000881, moderately similar to ACTIN 6.	1950	99
1556	gi139383	Homo sapiens		1949	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
=_	19	·	IMAGE:3349184, mRNA, complete cds.		
1557	gi623545	Oryctolagus cuniculus	sarcoplasmic reticulum glycoprotein	2366	96
1557	gi164861	Oryctolagus cuniculus	sarcolumenin precursor	2307	97
1557	gi496325	Gallus gallus	53 kDa glycoprotein	2160	87
1558	AAB946 41	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15526.	1379	98
1558	AAG644 03	Homo sapiens	SHAN- Human paneth cell enhanced expression-like protein.	1379	98
1558	AAM940 28	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 126.	1379	98
1559	gi874531 5	Homo sapiens	putative GTP-binding protein (GTPBP2) mRNA, partial cds.	2742	99
1559	gi135610 07	Homo sapiens	Human DNA sequence from clone RP11-22124 on chromosome 6 Contains the 3' part of the POLH gene for DNA directed polymerase eta and the GTPBP2 gene for GTP binding protein 2, ESTs, STSs, GSSs and a CpG island, complete sequence.	2742	99
1559	gi874531	Mus musculus	putative GTP-binding protein	2731	99
1560	AAG026 53	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 6734.	425	100
1560	gi150804 59	Homo sapiens	clone MGC:9017 IMAGE:3860059, mRNA, complete cds.	425	100
1560	gi233792 0	Homo sapiens	Human syntaxin 7 mRNA, complete cds.	421	98
1561	AAB944 68	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15128.	4375	99
1561	gi104349 44	Homo sapiens	cDNA FLJ13089 fis, clone NT2RP3002108, weakly similar to DEC1 PROTEIN.	4375	99
1561	gi730058	Drosophila melanogaster	CG4845 gene product	1083	31
1562	AAU121 77	Homo sapiens	GETH Human PRO305 polypeptide sequence.	226	100
1562	AAY647 34	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:895.	226	100
1562	AAY814 87	Homo sapiens	FUJY Human cathepsin L2.	226	100
1563	gi120527 26	Homo sapiens	mRNA; cDNA DKFZp761N0411 (from clone DKFZp761N0411); complete cds.	2381	99
1563	gi142509 20	Homo sapiens	mRNA for SMC6 protein.	2374	99
1563	gi142509 22	Mus musculus	SMC6 protein	2163	88
1564	gi149705	Homo sapiens	mRNA for WDR9 protein	524	98

SEQ	Hit ID	Speicies	Description	S score	Percent
ID	-			J SCOLU	identity
1554	62		(WDR9 gene), form A.		
1564	gi149705 91		WDR9 protein, form A	363	79
1564	AAB344 87	Homo sapiens	HUMA- Human secreted protein BLAST search protein SEQ ID NO: 105.	169	52
1565	gi680832 9	•	mRNA; cDNA DKFZp434K0410 (from clone DKFZp434K0410); partial cds.	787	100
1565	AAB931 88	Homo sapiens	HELI- Human protein sequence SEQ ID NO:12140.	528	51
1565	AAB927 02	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11102.	528	51
1566	gi128038 41	Homo sapiens	Similar to retinoic acid induced 12, clone MGC:3373 IMAGE:3629369, mRNA, complete cds.	1576	99
1566	AAB267 93	Homo sapiens	UYFU- Human melanoma growth related factor-1 amino acid sequence.	1199	95
1566	gi132777 02	Mus musculus	retinoic acid induced 12	1182	75
1567	AAB534 05	Homo sapiens	HUMA- Human colon cancer antigen protein sequence SEQ ID NO:945.	1288	93
1567	gi29587	Homo sapiens	Human mRNA for carbonic anhydrase II (EC 4.2.1.1).	1288	93
1567	gi179795	Homo sapiens	Human carbonic anhydrase II mRNA, complete cds.	1288	93
1568	gi182146	Homo sapiens	eosinophil peroxidase (EPP) gene, exon 12 and complete cds.	3757	100
1568	gi31183	Homo sapiens	Human mRNA for eosinophil peroxidase.	3549	97
1568	gi 1 <i>777</i> 37 8	Mus musculus	eosinophil peroxidase	3376	89
1569	AAB941 83	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14500.	2405	100
1569	gi104342 15	Homo sapiens	cDNA FLJ12618 fis, clone NT2RM4001666, weakly similar to HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.	2405	100
1569	gi135439 55	Homo sapiens	Similar to hypothetical protein FLJ12618, clone MGC:12994 IMAGE:3504996, mRNA, complete cds.	2082	94
1570	AAB939 04	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13862.	2499	99
1570	gi142862 14	Homo sapiens	hypothetical protein FLJ12150, clone MGC:15043 IMAGE:3634992, mRNA, complete cds.	2499	99
1570	gi104335 59	Homo sapiens	cDNA FLJ12150 fis, clone MAMMA1000422.	2499	99
1571	gi768460 5	Mus musculus	smoothelin B	640	54
1571	gi768460	Mus musculus	smoothelin A	640	54

SEQ . ID	Hit ID	Speicies	Description	S score	Percent identity
	4				
1571	gi754725 8	Mus musculus	smoothelin small isoform S1	640	54
1572	AAB950 33	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16784.	1174	100
1572	gi104334 42	Homo sapiens	cDNA FLJ12056 fis, clone HEMBB1002050.	1174	100
1572	gi530876	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 468; amino acid feature: globular protein domain, aa 32 265	142	26
1573	gi128572 47	Mus musculus	putative	2111	92
1573	gi107279 09	Drosophila melanogaster	CG6169 gene product	688	48
1573	gi238891 1	Schizosaccharom yces pombe	hypothetical PSU1-like protein	585	47
1574	AAB419 54	Homo sapiens	CURA- Human ORFX ORF1718 polypeptide sequence SEQ ID NO:3436.	1765	97
1574	AAB427 73	Homo sapiens	CURA- Human ORFX ORF2537 polypeptide sequence SEQ ID NO:5074.	1134	93
1574	gi175122 54	Homo sapiens	hypothetical protein FLJ21156, clone MGC:29459 IMAGE:5020837, mRNA, complete cds.	1089	100
1575	AAY400 90	Homo sapiens	HUMA- Peptide sequence derived from a human secreted protein.	918	98
1575	gi128546 39	Mus musculus	putative	443	69
1575	gi170661 07	Homo sapiens	partial TTN gene for titin.	86	25
1576	gi104384 73	Homo sapiens	cDNA: FLJ22184 fis, clone HRC00983.	3291	99
1576	gi102417 12	Homo sapiens	mRNA; cDNA DKFZp761K0816 (from clone DKFZp761K0816).	1238	99
1576	gi600118	Zea mays	extensin-like protein	666	33
1577	gi165492 61	Homo sapiens	cDNA FLJ30107 fis, clone BNGH41000198, weakly similar to TETRACYCLINE RESISTANCE PROTEIN, CLASS E.	1453	100
1577	gi147150 55	Homo sapiens	Similar to RIKEN cDNA 1110002C08 gene, clone MGC:9564 IMAGE:3872267, mRNA, complete cds.	1453	100
1577	gi128338 45	Mus musculus	putative	1339	90
1578	gi104376 69	Homo sapiens	cDNA: FLJ21551 fis, clone COL06266.	1925	99
1578	AAE0179 1	Homo sapiens	HUMA- Human gene 22 encoded secreted protein HOHDF66, SEQ ID NO:112.	1840	99
1578	AAB417	Homo sapiens	CURA- Human ORFX	1473	99

SEQ ID		Speicies	Description	S score	Percent identity
	11		ORF1475 polypeptide sequence SEQ ID NO:2950.		Identity
1579	gi143279 15	•	clone MGC:11186 IMAGE:3844322, mRNA, complete cds.	3446	100
1579	gi140431 03	Homo sapiens	clone MGC:15388 IIVIAGE:3350378, mRNA, complete cds.	3446	100
1579	AAB947 22	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15741.	3439	99
1580	gi134461 90	Homo sapiens	Human DNA sequence from clone RP4-717M23 on chromosome 20 Contains the gene encoding a CRP2 binding protein (CRP2BP), a pseudogene, ESTs, STSs, GSSs and CpG islands, complete sequence.	3955	97
1580	gi140431 03	Homo sapiens	clone MGC:15388 IMAGE:3350378, mRNA, complete cds.	3952	97
1580	gi143279 15	Homo sapiens	clone MGC:11186 IMAGE:3844322, mRNA, complete cds.	3281	96
1581	gi165516 10	Homo sapiens	cDNA FLJ31697 fis, clone NT2RI2005851, weakly similar to PLECTIN.	1911	99
1581	AAM664 35	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 26741.	588	100
1581	AAM540 44	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 26149.	588	100
1582	AAU204 43	Homo sapiens	HUMA- Human secreted protein, Seq ID No 435.	940	94
1582	AAM937 13	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3654.	756	100
1582	gi171490 39	Homo sapiens	MTO1-like protein gene, complete cds; nuclear gene for mitochondrial product.	756	100
1583	ABB1222 0	Homo sapiens	HYSE- Human peroxisomal Cadependent solute carrier homologue, SEQ:2590.	344	100
1583	gi128536 85	Mus musculus	putative putative	168	52
1583	AAM800 61	Homo sapiens	HYSE- Human protein SEQ ID NO 3707.	165	55
1584	gi143491 25	Homo sapiens	mRNA for alpha2- glucosyltransferase (ALG10 gene).	716	93
1584	gi351345 1	Rattus norvegicus	potassium channel regulator 1	681	90
584	AAB257 15	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 3 SEQ ID NO:104.	617	93
585	gi126979 39	Homo sapiens	mRNA for KIAA1697 protein, partial cds.	1904	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1585	gi 1 0 4 4 0 2 4 9	Homo sapiens	cDNA: FLJ23529 fis, clone LNG06042.	1897	99
1585	gi729341 5	Drosophila melanogaster	Dhc16F gene product	786	44
1586	AAZ3583 4_aa1	Homo sapiens	INCY- Human vesicle trafficking protein 2 encoding cDNA.	804	84
1586	AAB936 64	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13188.	804	84
1586	AAY499 59	Homo sapiens	INCY- Human vesicle trafficking protein 2.	804	84
1587	AAY765 61	Homo sapiens	META- Human ovarian tumor EST fragment encoded protein 57.	623	92
1587	gi136235 85	Homo sapiens	Similar to RIKEN cDNA 1500034E06 gene, clone MGC:14151 IMAGE:3690202, mRNA, complete cds.	623	92
1587	gi128586 76	Mus musculus	putative	595	88
1588	AAU206 47	Homo sapiens	HUMA- Human secreted protein, Seq ID No 639.	927	99
1588	AAU205 23	Homo sapiens	HUMA- Human secreted protein, Seq ID No 515.	927	99
1588	AAB954 32	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17854.	927	99
1589	AAB591 91	Homo sapiens	UYCO Human NADE.	293	57
1589	gi845289 4	Homo sapiens	p75NTR-associated cell death executor (NADE) mRNA, complete cds.	293	57
1589	gi189379	Homo sapiens	Human unknown protein from clone pHGR74 mRNA, complete cds.	293	57
1590	AAG017 16	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5797.	894	99
1590	AAY824 73	Homo sapiens	LLTL- Human APG12 protein sequence.	724	100
1590	gi411573	Homo sapiens	mRNA for Apg12, complete cds.	724	100
1591	AAW877 01	Homo sapiens	INCY- A human membrane fusion protein designated SYTAX1.	1357	99
1591	gi420024	Homo sapiens	H.sapiens gene from PAC 42616, similar to syntaxin 7.	1325	100
1591	gi147150 19	Mus musculus	Unknown (protein for MGC:6471)	1280	93
1592	AAA540 89 aa1	Homo sapiens	GETH PRO211 cDNA.	1944	87
1592	AAB530 75	Homo sapiens	GETH Human angiogenesis- associated protein PRO211, SEQ ID NO:57.	1944	87
1592	AAB612 31	Homo sapiens	MILL- Human TANGO 331 protein.	1944	87
1593	gi668159	Homo sapiens	HSJ2 mRNA for DnaJ homolog, complete cds.	1567	93
1593	gi 128032	Homo sapiens	MRJ gene for a member of the	1567	93

SEC	Hit ID	Speicies	Description	S score	Domount
D				3 score	Percent identity
	63		DNAJ protein family, clone MGC:1152 IMAGE:3346070, mRNA, complete cds.		
1593	66	Homo sapiens	INCY- Human DnaJ-like protein, HSPJ2.	1516	98
1594	58	Homo sapiens	mRNA for HMG-box transcription factor TCF-3, complete cds.	3096	100
1594	8	Mus musculus	TCF-3 protein	2934	95
1594	gi142799 82	Xenopus laevis	T-cell factor XTCF-3	2195	77
1595	gi163070 74	Homo sapiens	hypothetical protein FLJ22724, clone MGC:16791 IMAGE:3900548, mRNA, complete cds.	932	100
1595	gi104392 25	Homo sapiens	cDNA: FLJ22724 fis, clone HSI14868.	932	100
1595	gi128543 96	Mus musculus	putative	618	68
1596	gi100472 29	Homo sapiens	mRNA for KIAA1577 protein, partial cds.	3874	100
1596	gi795928 3	Homo sapiens	mRNA for KIAA1511 protein, partial cds.	3002	74
1596	gi104404 18	Homo sapiens	mRNA for FLJ00044 protein, partial cds.	2010	63
1597	AAY131 17	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 131.	268	100
1597	gi138164 07	Sulfolobus solfataricus	Dehydrogenase, putative	66	43
1597	gi151400 82	Sinorhizobium meliloti	HYPOTHETICAL PROTEIN	66	37
1598	gi169437 20	Homo sapiens	mRNA for SOX7 protein.	2106	100
1598	gi165503 14	Homo sapiens	cDNA FLJ30994 fis, clone HLUNG1000076, highly similar to Mus musculus mRNA for mSox7.	2106	100
1598	gi132791 64	Homo sapiens	Similar to SRY-box containing gene 7, clone MGC:10895 IMAGE:3622936, mRNA, complete cds.	2106	100
1599	gi176461 46	Homo sapiens	B lymphocyte activation-related protein mRNA, complete cds.	1111	97
1599	gi120062 23	Homo sapiens	NPD017 mRNA, complete cds.	1111	97
1599	gi151267 45	Homo sapiens	hypothetical protein FLJ21174, clone MGC:5372 IMAGE:3445403, mRNA, complete cds.	1105	97
1600	gi143288 79	Homo sapiens	CUB domain containing protein 1 (CDCP1) mRNA, complete cds.	4394	100
1600	15	Homo sapiens	cDNA: FLJ22969 fis, clone KAT10759.	4385	99
1600	AAY914	Homo sapiens	HUMA- Human secreted protein	3633	98

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	56		sequence encoded by gene 6 SEQ ID NO:129.		
1601	gi120528 46	Homo sapiens	mRNA; cDNA DKFZp564K2464 (from clone DKFZp564K2464); complete cds.	2152	100
1601	gi126527 23	Homo sapiens	clone MGC:3295 IMAGE:3508204, mRNA, complete cds.	2035	100
1601	AAW790 88	Homo sapiens	GEMY Human secreted protein bi129_2.	1115	100
1602	gi508161 0	Mus musculus	huntington yeast partner C	4295	94
1602	gi156368 98	Gallus gallus	formin binding protein 11- related protein	2507	55
1602	gi508160 8	Mus musculus	formin binding protein 11	2505	54
1603	gi508161 0	Mus musculus	huntington yeast partner C	4046	90
1603	gi680803 8	Homo sapiens	mRNA; cDNA DKFZp434H2121 (from clone DKFZp434H2121); partial cds.	2341	100
1603	gi156368 98	Gallus gallus	formin binding protein 11- related protein	2339	52
1604	AAB950 53	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16855.	680	100
1604	gi104335 25	Homo sapiens	cDNA FLJ12122 fis, clone MAMMA1000129.	680	100
1604	AAE0609 6	Homo sapiens	HUMA- Human gene 56 encoded secreted protein HRABA80, SEQ ID NO:158.	151	48
1605	AAB943 09	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14777.	2318	99
1605	gi104345 01	Homo sapiens	cDNA FLJ12800 fis, clone NT2RP2002079, weakly similar to HISTONE H1, GONADAL.	2318	99
1605	gi173912 25	Mus musculus	Similar to hypothetical protein FLJ12800	1515	70
1606	AAG645 02	Homo sapiens	UYFU- Human EPIP2 (endometrial progesterone- induced protein).	1914	100
1606	gi173902 89	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:9290 IMAGE:3883843, mRNA, complete cds.	1914	100
1606	gi134360 74	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:10519 IMAGE:3938160, mRNA, complete cds.	1914	100
1607	gi532680 2	Homo sapiens	phosphoserine aminotransferase (PSA) mRNA, complete cds.	1673	100
1607	AAG645 02	Homo sapiens	UYFU- Human EPIP2 (endometrial progesterone- induced protein).	1616	87
1607	gi173902 89	Homo sapiens	Similar to phosphoserine aminotransferase, clone MGC:9290 IMAGE:3883843,	1616	87

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			mRNA, complete cds.		- tubilitity
1608	gi134477 61	•	cystatin and DUF19 domain- containing protein 1 (CSDUFD1) mRNA, complete cds.	736	100
1608	AAG745	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5277.	570	100
1608	AAB937 98	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13564.	281	47
1609	gi104402 30	Homo sapiens	cDNA: FLJ23514 fis, clone LNG04628.	2005	100
1609	gi128529 73	Mus musculus	putative	1509	69
1609	gi124077 49	Arabidopsis thaliana	initiation factor 3a	138	22
1610	AAY649 94	Homo sapiens	GEST Human 5' EST related polypeptide SEQ ID NO:1155.	372	100
1610	AAM008 52	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 215.	69	39
1610	gi332565	Orf virus	ORF2	68	42
1611	gi104397 05	Homo sapiens	cDNA: FLJ23121 fis, clone LNG07996.	3137	100
1611	AAB949 96	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16625.	1618	99
1611	gi104332 57	Homo sapiens	cDNA FLJ11889 fis, clone HEMBA1007251, weakly similar to Homo sapiens F-box protein FBX29 (FBX29) mRNA.	1618	99
1612	AAB952 34	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17375.	3584	100
1612	gi104346 74	Homo sapiens	cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mRNA.	3584	100
1612	gi505203 1	Mus musculus	axotrophin	2983	85
1613	gi965095 4	Mus musculus	beta-1,6-N- acetylglucosaminyltransferase B	1254	73
1613	AAV160 00_aa1	Homo sapiens	LJOL- Human beta-1,6-N-acetylglucosaminyltransferase (IGnT) encoding cDNA.	1044	65
1613	AAQ892 01_aa1	Homo sapiens	LJOL- I-branching enzyme cDNA.	1044	65
1614	gi100473 11	Homo sapiens	mRNA for KIAA1617 protein, partial cds.	4792	100
1614	gi663535 3	Homo sapiens	RU1 (RU1) mRNA, complete cds.	2467	55
1614	gi157790 95	Homo sapiens	Similar to RU1, clone MGC:3342 IMAGE:3029598, mRNA, complete cds.	2467	55
1615	gi468069 3	Homo sapiens	CGI-27 protein mRNA, complete cds.	1414	92
1615	gi175117 62	Homo sapiens	CGI-27 protein, clone MGC:31852 IMAGE:4851517, mRNA, complete cds.	1414	92
1615	gi170463	Homo sapiens	C21 orf19-like protein mRNA,	1414	92

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	03		complete cds.		
1616	gi100472 69	Homo sapiens	mRNA for KIAA1597 protein, partial cds.	4638	99
1616	gi136470 69	Mus musculus	synaptotagmin-like protein 2-a delta 2S-III	3717	81
1616	gi136470 09	Mus musculus	synaptotagmin-like protein 2-a	3666	77
1617	AAM937 72	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3778.	1945	98
1617	ABB1173	Homo sapiens	HYSE- Human granuphilin-a homologue, SEQ ID NO:2101.	1945	98
1617	gi159302 18	Homo sapiens	synaptotagmin-like 2, clone MGC:9588 IMAGE:3887570, mRNA, complete cds.	1945	98
1618	gi776873 9	Homo sapiens	genomic DNA, chromosome 21q, section 89/105.	3747	100
1618	gi128573 81	Mus musculus	putative	1233	78
1618	gi488438 6	Homo sapiens	mRNA; cDNA DKFZp586F0422 (from clone DKFZp586F0422); partial cds.	870	80
1619	AAR225 46	Homo sapiens	NEUR- Truncated Dopamine D1 receptor encoded by pseudogene clone GL-39.	1157	93
1619	AAR210 82	Homo sapiens	NEUR- Dopamine D1 receptor encoded by clone GL-30.	1028	85
1619	gi32049	Homo sapiens	Human HD5DR gene for D5 dopamine receptor.	1028	85
1620	AAE1032 9	Homo sapiens	INCY- Human transporter and ion channel-6 (TRICH-6) protein.	1339	92
1620	AAM258 77	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1392.	1284	100
1620	gi128565 98	Mus musculus	putative	382	64
1621	AAB942 78	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14707.	1465	100
1621	gi135434 48	Homo sapiens	hypothetical protein FLJ12750, clone MGC:4691 IMAGE:3533384, mRNA, complete cds.	1465	100
1621	gi104344 28	Homo sapiens	cDNA FLJ12750 fis, clone NT2RP2001168, weakly similar to VERPROLIN.	1465	100
1622	AAY026 69	Homo sapiens	HUMA- Human secreted protein encoded by gene 20 clone HMKAH10.	288	100
1622	gi751042	Caenorhabditis elegans	hypothetical protein Y6G8.1 - Caenorhabditis elegans >	66	37
1623	AAB953 93	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17745.	795	100
1623	gi104352 17	Homo sapiens	cDNA FLJ13265 fis, clone OVARC1000937.	795	100
1623	AAB570 19	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1597.	275	91
1624	AAG892	Homo sapiens	GEST Human secreted protein,	936	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	81		SEQ ID NO: 401.		
1624	AAU159 32	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 885.	936	100
1624	gi104391 93	Homo sapiens	cDNA: FLJ22700 fis, clone HSI12073.	936	100
1625	gi128579 64	Mus musculus	putative	1533	86
1625	gi102413 97	Homo sapiens	Human DNA sequence from clone RP3-336K20 on chromosome 6 Contains parts of 2 genes for novel proteins, ESTs, STSs and GSSs, complete sequence.	964	100
1625	gi165523 03	Homo sapiens	cDNA FLJ32234 fis, clone PLACE6004687.	721	97
1626	gi104381 58	Homo sapiens	cDNA: FLJ21940 fis, clone HEP04512.	3307	99
1626	AAG737 12	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4476.	455	98
1626	gi104406 14	Oryza sativa	putative ATP-dependent RNA helicase	452	32
1627	gi104378 37	Homo sapiens	cDNA: FLJ21687 fis, clone COL09385.	1466	100
1627	gi618017 8	Homo sapiens	transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha-1 subunit gene, partial cds, complete sequence.	1182	98
1627	ABB1156 1	Homo sapiens	HYSE- Human JM10 protein homologue, SEQ ID NO:1931.	947	100
1628	AAM252 27	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:742.	2069	100
1628	AAB853 62	Homo sapiens	INCY- Human phosphatase (PP) (clone ID 2522707CD1).	2021	100
1628	gi150805 05	Homo sapiens	Similar to RIKEN cDNA 5730568A12 gene, clone MGC:17651 IMAGE:3857480, mRNA, complete cds.	1907	100
1629	gi656284 5	Rattus norvegicus	type A/B hnRNP p40	1661	91
1629	gi337727 9	Rattus norvegicus	AIF-C1	1654	91
1629	gi181427 4	Homo sapiens	Human apobec-1 binding protein 1 mRNA, complete cds.	1631	92
1630	AAY360 83	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 468.	430	98
1630	AAG005 83	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4664.	414	100
1630	gi358259	Cnemidophorus	NADH dehydrogenase subunit 4	66	37

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	4	tigris			
1631	AAB102 84	Homo sapiens	GEMY Human fetal placenta protein fragment AC175_2i.	852	94
1631	gi398346 3	Homo sapiens	microfibril-associated glycoprotein 2 (MAGP2) gene, exon 10 and complete cds.	852	94
1631	gi135434 86	Homo sapiens	Microfibril-associated glycoprotein-2, clone MGC:14490 IMAGE:4247343, mRNA, complete cds.	852	94
1632	gi161984 56	Homo sapiens	Similar to RIKEN cDNA 0610040E02 gene, clone MGC:17973 IMAGE:3919892, mRNA, complete cds.	1339	99
1632	AAY026 61	Homo sapiens	HUMA- Human secreted protein encoded by gene 12 clone HFTCU19.	1142	99
1632	gi167406 89	Mus musculus	RIKEN cDNA 0610040E02	1059	77
1633	AAB530 94	Homo sapiens	GETH Human angiogenesis- associated protein PRO826, SEQ ID NO:158.	510	100
1633	AAB509 16	Homo sapiens	GETH Human PRO826 protein.	510	100
1633	AAB652 04	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	510	100
1634	AAB530 94	Homo sapiens	GETH Human angiogenesis- associated protein PRO826, SEQ ID NO:158.	413	85
1634	AAB509 16	Homo sapiens	GETH Human PRO826 protein.	413	85
1634	AAB652 04	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	413	85
1635	gi104390 08	Homo sapiens	cDNA: FLJ22573 fis, clone HSI02387.	1937	100
1635	AAM878 76	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:15469.	187	45
1635	gi133464	Xenopus laevis	APEG precursor protein	93	37
1636	gi104390 08	Homo sapiens	cDNA: FLJ22573 fis, clone HSI02387.	578	100
1636	AAM878 76	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:15469.	155	94
1636	gi394136	Homo sapiens	I-REL gene, exon 12 and complete cds.	79	37
1637	AAM938 71	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3980.	3761	99
1637	gi143311 31	Homo sapiens	scinderin mRNA, complete cds.	3749	99
1637	AAR804 81	Homo sapiens	NAKA/ Recombinant human adseverin.	3527	92
1638	gi104369 70	Homo sapiens	cDNA: FLJ20991 fis, clone CAE02103.	239	67

SEQ	Hit ID	Speicies	Description	S score	Percent
ID	1.51500			}	identity
1638	gi646024 0	Deinococcus radiodurans	DNA-binding response regulator	86	37
1638	gi167548 77	Cyprinus carpio	Smad4 type4	79	27
1639	AAY849 01	Homo sapiens	INCY- A human proliferation and apoptosis related protein.	2821	95
1639	gi120532 25	Homo sapiens	mRNA; cDNA DKFZp434P2235 (from clone DKFZp434P2235); complete cds.	2806	95
1639	gi37330	Homo sapiens	H.sapiens mRNA for tre oncogene (clone 210).	2053	78
1640	AAY849 01	Homo sapiens	INCY- A human proliferation and apoptosis related protein.	2846	96
1640	gi120532 25	Homo sapiens	mRNA; cDNA DKFZp434P2235 (from clone DKFZp434P2235); complete cds.	2834	95
1640	gi37330	Homo sapiens	H.sapiens mRNA for tre oncogene (clone 210).	2050	77
1641	gi139362 85	Mus musculus	TRH4	1522	77
1641	gi128455 40	Mus musculus	putative	1520	77
1641	AAU007 82	Homo sapiens	INCY- Human apoptosis protein, APOP-2.	1345	98
1642	gi172253 31	Homo sapiens	MY0876G05 protein (MY876) mRNA, complete cds.	1209	100
1642	gi120020 42	Homo sapiens	brain my048 protein mRNA, complete cds.	1209	100
1642	gi176461 46	Homo sapiens	B lymphocyte activation-related protein mRNA, complete cds.	911	78
1643	gi104373 07	Homo sapiens	cDNA: FLJ21240 fis, clone COL01132.	2090	100
1643	AAB747 30	Homo sapiens	INCY- Human membrane associated protein MEMAP-36.	856	42
1643	AAY949 06	Homo sapiens	GEMY Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	853	42
1644	AAY144 48	Homo sapiens	HUMA- Human secreted protein encoded by gene 38 clone HFGAH44.	316	100
1645	gi103344 43	Homo sapiens	Human DNA sequence from clone RP11-291L22 on chromosome 10 Contains the 3' end of the HSD17B7 (hydroxysteroid (17-beta) dehydrogenase 7) gene, part of a gene similar to CDC10 (cell division cycle 10, S. cerevisiae, homolog), part of a novel gene, a novel pseudogene, STSs, GSSs and a CpG Island, complete sequence.	256	100
1645	gi560623	human, fetal lung, mRNA, 2314 nt]. [Homo	hCDC10=CDC10 homolog	236	72

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
		sapiens			
1645	gi286460	Mus musculus	CDC10	236	72
1646	AAB189 69	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	1707	95
1646	AAB495 04	Homo sapiens	HUMA- Clone HNTMH27.	1370	94
1646	gi163075	Mus musculus	RIKEN cDNA 2210021G21 gene	1325	90
1647	gi100472 31	Homo sapiens	mRNA for KIAA1578 protein, partial cds.	2083	95
1647	gi684119 4	Homo sapiens	HSPC272	281	81
1647	gi108003 75	Caenorhabditis elegans	Hypothetical protein Y67D8C.5	192	21
1648	gi143493 55	Homo sapiens	hypothetical protein FLJ23323, clone MGC:14873 IMAGE:3948222, mRNA, complete cds.	1771	100
1648	gi104399 69	Homo sapiens	cDNA: FLJ23323 fis, clone HEP12456.	1771	100
1648	gi128525 02	Mus musculus	putative	1540	65
1649	AAY413 60	Homo sapiens	HUMA- Human secreted protein encoded by gene 53 clone HJPAD75.	490	100
1649	AAM244 06	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1931.	335	100
1649	AAY414 70	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 53.	84	100
1650	AAY413 60	Homo sapiens	HUMA- Human secreted protein encoded by gene 53 clone HJPAD75.	267	63
1650	AAM244 06	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1931.	199	90
1650	AAY414 70	Homo sapiens	HUMA- Fragment of human secreted protein encoded by gene 53.	84	100
1651	gi165503 12	Homo sapiens	cDNA FLJ30993 fis, clone HLUNG1000064, weakly similar to KARYOGAMY PROTEIN KAR4.	2449	100
1651	gi163068 92	Homo sapiens	clone MGC:2902 IMAGE:3010654, mRNA, complete cds.	2449	100
1651	gi139385 95	Homo sapiens	Similar to CG7818 gene product, clone MGC:4531 IMAGE:3010654, mRNA, complete cds.	2449	100
1652	AAG671 58	Homo sapiens	MILL- Amino acid sequence of a human 20685 transporter polypeptide.	1586	100
1652	gi132741 22	Homo sapiens	Human DNA sequence from clone RP1-55C23 on chromosome 6q22.3-23.3 Contains the VNN1 and VNN2	1586	100

SEQ	Hit ID	Speicies	Description	S score	Percent
			genes for vanin 1 and 2, the gene for vanin 3 (VNN3), a HLF (hepatic leukemia factor) pseudogene, a CCNG1 (cyclin G1) pseudogene, the 3' part of a		identity
1652	c:157050	177	novel gene, ESTs, GSSs, and STSs, complete sequence.		
L	gi157958 17		unnamed protein product	1586	100
1653	AAB541 63	Homo sapiens	HUMA- Human pancreatic cancer antigen protein sequence SEQ ID NO:615.	322	63
1653	gi180886		Human colipase mRNA, complete cds.	322	63
1653	gi173897 64		colipase, pancreatic, clone MGC:23801 IMAGE:4251084, mRNA, complete cds.	322	63
1654	AAU171 98	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 763.	1359	100
1654	gi159874 93	Homo sapiens	tumor endothelial marker 6 (TEM6) mRNA, complete cds.	1359	100
1654	gi143257 70	Homo sapiens	mRNA for thyroid specific PTB domain protein, complete cds.	1359	100
1655	AAG011 18	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5199.	360	100
1655	gi154189 66	Xenopus laevis	annexin 4	66	44
1656	gi104370 31	Homo sapiens	cDNA: FLJ21034 fis, clone CAE09073.	1403	100
1656	gi163071 59	Mus musculus	Unknown (protein for IMAGE:3493084)	1060	50
1656	gi138795 51	Mus musculus	Unknown (protein for IMAGE:3709003)	1060	50
1657	AAM800 47	Homo sapiens	HYSE- Human protein SEQ ID NO 3693.	820	91
1657	AAM790 63	Homo sapiens	HYSE- Human protein SEQ ID NO 1725.	820	89
1657	ABB1214 4	Homo sapiens	HYSE- Human HSPP-29 protein homologue, SEQ ID NO:2514.	820	91
1658	gi581382 3	Homo sapiens	SUII isolog mRNA, complete cds.	470	86
1658	gi450281	Homo sapiens	suilisol mRNA, complete cds.	470	86
1658	gi142505 20	Homo sapiens	putative translation initiation factor, clone MGC:15684 IMAGE:3350981, mRNA, complete cds.	470	86
1659	gi168771 87	Homo sapiens	clone MGC:17299 IMAGE:3845811, mRNA, complete cds.	1094	100
1659	AAY129 52	Homo sapiens	HUMA- Amino acid sequence of a human secreted peptide.	362	98
1659	gi239437 6	Cercopithecus aethiops	thromboxane A2 receptor; TBXA2R	94	29
1660	gi104389 46	Homo sapiens	cDNA: FLJ22527 fis, clone HRC12820.	1017	97
1660	gi165493	Homo sapiens	cDNA FLJ30149 fis, clone	665	90

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	12		BRACE2000280, weakly similar to MNN4 PROTEIN.		
1660	gi729920	Drosophila melanogaster	CG16789 gene product	519	42
1661	AAB955 72	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18221.	2231	100
1661	gi 104359 27	Homo sapiens	cDNA FLJ13798 fis, clone THYRO1000124.	2231	100
1661	gi128516 20	Mus musculus	putative	1745	77
1662	AAY482 56	Homo sapiens	META- Human prostate cancerassociated protein 42.	242	75
1662	gi382085 7	Euglena spirogyra	maturase-like protein	81	30
1662	gi115596 49	Leuconostoc mesenteroides	dextransucrase Dsrb742	79	39
1663	gi140177 83	Homo sapiens	mRNA for KIAA1783 protein, partial cds.	2287	100
1663	AAU171 93	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 758.	1725	100
1663	AAY578 95	Homo sapiens	INCY- Human transmembrane protein HTMPN-19.	1634	100
1664	gi104369 92	Homo sapiens	cDNA: FLJ21007 fis, clone CAE03871.	3436	100
1664	gi137849 43	Mus musculus	Unknown (protein for MGC:11761)	2930	84
1664	gi178628 68	Drosophila melanogaster	RE01471p	308	28
1665	AAG933 18	Homo sapiens	NISC- Human protein HP10505.	465	100
1665	gi163068 68	Homo sapiens	mitochondrial ribosomal protein S21, clone MGC:2680 IMAGE:2819715, mRNA, complete cds.	465	100
1665	gi136209 11	Homo sapiens	MRPS21 mRNA for mitochondrial ribosomal protein S21, complete cds.	465	100
1666	AAU276 52	Homo sapiens	ZYMO Human protein AFP213641.	1484	100
1666	gi158624 70	Homo sapiens	unnamed protein product	1484	100
1666	AAE0607	Homo sapiens	HUMA- Human gene 31 encoded secreted protein HBJLF01, SEQ ID NO:133.	1284	100
1667	AAW781 32	Homo sapiens	HUMA- Human secreted protein encoded by gene 7 clone HPEBD85.	246	100
1668	AAM502 13	Homo sapiens	CURA- Human interleukin-11- like AMF7 C-terminal polypeptide.	2219	99
1668	gi165489 21	Homo sapiens	unnamed protein product	2219	99
1668	AAB948 03	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15937.	1358	100
1669	gi120533	Homo sapiens	mRNA; cDNA DKFZp586O0222 (from clone	2747	100

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SEQ	Hit ID	Speicies	Description	S score	Percent
·			DKFZp586O0222); complete cds.		identity
1669	gi936853 8	Homo sapiens	mRNA full length insert cDNA clone EUROIMAGE 1987170.	2687	98
1669	gi996590 5	Mus musculus	synembryn	2383	86
1670	gi104402 80	Homo sapiens	DNA: FLJ23554 fis, cione LNG09359.	3757	100
1670	gi128552 47	Mus musculus	putative	1339	64
1670	gi146026 09	Homo sapiens	hypothetical protein FLJ23554, clone MGC:14866 IMAGE:3946091, mRNA, complete cds.	1236	99
1671	gi104417 32	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds.	4286	99
1671	gi173828 94	Homo sapiens	unnamed protein product	3899	93
1671	gi173828 82	Mus musculus	unnamed protein product	3477	84
1672	AAB941 18	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14362.	1936	100
1672	gi104341 08	Homo sapiens	cDNA FLJ12552 fis, clone NT2RM4000712, moderately similar to Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA.	1936	100
1672	AAB958 06	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18793.	1930	99
1673	AAB482 93	Homo sapiens	UYYA Human ZF5 protein.	1407	80
1673	gi645611 4	Mus musculus	F-box protein FBX16	1407	80
1673	ABB1559 0	Homo sapiens	HUMA- Human nervous system related polypeptide SEQ ID NO 4247.	831	90
1674	gi100471 63	Homo sapiens	mRNA for KIAA1549 protein, partial cds.	7563	100
1674	AAM791 57	Homo sapiens	HYSE- Human protein SEQ ID NO 1819.	948	28
1674	AAM801 41	Homo sapiens	HYSE- Human protein SEQ ID NO 3787.	941	30
1675	gi167686 54	Drosophila melanogaster	HL01494p	911	39
1675	gi729229 9	Drosophila melanogaster	CG1271 gene product	888	38
1675	gi498199 5	Thermotoga maritima	glycerol kinase	846	38
1676	gi128528 37	Mus musculus	putative	892	69
1676	gi322823 7	Homo sapiens	UHS KerB gene.	871	71
676	gi200962	Mus musculus	serine 1 ultra high sulfur protein	827	65
1677	gi173901 82	Homo sapiens	clone IMAGE:4797244, mRNA, partial cds.	1694	99
677	AAY761	Homo sapiens	HUMA- Human secreted protein	863	99

SEQ ID	Hit ID	Speicles	Description	S score	Percent identity
10	77		encoded by gene 54.		
677	AAY043 06	Homo sapiens	HUMA- Human secreted protein encoded by gene 14.	328	93
678	gi568941	Homo sapiens	mRNA for KIAA 1040 protein, partial cds.	2793	99
678	gi107286 60	Drosophila melanogaster	CG8683 gene product	2736	48
678	AAY023 67	Homo sapiens	ONOY Polypeptide identified by the signal sequence trap method.	2663	99
679	gi104399 64	Homo sapiens	cDNA: FLJ23320 fis, clone HEP12381.	3605	99
1679	AAG744 99	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:5263.	623	95
679	gi128306 79	Drosophila helvetica	putative transposase	220	24
680	gi104382	Homo sapiens	cDNA: FLJ22028 fis, clone HEP08589.	2454	100
1680	AAB736 81	Homo sapiens	INCY- Human oxidoreductase protein ORP-14.	2337	100
1680	gi729865	Drosophila melanogaster	CG10721 gene product	882	43
1681	AAB943 93	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14957.	3231	99
1681	gi104347 65	Homo sapiens	cDNA FLJ12973 fis, clone NT2RP2006023.	3231	99
1681	gi128604 50	Mus musculus	putative	1177	64
1682	gi104377 48	Homo sapiens	cDNA: FLJ21615 fis, clone COL07393.	876	100
1682	gi131951 51	Homo sapiens	transcription factor TZP (TZP) mRNA, complete cds.	362	47
1682	gi102414 61	Homo sapiens	Human DNA sequence from clone RP5-1121G12 on chromosome 20 Contains the 3' end of a gene encoding the hepatocellular carcinoma-associated antigen 58 (HCA58), the SCAND1 gene encoding the domain-containing 1 protein, a novel gene, 2 CpG islands, ESTs, STSs and GSSs, complete sequence.	362	47
1683	AAB439 00	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1345.	483	87
1683	gi168491 7	Homo sapiens	Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.	483	87
1683	gi128047 05	Homo sapiens	ribosomal protein L44, clone MGC:2064 IMAGE:3353669, mRNA, complete cds.	483	87
1684	AAY079 31	Homo sapiens	HUMA- Human secreted protein fragment encoded from gene 80.	213	100
1684	gi593200	Mus musculus	neuronal apoptosis inhibitory	68	50

SEQ	Hit ID	Speicies	Description	S score	Damant
ID		Specials		S score	Percent identity
1.50	3		protein-rs6		
1684	gi593200 8		neuronal apoptosis inhibitory protein	68	50
1685	gi140304 07		keratin-associated protein 16.4	380	77
1685	gi140304 09	Mus musculus	keratin-associated protein 16.5	309	64
1685	gi140304 01	Mus musculus	keratin-associated protein 16.1	302	67
1686	gi153417 94	Homo sapiens	hypothetical protein FLJ12787, clone MGC:16870 IMAGE:3048487, mRNA, complete cds.	1433	100
1686	AAB951 82	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17250.	1426	99
1686	gi104344 81	Homo sapiens	cDNA FLJ12787 fis, clone NT2RP2001943.	1426	99
1687	AAY384 01	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 16.	230	88
1687	AAB256 87	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 23 SEQ ID NO:76.	66	38
1688	gi127449 21	Homo sapiens	tethering factor SEC34 (SEC34) mRNA, complete cds.	4223	100
1688	gi145496 69	Homo sapiens	vesicle docking protein SEC34 mRNA, complete cds.	4212	99
1688	gi152915 37	Drosophila melanogaster	GH25768p	1691	43
1689	AAB907 46	Homo sapiens	GEMY Human DF989_3 protein sequence SEQ ID 192.	545	97
1689	AAW644 71	Homo sapiens	GEMY Human secreted protein from clone DF989_3.	545	97
1689	gi282930 2	Homo sapiens	mRNA for Efs1, complete cds.	74	37
1690	AAW136 58	Homo sapiens	UYMC- Human cytidine deaminase.	657	87
1690	gi598149	Homo sapiens	cytidine deaminase (CDA) mRNA, complete cds.	657	87
1690	gi432179 3	Homo sapiens	cytidine deaminase gene, exon 4 and complete cds.	657	87
1691	gi126980 79	Homo sapiens	mRNA for KIAA1767 protein, partial cds.	4013	99
1691	AAM255 78	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1093.	3955	99
1691	AAE0618 6	Homo sapiens	HUMA- Human gene 58 encoded secreted protein fragment, SEQ ID NO:248.	3521	99
1692	gi255901 0	Homo sapiens	chaperonin containing t-complex polypeptide 1, eta subunit (Ccth) mRNA, complete cds.	890	100
1692	gi 141983 88	Mus musculus	chaperonin subunit 7 (eta)	879	98
1692	gi468504	Mus musculus	CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT)	879	98
1693	gi 165520 36	Homo sapiens	cDNA FLJ32028 fis, clone NTONG1000257.	918	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1693	AAB747 68	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 13 SEQ ID NO:77.	592	99
693	AAB747 45	Homo sapiens	HUMA- Human secreted protein sequence encoded by gene 13 SEQ ID NO:54.	592	99
694	gi100471 57	Homo sapiens	mRNA for KIAA1546 protein, partial cds.	3652	100
694	gi126978	Homo sapiens	mRNA for KIAA1676 protein, partial cds.	613	39
694	gi729228	Drosophila melanogaster	CG2083 gene product	534	35
695	AAG000 78	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4159.	164	80
695	gi237020	Homo sapiens	mRNA for procollagen alpha 2(V).	164	80
1695	gi179698	Homo sapiens	Human collagen type V alpha-2 mRNA, 5' end.	164	80
1696	gi165525 96	Homo sapiens	cDNA FLJ32466 fis, clone SKNMC2000065.	2609	99
1696	gi140178 27	Homo sapiens	mRNA for KIAA1805 protein, partial cds.	2609	99
1696	gi152079 87	Macaca fascicularis	hypothetical protein	2588	99
1697	AAB928 79	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11475.	639	73
1697	AAM414 35	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6366.	639	73
1697	AAM396 49	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2794.	639	73
1698	AAM254 87	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1002.	586	100
1698	AAG036 67	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7748.	582	99
1698	gi128500	Mus musculus	putative	557	93
1699	AAE0477 4	Homo sapiens	INCY- Human vesicle trafficking protein-17 (VETRP- 17) protein.	748	100
1699	AAB416 37	Homo sapiens	CURA- Human ORFX ORF1401 polypeptide sequence SEQ ID NO:2802.	748	100
1699	gi331995	Homo sapiens	mRNA for TOM1 protein.	638	82
1700	gi141401 00	Homo sapiens	OTT gene for one twenty two proteins (spliced and unspliced forms).	4797	.99
1700	AAB951	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17093.	4779	99
1700	gi141613 69	Homo sapiens	putative RNA-binding motif protein 15 short form (RBM15) mRNA, complete cds, alternatively spliced.	4779	99
1701	AAB938 79	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13792.	2228	100
1701	AAG667	Homo sapiens	BIOD- Human cell growth inhibition protein 48.	2228	100

SEC		Speicies	Description	S score	Percent identity
1701	27		clone MGC:15047 IMAGE:3535485, mRNA, complete cds.	2228	100
1702	0		INCY- Human kinase (PKIN)- 14 protein.	4186	100
1702	17		gklp mRNA for kinase-like protein spiice variant 1, complete cds.	4186	100
1702	AAB656 79	Homo sapiens	SUGE- Novel protein kinase, SEQ ID NO: 207.	4158	97
1703	53	Homo sapiens	GETH Human PRO5774 polypeptide sequence.	440	74
1703	AAY307 34	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	258	96
1703	gi118166 9	Saccharomyces cerevisiae	Tel2p	75	24
1704	gi104397 62	Homo sapiens	cDNA: FLJ23164 fis, clone LNG09764.	3205	100
1704	gi104403 12	Homo sapiens	cDNA: FLJ23577 fis, clone LNG12640.	1755	98
1704	gi126980 85	Homo sapiens	mRNA for KIAA1770 protein, partial cds.	1614	99
1705	AAM418 06	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6737.	1194	77
1705	AAM400 20	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3165.	1194	77
1705	ABB1223	Homo sapiens	HYSE- Human novel protein, SEQ ID NO:2601.	1194	77
1706	gi152775 65	Mus musculus	RIKEN cDNA 2510039018 gene	3091	91
1706	gi128469 32	Mus musculus	putative	3088	91
1706	AAB430 28	Homo sapiens	CURA- Human ORFX ORF2792 polypeptide sequence SEQ ID NO:5584.	2246	95
1707	gi160411 36	Macaca fascicularis	hypothetical protein	702	92
1707	AAB652 16	Homo sapiens	GETH Human PRO1004 (UNQ488) protein sequence SEQ ID NO:227.	569	92
1707	AAY666 93	Homo sapiens	GETH Membrane-bound protein PRO1004.	569	92
1708	AAB956 36	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18369.	2429	100
1708	gi104363 57	Homo sapiens	cDNA FLJ14009 fis, clone Y79AA1002431, weakly similar to TRANSDUCIN-LIKE ENHANCER PROTEIN 2.	2429	100
1708	gi503043 9	Homo sapiens	chromosome 19, cosmid R26610, complete sequence.	1569	80
1709	gi157051 43	Mus musculus	suppressor of cytokine signalling	2071	86
1709	AAM007 59	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 122.	1712	100
1709	AAM008 72	Homo sapiens	HYSE- Human bone marrow protein, SEQ ID NO: 348.	1215	99
1710	gi104387	Homo sapiens	cDNA: FLJ22408 fis, clone	1934	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	85		HRC08416.		
1710	AAM399 17	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3062.	837	45
1710	AAM417 03	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 6634.	836	45
1711	gi104374 28	Homo sapiens	cDNA: FLJ21343 fis, clone COL02679.	1836	100
1711	gi120531 45	Homo sapiens	mRNA; cDNA DKFZp434A0926 (from clone DKFZp434A0926); complete cds.	1388	99
1711	gi568953 7	Homo sapiens	mRNA for KIAA1100 protein, complete cds.	1261	68
1712	AAG032 54	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7335.	438	89
1712	gi730038 3	Drosophila melanogaster	CG7671 gene product	366	27
1712	AAB945 51	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15312.	309	100
1713	gi144956 58	Homo sapiens	hypothetical protein FLJ12687, clone MGC:15791 IMAGE:3504468, mRNA, complete cds.	2639	99
1713	AAB942 41	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14627.	2631	99
1713	gi104343 33	Homo sapiens	cDNA FLJ12687 fis, clone NT2RM4002532, weakly similar to PROTEIN HOM1.	2631	99
1714	AAC623 51_aa1	Homo sapiens	CELL- Nucleotide sequence of lysophosphatidic acid acyltransferase-beta.	834	100
1714	AAA392 92_aa1	Homo sapiens	CELL- Human lysophosphatidic acid acyltransferase beta encoding cDNA.	834	100
1714	AAB306 23	Homo sapiens	CELL- Amino acid sequence of lysophosphatidic acid acyltransferase-beta.	834	100
1715	AAB958 47	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18896.	675	100
1715	gi104367 63	Homo sapiens	cDNA FLJ14326 fis, clone PLACE4000247.	675	100
1715	gi165529 00	Homo sapiens	cDNA FLJ32711 fis, clone TEST12000707, weakly similar to DOUBLESEX PROTEIN, MALE-SPECIFIC.	90	35
1716	AAB530 94	Homo sapiens	GETH Human angiogenesis- associated protein PRO826, SEQ ID NO:158.	278	100
1716	AAB509 16	Homo sapiens	GETH Human PRO826 protein.	278	100
1716	AAB652 04	Homo sapiens	GETH Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.	278	100
1717	AAB949 15	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16349.	961	100
1717	gi146026 23	Homo sapiens	hypothetical protein FLJ11526, clone MGC:15059	961	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
			IMAGE:3937610, mRNA, complete cds.		Identity
1717	gi104327 97	Homo sapiens	cDNA FLJ11526 fis, clone HEMBA1002555, weakly similar to Homo sapiens mSin3A associated polypeptide p30 mRNA.	961	100
1718	AAY124 39	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID NO:470.	453	94
1718	gi134771 83	Homo sapiens	Similar to hypothetical protein FLJ20859, clone MGC:12940 IMAGE:2822127, mRNA, complete cds.	453	94
1718	gi128308 10	Homo sapiens	false p73 target protein gene, complete cds.	453	94
1719	gi159289 65	Homo sapiens	hypothetical protein FLJ11354, clone MGC:22961 IMAGE:4865798, mRNA, complete cds.	3522	100
1719	AAB937 08	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13299.	3514	99
1719	gi104325 95	Homo sapiens	cDNA FLJ11354 fis, clone HEMBA1000129, weakly similar to HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I.	3514	99
1720	gi147173 96	Homo sapiens	potassium-dependent Na/Ca exchanger NCKX3 (SLC24A3) mRNA, partial cds.	3108	97
1720	gi125974 41	Mus musculus	K+-dependent Na/Ca exchanger	3027	94
1720	gi120003 97	Rattus norvegicus	potassium-dependent sodium- calcium exchanger NCKX3	3025	94
1721	gi150724 54	Mus musculus	von Willebrand factor A-related protein	1614	72
1721	AAB425 81	Homo sapiens	CURA- Human ORFX ORF2345 polypeptide sequence SEQ ID NO:4690.	1358	93
1721	AAB883 40	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0053.	1288	98
1722	AAE0382 2	Homo sapiens	HUMA- Human gene 5 encoded secreted protein HETKL27, SEQ ID NO: 68.	935	100
1722	AAB825 97	Homo sapiens	HUMA- Human transmembrane protein encoded by cDNA clone HNALE36.	935	100
1722	gi157064 37	Homo sapiens	clone MGC:17366 IMAGE:3860009, mRNA, complete cds.	935	100
	AAG665 03	Homo sapiens	BIOD- Human ATP-dependent helicase 31.	1441	100
	AAM257 80	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1295.	1441	100
	gi136763 56	Homo sapiens	clone MGC:2679 IMAGE:2819663, mRNA, complete cds.	1434	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1724	AAG673 94	Homo sapiens	SUGE- Amino acid sequence of human protein kinase SGK269.	2322	100
1724	gi104371 81	Homo sapiens	cDNA: FLJ21140 fis, clone CAS07548.	1730	100
1724	AAG673	Homo sapiens	SUGE- Amino acid sequence of human protein kinase SGK223.	952	46
1725	AAF2449 8 aa1	Homo sapiens	GEST Human PG-3 coding sequence.	4362	99
1725	AAB354 01	Homo sapiens	GEST Human PG-3.	4355	99
1725	gi133968 64	Homo sapiens	unnamed protein product	4355	99
1726	AAB427 84	Homo sapiens	CURA- Human ORFX ORF2548 polypeptide sequence SEQ ID NO:5096.	817	99
1726	gi122248 87	Homo sapiens	mRNA; cDNA DKFZp547H027 (from clone DKFZp547H027); complete cds.	817	99
1726	gi104384 59	Homo sapiens	cDNA: FLJ22174 fis, clone HRC00767.	817	99
1727	gi167405 66	Homo sapiens	Similar to hypothetical protein FLJ13087, clone MGC:15009 IMAGE:3536735, mRNA, complete cds.	1854	100
1727	AAB952 97	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17525.	807	95
1727	gi104349 41	Homo sapiens	cDNA FLJ13087 fis, clone NT2RP3002099.	807	95
1728	AAB940 75	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14267.	3506	97
1728	AAM939 95	Homo sapiens	HELI- Human stomach cancer expressed polypeptide SEQ ID NO 59.	3506	97
1728	gi140421 45	Homo sapiens	cDNA FLJ14550 fis, clone NT2RM2001696.	3506	97
1729	AAG008 97	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4978.	392	93
1729	AAG008 98	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 4979.	130	100
1729	AAB425 97	Homo sapiens	CURA- Human ORFX ORF2361 polypeptide sequence SEQ ID NO:4722.	130	100
1730	ABB1161 3	Homo sapiens	HYSE- Human sorting nexin 7 homologue, SEQ ID NO:1983.	2341	100
1730	AAG741 74	Homo sapiens	HUMA- Human colon cancer antigen protein SEQ ID NO:4938.	2309	99
1730	gi488424 1	Homo sapiens	mRNA; cDNA DKFZp564F052 (from clone DKFZp564F052); partial cds.	2148	99
1731	gi134456 60	Homo sapiens	MP19 (LIM2) mRNA, complete cds, alternatively spliced.	933	100
1731	gi111775 46	Homo sapiens	LIM2 (LIM2) and natural killer group 7 (NKG7) genes, complete cds.	933	100
1731	gi134456 58	Homo sapiens	MP19ins (LIM2) mRNA, complete cds, alternatively	880	80

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
L			spliced.		Achuty
1732	91		CURA- Human ORFX ORF355 polypeptide sequence SEQ ID NO:710.	1056	100
1732	gi156174 58	cuniculus	Rab11 family interacting protein	869 .	48
1732	AAY294 88	Momo sapiens	CORI- Human lung lumour protein LT86-7 predicted amino acid sequence.	557	87
1733	gi104377 50	Homo sapiens	cDNA: FLJ21616 fis, clone COL07477.	1680	99
1733	gi143493 60	Homo sapiens	Similar to hypothetical protein FLJ21616, clone MGC:14941 IMAGE:3947903, mRNA, complete cds.	1443	99
1733	gi128054 73	Mus musculus	Unknown (protein for IMAGE:3490304)	1410	97
1734	gi104377 50	Homo sapiens	cDNA: FLJ21616 fis, clone COL07477.	1645	92
1734	gi143493 60	Homo sapiens	Similar to hypothetical protein FLJ21616, clone MGC:14941 IMAGE:3947903, mRNA, complete cds.	1565	99
1734	gi128054 73	Mus musculus	Unknown (protein for IMAGE:3490304)	1412	96
1735	AAB950 36	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16791.	863	100
1735	gi104334 48	Homo sapiens	cDNA FLJ12060 fis, clone HEMBB1002142.	863	100
1735	gi153419 04	Homo sapiens	clone MGC:21051 IMAGE:4476886, mRNA, complete cds.	751	99
1736	gi140437 83	Homo sapiens	clone MGC:14256 IMAGE:4129368, mRNA, complete cds.	2232	100
1736	gi104368 57	Homo sapiens	cDNA: FLJ20897 fis, clone ADKA03573.	2232	100
1736	gi126537 85	Homo sapiens	clone IMAGE:3349601, mRNA, partial cds.	1783	99
1737	gi142498 50	Homo sapiens	clone MGC:15062 IMAGE:2959567, mRNA, complete cds.	1535	99
1737	AAM795 39	Homo sapiens	HYSE- Human protein SEQ ID NO 3185.	1523	53
1737	AAM785 55	Homo sapiens	HYSE- Human protein SEQ ID NO 1217.	1523	53
1738	gi131833 38	Homo sapiens	calneuron 1 (CALN1) mRNA, complete cds.	881	100
1738	gi131833 40	Mus musculus	calneuron 1	880	99
1738	gi767034 4	Mus musculus	unnamed protein product	880	99
1739	gi499592 7	Xenopus laevis	p33 ringo	545	49
1739	gi102802 85	Xenopus sp.	unnamed protein product	545	49
1739	gi446879	Xenopus laevis	speedy protein	540	48

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	0				
1740	gi152815 53	Homo sapiens	solute carrier family 12 member 8 (SLC12A8) gene, partial cds.	1905	80
1740	gi172249 40	Mus musculus	cation-chloride cotransporter	1761	74
1740	gi104397 94	Homo sapiens	cDNA: FLJ23188 fis, clone LNG12038.	1613	99
1741	gi633016 3	Homo sapiens	mRNA for KIAA1161 protein, partial cds.	1137	99
1741	gi730133 3	Drosophila melanogaster	CG11909 gene product	485	41
1741	gi64404	Torpedo californica	4-acetamido-4'- isothiocyanostilbene-2, 2'- disulphonic acid-binding protein	415	38
1742	AAM678 57	Homo sapiens	MOLE- Human bone marrow expressed probe encoded protein SEQ ID NO: 28163.	1553	100
1742	AAM554 71	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 27576.	1553	100
1742	gi156208 49	Homo sapiens	mRNA for KIAA1895 protein, partial cds.	1553	100
1743	gi285264 0	Homo sapiens	cione 23856 unknown mRNA, partial cds.	942	99
1743	gi133252 81	Homo sapiens	hypothetical protein MGC2683, clone MGC:4313 IMAGE:2819900, mRNA, complete cds.	700	100
1743	gi126544 85	Homo sapiens	clone MGC:2683 IMAGE:2819900, mRNA, complete cds.	700	100
1744	gi139383 07	Homo sapiens	clone MGC:15626 IMAGE:3343642, mRNA, complete cds.	526	62
1744	AAB907 65	Homo sapiens	NOJI/ Human shear stress- response protein SEQ ID NO: 30.	524	64
1744	AAB621 59	Homo sapiens	NEUR- Human arginine-rich protein.	524	64
1745	gi724320	Homo sapiens	mRNA for KIAA1413 protein, partial cds.	7273	99
1745	AAB930 57	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11862.	3014	99
1745	gi702286 1	Homo sapiens	cDNA FLJ10680 fis, clone NT2RP2006573, weakly similar to 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37).	3014	99
1746	gi724320 7	Homo sapiens	mRNA for KIAA1413 protein, partial cds.	7245	98
1746	AAB930 57	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11862.	3014	99
1746	gi702286 1	Homo sapiens	cDNA FLJ10680 fis, clone NT2RP2006573, weakly similar to 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37).	3014	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1747	AAE1033 0	Homo sapiens	INCY- Human transporter and ion channel-7 (TRICH-7) protein.	1520	100
1747	AAM394 22	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2567.	694	48
1747	AAM793 97	Homo sapiens	HYSE- Human protein SEQ ID NO 3043.	694	48
1748	gi104397 44	Homo sapiens	cDNA: FLJ23151 fis, clone LNG09417.	2362	100
1748	gi128604 56	Mus musculus	putative	1732	70
1748	gi895406	Arabidopsis thaliana	Contains similarity to a transposable element Tip100 protein for transposase from Ipomoea purpurea gb 4063769 and is a member of the transmembrane 4 family PF 00335.	308	24
1749	gi175299 87	Homo sapiens	oxysterol-binding protein-like protein OSBPL3 (OSBPL3) mRNA, complete cds.	4671	100
1749	gi173893 82	Homo sapiens	oxysterol binding protein-like 3, clone MGC:21526 IMAGE:3909164, mRNA, complete cds.	4671	100
1749	gi108809 73	Homo sapiens	oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds.	4671	100
1750	AAB948 79	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16094.	2813	100
1750	gi104363 38	Homo sapiens	cDNA FLJ13998 fis, clone Y79AA1002229, weakly similar to DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.	2813	100
1750	AAB943 19	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14797.	2330	99
1751	AAB193 90	Homo sapiens	LEXI- Amino acid sequence of a human lipoxygenase protein.	3836	100
1751	gi133781 70	Homo sapiens	partial ALOXE3 gene for arachidonate lipoxygenase 3, exons 1 to 4B (and joined CDS).	3836	100
1751	gi104410 04	Homo sapiens	epidermal lipoxygenase (ALOXE3) mRNA, complete cds.	3830	99
1752	AAM932 41	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 2671.	664	95
1752	gi150302 70	Homo sapiens	clone MGC:9889 IMAGE:3868330, mRNA, complete cds.	664	95
1752	AAO102 85	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 24177.	486	78
1753	gi456191	Homo sapiens	H.sapiens mRNA for rho GDP- dissociation Inhibitor 1.	818	99
1753	gi337395	Homo sapiens	Human GDP dissociation inhibitor mRNA, complete cds.	818	99
1753	gi285979	Homo sapiens	Human rho GDI mRNA, complete cds.	818	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1754	AAQ435 49_aa1	Homo sapiens	HARD Gamma subunit of human retinal cGMP phosphodiesterase DNA.	472	100
1754	AAR931 17	Homo sapiens	HARD cGMP- phosphodiesterase gamma- subunit.	472	100
1754	AAR384 84	Homo sapiens	HARD Gamma subunit of human retinal cGMP phosphodiesterase.	472	100
1755	AAY194 46	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	590	98
1755	AAY195 99	Homo sapiens	HUMA- SEQ ID NO 317 from WO9922243.	590	98
1755	AAY196 02	Homo sapiens	HUMA- SEQ ID NO 320 from WO9922243.	137	100
1756	gi104373	Homo sapiens	cDNA: FLJ21313 fis, clone COL02176.	2197	99
1756	gi142503 21	Homo sapiens	hypothetical protein FLJ21313, clone MGC:16820 IMAGE:4148772, mRNA, complete cds.	2193	99
1756	gi128585	Mus musculus	putative	1936	86
1757	gi741435	Homo sapiens	Hox1.8 gene for homeobox protein.	478	100
1757	gi278967	Homo sapiens	homeobox protein A10 (HOXA10) gene, complete cds.	478	100
1757	gi155592 35	Homo sapiens	clone MGC:12859 IMAGE:4107013, mRNA, complete cds.	478	100
1758	gi189772	Homo sapiens	Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.	872	90
1758	gi135435 68	Homo sapiens	prostaglandin D2 synthase (21kD, brain), clone MGC:14559 IMAGE:4294999, mRNA, complete cds.	872	90
1758	gi129638 79	Homo sapiens	prostaglandin D synthase mRNA, complete cds.	872	90
1759	gi298250 8	Homo sapiens	mRNA for TCR beta chain, specific for Mage 3/HLA-A2.	1296	92
1759	gi300292 5	Homo sapiens	T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds.	1286	92
1759	gi36733	Homo sapiens	H.sapiens mRNA for T-cell antigen receptor beta-chain.	1047	75
1760	AAM257 28	Homo sapiens	HYSE- Human protein sequence SEQ ID NO:1243.	667	99
1760	gi155290 64	Homo sapiens	sorting nexin 14 (SNX14) mRNA, complete cds.	667	99
1760	gi134772 73	Homo sapiens	clone MGC:13217 IMAGE:3959086, mRNA, complete cds.	667	99
1761	AAB948 43	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16018.	1761	100
1761	gi104362 67	Homo sapiens	cDNA FLJ13955 fis, clone Y79AA1001177.	1761	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1761	gi163592 95	Mus musculus	Similar to hypothetical protein FLJ13955	1681	85
1762	AAE0205 8	Homo sapiens	HUMA- Human four disulfide core domain (FDCD)-containing protein.	1200	84
1762	gi128353 76	Mus musculus	putative	918	68
1762	gi126554 52	Homo sapiens	mRNA for keratin associated protein 4.7 (KRTAP4.7 gene).	892	68
1763	AAG674 85	Homo sapiens	LEXI- Amino acid sequence of a human transporter protein.	2391	99
1763	AAE1033 3	Homo sapiens	INCY- Human transporter and ion channel-10 (TRICH-10) protein.	2368	96
1763	gi127182 01	Homo sapiens	Human DNA sequence from clone RP11-305P22 on chromosome 20 Contains ESTs, STSs, GSSs and 7 CpG islands. Contains three novel genes and a novel gene for a helix-loop-helix DNA binding protein, complete sequence.	2243	100
1764	gi157789 48	Homo sapiens	Similar to thiamine pyrophosphokinase, clone MGC:14885 IMAGE:3622116, mRNA, complete cds.	717	100
1764	gi126672 03	Homo sapiens	thiamine pyrophosphokinase (TPK1) mRNA, complete cds.	717	100
1764	gi122489 15	Homo sapiens	hTPK1 mRNA for thiamin pyrophosphokinase, complete cds.	717	100
1765	gi104388 31	Homo sapiens	cDNA: FLJ22439 fis, clone HRC09236.	2525	99
1765	AAB422 37	Homo sapiens	CURA- Human ORFX ORF2001 polypeptide sequence SEQ ID NO:4002.	2084	99
1765	gi135592 84	Homo sapiens	Human DNA sequence from clone RP5-117516 on chromosome 20. Contains the 3' end of the gene for Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein), the 5' end of the gene encoding N-terminal acetyltransferase complex ard1 subunit, ESTs, STSs, GSSs and two CpG islands, complete sequence.	829	36
1766	gi958842 8	Homo sapiens	Human DNA sequence from clone RP5-1024N4 on chromosome 1p32.1-33. Contains the gene for a novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1), a pseudogene similar to part of butyrophilin family members, a novel gene, ESTs, STSs, GSSs and a putative CpG	2858	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
~~			island, complete sequence.		
1766	gi529056	Homo sapiens	Na+/glucose cotransporter (SGLT1) gene, exon 15 and complete cds.	1955	55
1766	gi364604 3	Homo sapiens	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Contains ESTs and STSs, complete sequence.	1955	55
1767	AAB734 85	Homo sapiens	MILL- Human aminopeptidase 22196.	3657	99
1767	gi125836 12	Homo sapiens	mRNA for neurolysin.	3657	99
1767	gi139224 67	Homo sapiens	unnamed protein product	3657	99
1768	gi101221 38	Rattus norvegicus	SynGAP-a	6651	99
1768	gi293544 8	Rattus norvegicus	synaptic ras GTPase-activating protein p135 SynGAP	6634	99
1768	gi662458 7	Homo sapiens	Human DNA sequence from clone RP4-570F3 on chromosome 6. Contains the 5' end of the gene for the ortholog of the rat synaptic ras GTPase-activating protein p135 SynGAP, gene LOC51596 for divalent cation tolerant protein CUTA or brain acetylcholinesterase putative membrane anchor, the PHF1 gene for PHD finger protein 1, the KNSL2 gene for kinesin-like protein 2, the gene for a novel protein similar to ribosomal protein L12 (RPL12) and the gene for a novel protein similar to lysophospholipase II (LYPLA2). Contains ESTs, STSs, GSSs and four CpG islands, complete sequence.	1040	100
1769	AAB958 63	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18931.		
1769	gi173892 83	Homo sapiens	hypothetical protein FLJ14346, clone MGC:21027 IMAGE:4415420, mRNA, complete cds.	1040	100
1769	gi104367 91	Homo sapiens	cDNA FLJ14346 fis, clone THYRO1001320.	1040	100
1770	AAB945 17	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15235.	2593	99
1770	gi104351 22	Homo sapiens	cDNA FLJ13203 fis, clone NT2RP3004504, highly similar to M.musculus mRNA for CPEB	2593	99

SEQ ID	Hit ID	Speicles	Description	S score	Percent identity
ļ			protein.		identity
1770	16		cytoplasmic polyadenylation element-binding protein short form (CPEB1) mRNA, complete cds.	2583	98
1771	AAB480 59	Homo sapiens	INCY- Human extracellular signaling molecule (EXCS) (ID 1493630CD1).	432	97
1771	AAY360 90	Homo sapiens	GEST Extended human secreted protein sequence, SEQ ID NO. 475.	420	95
1771	AAY117 68	Homo sapiens	GEST Human 5' EST secreted protein SEQ ID No: 368.	257	95
1772	AAB930 75	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11902.	2936	99
1772	gi140424 15	Homo sapiens	cDNA FLJ14710 fis, clone NT2RP3000632, weakly similar to ZINC FINGER PROTEIN 84.	2936	99
1772	gi165514 29	Homo sapiens	cDNA FLJ31551 fis, clone NT2RI2001083, moderately similar to ZINC FINGER PROTEIN 84.	1813	63
1773	AAY768 43	Homo sapiens	INCY- Human proton ATPase subunit (HPAS) protein sequence.	356	100
1773	AAY885 90	Homo sapiens	SATO/ Human tumour specific antigen amino acid sequence.	356	100
1773	AAW645 34	Homo sapiens	SAGA Human fibrosarcoma cell line HT-1080 clone HP00442 protein.	356	100
1774	gi124073 85	Homo sapiens	tripartite motif protein TRIM5 isoform gamma (TRIM5) mRNA, complete cds; alternatively spliced.	1818	99
1774	gi124073 87	Homo sapiens	tripartite motif protein TRIM5 isoform delta (TRIM5) mRNA, complete cds; alternatively spliced.	1559	99
1774	gi124073 83	Homo sapiens	tripartite motif protein TRIM5 isoform beta (TRIM5) mRNA, complete cds; alternatively spliced.	1557	100
1775	gi142506 01	Homo sapiens	hypothetical protein FLJ22056, clone MGC:3045 IMAGE:3343082, mRNA, complete cds.	2600	99
1775	gi 104383 15	Homo sapiens	cDNA: FLJ22056 fis, clone HEP09916.	1747	100
1775	gi729529 3	Drosophila melanogaster	CG8633 gene product	597	31
1776	gi104370 59	Homo sapiens	cDNA: FLJ21054 fis, clone CAS00538.	736	100
1776	gi115580 99	Mus musculus	syncoilin	653	89
1776	gi128354 05	Mus musculus	<u> </u>	552	84
1777	gi163076	Homo sapiens	hypothetical protein FLJ12270,	3045	100

SEQ ID	Hit ID	Speicles	Description	S score	Percent identity
	08		clone MGC:10176 IMAGE:3908004, mRNA, complete cds.	. •	
1777	gi156209 05	Homo sapiens	mRNA for KIAA1923 protein, partial cds.	3042	99
1777	AAB939 45	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13963.	2190	100
778	gi795981 9	Homo sapiens	PRO1430	299	100
1778	AAO078 40	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 21732.	75	54
778	AAO088 70	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 22762.	73	43
1779	AAG629 10	Homo sapiens	KLEE/ Amino acid sequence of a human xylosylytransferase (XT) isoform XT-II.	4625	100
1779	gi113222 70	Homo sapiens	mRNA for xylosyltransferase II (XT-II gene).	4625	100
1779	gi152096 53	Homo sapiens	human XT-II	4625	100
1780	gi992997	Macaca fascicularis	hypothetical protein	1778	96
1780	AAG787 40	Homo sapiens	BODE- Human transcriptional elongation factor IIS 24.	1162	99
780	ABB1122 0	Homo sapiens	HYSE- Human TFIISh homologue, SEQ ID NO:1590.	653	100
1781	gi152778 46	Homo sapiens	Similar to hypothetical protein FLJ21522, clone MGC:16817 IMAGE:3853503, mRNA, complete cds.	3122	99
1781	AAB643 72	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA4.	3100	99
1781	gi104376	Homo sapiens	cDNA: FLJ21522 fis, clone COL05884.	2892	94
1782	AAB946 25	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15483.	2688	100
1782	gi104353 87	Homo sapiens	cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MUSCLE.	2688	100
1782	gi165518 77	Homo sapiens	cDNA FLJ31903 fis, clone NT2RP7004260, weakly similar to MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B.	2429	92
1783	gi105681 12	Homo sapiens	ALR-like protein mRNA, complete cds.	17050	100
1783	gi563007 7	Homo sapiens	PAC clone RP5-98107 from 7q34-q36, complete sequence.	9606	100
1783	AAB422 30	Homo sapiens	CURA- Human ORFX ORF1994 polypeptide sequence SEQ ID NO:3988.	9583	99
1784	AAB688 76	Homo sapiens	INCY- Human RECAP polypeptide, SEQ ID NO: 6.	1895	85
1784	gi104381 74	Homo sapiens	cDNA: FLJ21952 fis, clone HEP04970.	1895	85
1784	gi169242	Homo sapiens	hypothetical protein FLJ21952,	1862	84

SEC		Speicies	Description	S score	Percent identity
	96		clone MGC:2790		luentity
ĺ	İ		IMAGE:2960984, mRNA,		İ
1505	1		complete cds.	ł	ł
1785	1	Homo sapiens	HUMA- Human novel secreted	1433	100
1785	26 gi140178		protein, Seq ID 979.		
1765	23	Homo sapiens	mRNA for KIAA1803 protein,	1433	100
1785		Homo sapiens	partial cds.	<u> </u>	i
1700	55	110mo sapiens	GEAT Human zinc finger	1168	99
	155		domain DNA binding protein S		- [
1786	AAG004	Homo sapiens	GEST Human secreted protein,	1207	
	05		SEQ ID NO: 4486.	397	98
1786	AAM906	Homo sapiens	HUMA- Human	215	
	02	1	immune/haematopoietic antigen	215	56
			SEQ ID NO:18195.		-
1786	AAM411	Homo sapiens	HYSE- Human polypeptide SEQ	84	34
	14		ID NO 6045.	1	134
1787	AAG020	Homo sapiens	GEST Human secreted protein,	302	100
1505	95		SEQ ID NO: 6176.		100
1787	gi665103	Mus musculus	similar to RNA binding protein	222	53
1787	2:100470	domesticus			
1/0/	gi128478 83	Mus musculus	putative	222	53
1788	gi979845	Home conjent	721		
2700	2	Homo sapiens	mRNA for putative capacitative	4470	100
1788	gi532685	Mus musculus	calcium channel (trp7 gene). receptor-activated calcium		
	4	111dS IIIdSCUIdS	channel	4392	98
1788	gi229590	Homo sapiens	Human putative calcium influx	3529	
	3		channel (htrp3) mRNA,	3329	81
			complete cds.	ĺ	1
1789	AAG023	Homo sapiens	GEST Human secreted protein,	377	98
1500	37		SEQ ID NO: 6418.		70
1789	AAM008	Homo sapiens	HYSE- Human bone marrow	72	31
1789	75		protein, SEQ ID NO: 351.		1
1707	gi166669 2	Mus musculus	alpha-NAC, muscle-specific	72	34
1790	AAB733	Homo sapiens	form gp220		
.,,,	81	1 Hollio Sapiens	NANF- Human gas vesicle	2838	99
1790	gi120055	Homo sapiens	protein homologue hGvpT-b. HT025 mRNA, complete cds.		
	09	110mio Supiciis	111 025 mkivA, complete cas.	2838	99
790	gi173914	Homo sapiens	clone MGC:2462	1600	+
	58		IMAGE:2964737, mRNA,	1699	99
			complete cds.		1
791	AAY994	Homo sapiens	GETH Human PRO1555	1300	100
	38		(UNQ763) amino acid sequence	1500	100
		· · · · · · · · · · · · · · · · · · ·	SEQ ID NO:338.		
791	AAB240	Homo sapiens	GETH Human PRO1555 protein	1300	100
701	37		sequence SEQ ID NO:49.		
791	gi126542	Homo sapiens	Similar to hypothetical protein,	1300	100
1	33		clone 1-2, clone MGC:5442		
			IMAGE:3449979, mRNA,		1 1
792	AAB638	Homo sapiens	complete cds.		
	60	110mo sapiens	LUDW- Human prostate cancer	297	50
1			associated antigen protein sequence SEQ ID NO:1222.		ļĺ
- 1			bodactice SEQ ID NO:1222.		1 1
792	AAM767	Homo sapiens		272	51

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
		· ·	SEQ ID NO: 37077.		
1792	AAM639 51	Homo sapiens	MOLE- Human brain expressed single exon probe encoded protein SEQ ID NO: 36056.	272	51
1793	AAB942 49	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14645.	799	99
1793	gi104343 56	Homo sapiens	cDNA FLJ12700 fis, clone NT2RP1000721.	799	99
1793	ABB1242 2	Homo sapiens	HYSE- Human bone marrow expressed protein SEQ ID NO: 261.	528	99
1794	AAB651 89	Homo sapiens	GETH Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.	1858	99
1794	AAB875 36	Homo sapiens	GETH Human PRO1013.	1858	99
1794	AAY666 66	Homo sapiens	GETH Membrane-bound protein PRO1013.	1858	99
1795	AAB651 89	Homo sapiens	GETH Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.	1655	93
1795	AAB875 36	Homo sapiens	GETH Human PRO1013.	1655	93
1795	AAY666 66	Homo sapiens	GETH Membrane-bound protein PRO1013.	1655	93
1796	gi777026	Homo sapiens	PRO3077	620	100
1796	gi158916 32	Agrobacterium tumefaciens	AGR_L_3035p	67	31
1797	AAY362 33	Homo sapiens	HUMA- Human secreted protein encoded by gene 10.	302	96
1797	gi298307	Rattus sp.	beta 3-adrenergic receptor; beta 3-AR	83	38
1797	gi241216	Rattus sp.	beta 3-adrenergic receptor	83	38
1798	ABB1203 7	Homo sapiens	HYSE-Human ribosomal protein L31 homologue, SEQ ID NO:2407.	341	100
1798	AAG038 94	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 7975.	341	100
1798	AAB437 07	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1152.	341	100
1799	AAE1099 5	Homo sapiens	INCY- Human lipid metabolism enzyme-4 (LME-4) protein.	2242	99
1799	AAB419 89	Homo sapiens	CURA- Human ORFX ORF1753 polypeptide sequence SEQ ID NO:3506.	2224	98
1799	AAB940 07	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14123.	1212	99
1800	AAY761 94	Homo sapiens	HUMA- Human secreted protein encoded by gene 71.	296	98
1800	AAY131 96	Homo sapiens	GEST Human secreted protein encoded by 5' EST SEQ ID NO: 210.	291	96
1800	AAY194 71	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	148	96
1801	ABB1242	Homo sapiens	HYSE- Human bone marrow	2841	99

SEC ID	Hit ID	Speicies	Description	S score	Percent
	2		expressed protein SEQ ID NO: 261.		identity
1801	6		PAC clone RP4-751H13 from 7q35-qter, complete sequence.	2830	100
1801	6	Mus musculus	unnamed protein product	2352	84 -
1802	82	Homo sapiens	GETH Human PRO792 polypeptide sequence.	1332	86
1802	16	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:155.	1332	86
1802	55	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:31.	1332	86
1803	82	Homo sapiens	GETH Human PRO792 polypeptide sequence.	1590	100
1803	AAB244 16	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:155.	1590	100
1803	AAB240 55	Homo sapiens	GETH Human PRO792 protein sequence SEQ ID NO:31.	1590	100
1804	AAB437 13	Homo sapiens	HUMA- Human cancer associated protein sequence SEQ ID NO:1158.	414	98
1804	AAR114 90	Homo sapiens	CALI- Tissue-plastin.	414	98
1804	gi339848	Homo sapiens	Human T-plastin mRNA, 5' end.	414	98
1805	AAY194 56	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	307	90
1805	gi138825 00	Mycobacterium tuberculosis CDC1551	conserved hypothetical transmembrane protein	70	32
1805	gi155071 4	Mycobacterium tuberculosis H37Rv	hypothetical protein Rv2673	70	32
1806	gi165528 50	Homo sapiens	cDNA FLJ32676 fis, clone TESTI1000168, weakly similar to PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22.	1265	100
1806	gi128599 36	Mus musculus	putative	962	78
1806	AAM388 77	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2022.	200	45
1807	AAY413 90	Homo sapiens	HUMA- Human secreted protein encoded by gene 83 clone HRAAB15.	813	100
1807	AAM399 90	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 3135.	581	44
1807	AAM389 99	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2144.	581	44
1808	gi128361 97	Mus musculus	putative	2154	75
1808	AAM823 98	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:9991.	750	90
1808	AAG040 69	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 8150.	491	100
1809	AAB952 52	Homo sapiens		3112	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1809	gi104347 29	Homo sapiens	cDNA FLJ12949 fis, clone NT2RP2005336, weakly similar to TRICHOHYALIN.	3112	99
1809	gi128040 75	Homo sapiens	hypothetical protein FLJ12949, clone MGC:11261 IMAGE:3942403, mRNA, complete cds.	1786	100
1810	AAY195 87	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	160	96
1811	gi156208 81	Homo sapiens	mRNA for KIAA1911 protein, partial cds.	1153	100
1811	AAM916 41	Homo sapiens	HUMA- Human immune/haematopoietic antigen SEQ ID NO:19234.	326	50
1811	gi128458 02	Mus musculus	putative	309	58
1812	gi104399 11	Homo sapiens	cDNA: FLJ23282 fis, clone HEP07626.	2677	100
1812	AAY996 53	Homo sapiens	INCY- Human GTPase associated protein-4.	2324	100
1812	gi101671	Rattus norvegicus	Fos-related antigen	2060	84
1813	AAY601 52	Homo sapiens	META- Human endometrium tumour EST encoded protein 212.	379	100
1813	AAY601 51	Homo sapiens	META- Human endometrium tumour EST encoded protein 211.	83	73
1813	AAB929 84	Homo sapiens	HELI- Human protein sequence SEQ ID NO:11704.	71	32
1814	gi146029 95	Homo sapiens	hypothetical protein FLJ23375, clone MGC:16634 IMAGE:4121449, mRNA, complete cds.	2299	100
1814	gi104400	Homo sapiens	cDNA: FLJ23375 fis, clone HEP16206.	2294	99
1814	AAB429 73	Homo sapiens	CURA- Human ORFX ORF2737 polypeptide sequence SEQ ID NO:5474.	725	98
1815	AAM787 22	Homo sapiens	HYSE- Human protein SEQ ID NO 1384.	1808	99
1815	gi150539 87	Homo sapiens	c-Mpl binding protein mRNA, complete cds.	1439	100
1815	AAE1019 9	Homo sapiens	HYSE- Human bone marrow derived contig polypeptide, SEQ ID NO: 64.	1231	85
1816	gi104404 74	Homo sapiens	mRNA for FLJ00074 protein, partial cds.	1001	100
1816	gi702096	Homo sapiens	cDNA FLJ20703 fis, clone KAIA1965.	546	. 63
1816	gi133251 42	Homo sapiens	DKFZP586I2223 protein, clone MGC:10840 IMAGE:3616057, mRNA, complete cds.	535	58
1817	gi100472 49	Homo sapiens	mRNA for KIAA1587 protein, partial cds.	5002	100
1817	gi136764 86	Macaca fascicularis	hypothetical protein	4641	92

SEQ	Hit ID	Speicies	Description	S score	Percent
1817	gi126591 40	Mus musculus	mage-e1	2474	identity 67
1818	AAY725 96	Homo sapiens	ZYMO Human cytokine alpha protein-27 (Zalpha27).	3538	99
1818	gi127102 97		unnamed protein product	3538	99
1818	gi104375 88		cDNA: FLJ21478 fis, clone COL05012.	2793	100
1819	gi128387 32		putative	1060	91
1819	gi657221 5	Homo sapiens	Human DNA sequence from clone RP1-37E16 on chromosome 22 Contains the 3' part of the gene for a novel VHS domain containing protein similar to predicted worm and human proteins, the SH3BP1 gene for SH3-domain binding protein 1, the gene for a novel protein similar to nitrophenylphosphatases from various organisms, the LGALS1 gene for soluble galactoside-binding lectin 1, a novel gene and the gene for a novel protein similar to mouse RIP3 (P116 Rho-interacting protein) and rat RB109, complete sequence.	647	46
1819	gi126531 07	Homo sapiens	hypothetical protein dJ37E16.5, clone MGC:8472 IMAGE:2821743, mRNA, complete cds.	647	46
1820	AAB736 90	Homo sapiens	INCY- Human oxidoreductase protein ORP-23.	2502	100
1820	gi104382 22	Homo sapiens	cDNA: FLJ21988 fis, clone HEP06320.	2502	100
1820	gi143367 19	Homo sapiens	16p13.3 sequence section 3 of 8.	2431	90
1821	gi372410 5	Homo sapiens	hHa4 gene for keratin type 1.	2029	99
1821	gi372410 1	Homo sapiens	hHa3-I gene for keratin type I.	1798	90
1821	gi 128526 06	Mus musculus	putative	1796	87
1822	gi322823 7	Homo sapiens	UHS KerB gene.	1079	88
1822	AAM794 04	Homo sapiens	HYSE- Human protein SEQ ID NO 3050.	877	81
1822	gi200962	Mus musculus	serine I ultra high sulfur protein	867	70
1823	AAB863 64	Homo sapiens	MEMO- Human ceramidase K2 protein.	1459	100
1823	AAB189 86	Homo sapiens	INCY- Amino acid sequence of a human transmembrane protein.	1459	100
1823	gi146694 36	Homo sapiens	alkaline phytoceramidase (APHC) mRNA, complete cds.	1459	100
1824	AAW616 01	Homo sapiens	INCY- Human metallothionein HMBP-I.	381	98

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1824	AAB571 83	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1761.	363	84
1824	AA0138 69	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 27761.	362	81
1825	gi159288 96	Homo sapiens	Similar to synaptotagmin-like 4, clone MGC:17313 IMAGE:3908307, mRNA, complete cds.	3496	100
1825	gi173859	Rattus norvegicus	granuphilin A	3225	91
1825	gi592673	Mus musculus	granuphilin-a	3187	90
1826	gi126531 47	Homo sapiens	signal sequence receptor, beta (translocon-associated protein beta), clone MGC:8566 IMAGE:2822983, mRNA, complete cds.	864	99
1826	gi452757	Homo sapiens	H.sapiens mRNA for TRAP beta subunit.	847	99
1826	gi173688 0	Homo sapiens	Human SSR2 mRNA for beta- signal sequence receptor, complete cds.	847	99
1827	AAB427 22	Homo sapiens	CURA- Human ORFX ORF2486 polypeptide sequence SEQ ID NO:4972.	2865	100
1827	AAB952 63	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17448.	2864	99
1827	gi104347 59	Homo sapiens	cDNA FLJ12969 fis, clone NT2RP2005841, weakly similar to Homo sapiens mRNA for ALEX3.	2864	99
1828	gi798129 7	Homo sapiens	Human DNA sequence from clone RP4-534K7 on chromosome 1p31.2-32.3. Contains the PGM1 gene for phosphoglucomutase 1, a novel gene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.	3323	100
1828	gi160418 46	Homo sapiens	clone MGC:9635 IMAGE:3915942, mRNA, complete cds.	3308	99
1828	gi140178	Homo sapiens	mRNA for KIAA1799 protein, partial cds.	3186	100
1829	gi943803 3	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1 (SR-A1) gene, complete cds.	6833	100
1829	gi104404 02	Homo sapiens	mRNA for FLJ00034 protein, partial cds.	6827	99
1829	gi143853 2	Rattus norvegicus	rAl	5019	82
1830	AAG812 94	Homo sapiens	ZYMO Human AFP protein sequence SEQ ID NO:106.	1128	100
1830	AAU035 89	Homo sapiens	INCY- Human DNA modification protein, DNAMP- 4.	1128	100

SEQ		Speicies	Description	S score	Percent
1830	gi173902 02	Homo sapiens	Similar to RIKEN cDNA 2510005D08 gene, clone MGC:27120 IMAGE:4793121, mRNA, complete cds.	1128	identity 100
1831	AAY652 82		GEST Human 5' EST related polypeptide SEQ ID NO:1443.	472	95
1831	gi128386 27	Mus musculus	putative	444	68
1831	gi651386 7	Strongylocentrot us purpuratus	tektin A1	292	40
1832	AAY108 37	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	434	100
1832	gi727160 6	Fowlpox virus	ORF FPV108 Virion envelope	72	28
1832	gi333523	Pigeonpox virus	major envelope antigen	72	28
1833	AAR561 66	Homo sapiens	USSH Neuroendocrine tumor	2003	95
1833	gi153419 94	Homo sapiens	clone MGC:17291 IMAGE:4347187, mRNA, complete cds.	2003	95
1833	gi155593 10	Homo sapiens	clone MGC:20310 IMAGE:4130556, mRNA, complete cds.	2000	94
1834	AAM514 65	Homo sapiens	TAKE Human G protein- coupled receptor protein TGR5.	1712	100
1834	AAY865 40	Homo sapiens	HUMA- Human gene 77- encoded protein fragment, SEQ ID NO:457.	679	98
1834	AAY862 91	Homo sapiens	HUMA- Human secreted protein HDPRK33, SEQ ID NO:206.	514	98
1835	gi165525 98	Homo sapiens	cDNA FLJ32467 fis, clone SKNMC2000097, moderately similar to M.musculus mRNA for protein Htf9C.	2883	99
1835	gi154264 94	Homo sapiens	HpaII tiny fragments locus 9C, clone MGC:14943 IMAGE:4054100, mRNA, complete cds.	2517	100
1835	gi104375 55	Homo sapiens	cDNA: FLJ21453 fis, clone COL04585.	2517	100
1836	gi724306 1	Homo sapiens	mRNA for KIAA1340 protein, partial cds.	2328	99
1836	gi388214 3	Homo sapiens	mRNA for KIAA0711 protein, complete cds.	311	28
1836	gi146029 92	Homo sapiens	clone MGC:16635 IMAGE:4121528, mRNA, complete cds.	309	29
1837	AAB947 27	Homo sapiens	HELI- Human protein sequence SEQ ID NO:15753.	2624	96
1837	gi104358 06	Homo sapiens	cDNA FLJ13710 fis, clone PLACE2000373, weakly similar to F-SPONDIN PRECURSOR.	2624	96
1837	gi142507 42		hypothetical protein FLJ13710, clone MGC:14171 IMAGE:4120678, mRNA, complete cds.	2473	98
838	AAB199	Homo sapiens	INCY- Human oxidoreductase	1900	99

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
==	31		OXRD-6.		
1838	gi170443 56	Homo sapiens	unnamed protein product	1900	99
1838	AAW677 37	Homo sapiens	REGC Human fsh05 gene protein product.	1528	100
1839	gi104400 14	Homo sapiens	cDNA: FLJ23356 fis, clone HEP14919.	1859	99
1839	gi152082 23	Macaca fascicularis	hypothetical protein	1798	96
1839	gi128536 89	Mus musculus	putative	1535	80
1840	gi142505 12	Homo sapiens	clone MGC:15468 IMAGE:2966921, mRNA, complete cds.	966	88
1840	gi140432 62	Homo sapiens	Similar to RIKEN cDNA 1500026B10 gene, clone MGC:15737 IMAGE:3355622, mRNA, complete cds.	966	88
1840	gi128377 54	Mus musculus	putative	710	68
1841	gi767162 9	Homo sapiens	Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein (MOG), the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a CpG island, complete sequence.	2247	90
1841	gi431182	Mus musculus	Zfp-57	674	39
1841	gi144956 50	Homo sapiens	zinc finger protein 331; zinc finger protein 463, clone MGC:15739 IMAGE:3355780, mRNA, complete cds.	444	29
1842	gi104399 51	Homo sapiens	cDNA: FLJ23311 fis, clone HEP11681.	2175	99
1842	ABB1246	Homo sapiens	HYSE- Human bone marrow expressed protein SEQ ID NO: 300.	259	100
1842	gi554172 2	Arabidopsis thaliana	putative protein	218	44
1843	gi999288 4	Homo sapiens	vacuolar proton pump 116 kDa accessory subunit (ATP6N1B) mRNA, complete cds, alternatively spliced.	4378	100
1843	AAB601 00	Homo sapiens	INCY- Human transport protein TPPT-20.	4331	99
1843	gi169032 13	Mus musculus	H-ATPase accessory subunit a4	3809	85
1844	AAM938 59	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3953.	3149	100
1844	gi172249 57	Homo sapiens	cationic amino acid transporter (SLC7A3) mRNA, complete cds.	3149	100
1844	AAM933	Homo sapiens	HELI- Human polypeptide, SEQ	3142	99

SEQ	Hit LD	Speicies	Description	S score	Percent
ID			Description	Sicore	identity
12.12	85		ID NO: 2970.		
1845	gi120530 07	Homo sapiens	mRNA; cDNA DKFZp434D1812 (from clone DKFZp434D1812); complete cds.	6038	99
1845	gi424019 5	Homo sapiens	mRNA for KIAA0853 protein, partial eds.	4974	100
1845	AAB670 47	Homo sapiens	INCY- Human immune response molecule (IMUN) protein SEQ ID NO: 1.	3777	99
1846	AAB941 08	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14340.	2903	100
1846	AAU045 57	Homo sapiens	GETH Human Stra6 homologue, PRO10282.	2903	100
1846	gi135609 66	Homo sapiens	STRA6 isoform 1 mRNA, complete cds, alternatively spliced.	2903	100
1847	AAB583 63	Homo sapiens	ROSE/ Lung cancer associated polypeptide sequence SEQ ID 701.	309	100
1847	AAY485 07	Homo sapiens	META- Human breast tumour- associated protein 52.	308	98
1847	AAM239 52	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1477.	294	98
1848	AAM937 37	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3705.	929	49
1848	gi317060 9	Rattus norvegicus	monocarboxylate transporter MCT3	631	35
1848	gi767044 6	Mus musculus	unnamed protein product	631	47
1849	AAB953 59	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17661.	3130	99
1849	gi104350 88	Homo sapiens	cDNA FLJ13181 fis, clone NT2RP3004016, weakly similar to TRANSCRIPTION INTERMEDIARY FACTOR 1- BETA.	3130	99
1849	gi729735 7	Drosophila melanogaster	CG8419 gene product	746	29
1850	gi104368 13	Homo sapiens	cDNA: FLJ20859 fis, clone ADKA01617.	2426	100
1850	gi134771 83	Homo sapiens	Similar to hypothetical protein FLJ20859, clone MGC:12940 IMAGE:2822127, mRNA, complete cds.	2357	98
1850	gi128308 10	Homo sapiens	false p73 target protein gene, complete cds.	2239	99
1851	AAM243 67	Homo sapiens	HYSE- Human EST encoded protein SEQ ID NO: 1892.	546	100
1851	AAY275 76	Homo sapiens	HUMA- Human secreted protein encoded by gene No. 10.	394	96
1851	gi30478	Homo sapiens	Human mRNA for dopamine beta-hydroxylase type b (EC 1.14.17.1).	68	26
1852	gi165515 61	Homo sapiens	cDNA FLJ31657 fis, clone NT2RI2004304, moderately similar to Homo sapiens NY-	2859	92

SEQ Hit ID		Speicles	Description	S score	Percent identity	
10			REN-2 antigen mRNA.			
1852	AAB366 26	Homo sapiens	INCY- Human FLEXHT-48 protein sequence SEQ ID NO:48.	2056	67	
1852	gi128034 69	Homo sapiens	high-glucose-regulated protein 8, clone MGC:739 IMAGE:3139250, mRNA, complete cds.	2056	67	
1853	gi776873	Homo sapiens	genomic DNA, chromosome 21q, section 87/105.	4306	99	
1853	gi142457 29	Homo sapiens	ANKRD3 mRNA for dual- specificity Ser/Thr/Tyr kinase, complete cds.	4003	94	
1853	gi988671 1	Homo sapiens	mRNA for protein kinase (dik gene).	3999	94	
1854	gi104391 29	Homo sapiens	cDNA: FLJ22655 fis, clone HSI07590.	960	100	
1854	AAG014 59	Homo sapiens	GEST Human secreted protein, SEQ ID NO: 5540.	668	100	
1854	AAU173 65	Homo sapiens	HUMA- Novel signal transduction pathway protein, Seq ID 930.	523	100	
1855	gi100471 85	Homo sapiens	mRNA for KIAA1560 protein, partial cds.	3397	100	
1855	gi175124 95	Mus musculus	Mus musculus glycerol-3-phosphate 3371 acyltransferase, mitochondrial		93	
1855	gi193367	Mus musculus	glycerol-3-phosphate acyltransferase	3363	93	
1856	ABB1223 6	Homo sapiens	HYSE- Human eppin-1 homologue, SEQ ID NO:2606.	472	100	
1856	gi139373 34	Homo sapiens	Human DNA sequence from clone RP3-461P17 on chromosome 20q12-13.2. Contains two novel genes, gene HE4 for Major Epididymisspecific protein E4 precursor (Epididymis Secretory protein E4), RPL5 (60S Ribosomal Protein L5), COX6C (Cytochrome C Oxidase subunit VIC) and HSPDI (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL, HUCHA60) pseudogenes, the SPINT3 gene for Kunitz type serine protease inhibitor 3 (HKIB9), two genes for novel Kunitz/Bovine pancreatic trypsin inhibitor and WAP-type (Whey Acidic Protein) 'four-disulfide core' domains containing proteins and the gene for Eppin-1, -2 and -3. Contains ESTs, STSs, GSSs and a CpG island, complete	415	98	
1856	gi135917	Oryctolagus	sequence.	257	66	

SEQ ID	Hit ID	Speicies	Description	S score	Percent
1857	gi128558	Mus musculus	putative	758	identity 57
1857	gi177366 46	Homo sapiens	Human DNA sequence from clone RP3-341D10 on chromosome X Contains a gene for a novel protein, part of the gene for a protein similar to	424	100
			ADP ribosylation factor 3, part of a gene similar to HTF9C and a CpG island, complete sequence.		
1857	AAM389 58	Homo sapiens	HYSE- Human polypeptide SEQ ID NO 2103.	421	43
1858	gi104395 20	Homo sapiens	cDNA: FLJ22973 fis, clone KAT11042.	2289	100
1858	gi116123 88	Homo sapiens	zinc finger transcription factor Pegasus mRNA, complete cds.	2279	99
1858	AAU161 42	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1095.	1745	98
1859	gi135440 26	Homo sapiens	putative zinc finger protein from EUROIMAGE 566589, clone MGC:13109 IMAGE:3959436, mRNA, complete cds.	1481	99
1859	AAB939 32	Homo sapiens	HELI- Human protein sequence SEQ ID NO:13929.	1474	99
1859	gi104336 47	Homo sapiens	cDNA FLJ12222 fis, clone MAMMA1001105, moderately similar to OVO PROTEIN.	1474	99
1860	AAG786 15	Homo sapiens	SHAN- Human zinc finger transcription factor BioZFTF45.	1760	89
1860	gi136234 31	Homo sapiens	clone MGC:13132 IMAGE:4124255, mRNA, complete cds.	1753	100
1860	gi131118 97	Homo sapiens	Similar to KIAA0414 protein, clone MGC:2629 IMAGE:3503643, mRNA, complete cds.	1753	100
1861	AAB622 01	Homo sapiens	RIGE- Cell cycle protein Radh- isoform 1.	3697	99
1861	gi816380 4	Mus musculus	putative repair and recombination helicase RAD26L	3215	89
1861	AAB622 02	Homo sapiens	RIGE- Cell cycle protein Radh- isoform 2.	2142	99
1862	gi259856 5	Mus musculus	rab19	1008	88
1862	AAM789 77	Homo sapiens	HYSE- Human protein SEQ ID NO 1639.	603	56
1862	gi729512 7	Drosophila melanogaster	Rab-RP3 gene product	523	55
1863	gi173840 67	Homo sapiens	Human DNA sequence from clone RP11-146P21 on chromosome 10 Contains the 3'end of a novel gene, a novel gene, the 5'end of the gene for KIAA0608 and a CpG island, complete sequence.	2467	99
1863	gi140399	Cricetulus	hypothetical protein 1-2	2311	92

SEQ ID	Hit ID			S score	Percent identity
	64	griseus			
1863	AAB951 96	Homo sapiens	HELI- Human protein sequence SEQ ID NO:17284.	2183	99
1864	gi126539 87	Homo sapiens	cutaneous T-cell lymphoma tumor antigen se70-2, clone MGC:5291 IMAGE:3451565, mRNA, complete cds.	1237	99
1864	gi113856 62	Homo sapiens	CTCL tumor antigen se70-2 mRNA, complete cds.	1237	99
1864	gi104369 25	Homo sapiens	cDNA: FLJ20957 fis, clone ADSE02053.	1233	99
1865	gi104399 11	Homo sapiens	cDNA: FLJ23282 fis, clone HEP07626.	2579	100
1865	AAY996 53	Homo sapiens	INCY- Human GTPase associated protein-4.	2544	100
1865	gi101671 2	Rattus norvegicus	Fos-related antigen	2256	84
1866	AAB530 73	Homo sapiens	GETH Human angiogenesis- associated protein PRO195, SEQ ID NO:46.	331	100
1866	AAB884 28	Homo sapiens	HELI- Human membrane or secretory protein clone PSEC0203.	331	100
1866	AAU123 07	Homo sapiens	GETH Human PRO195 polypeptide sequence.	331	100
1867	AAB941 97	Homo sapiens	HELI- Human protein sequence SEQ ID NO:14532.	4854	99
1867	gi104342 43	Homo sapiens	cDNA FLJ12634 fis, clone NT2RM4001858, weakly similar to T-BOX CONTAINING PROTEIN TBX6L.	4854	99
1867	gi669260 7	Mus musculus	MGA protein	4810	84
1868	AAB957 79	Homo sapiens	HELI- Human protein sequence SEQ ID NO:18726.	1326	100
1868	AAB428 78	Homo sapiens	CURA- Human ORFX ORF2642 polypeptide sequence SEQ ID NO:5284.	1326	100
1868	gi104366 25	Homo sapiens	cDNA FLJ14220 fis, clone NT2RP3003828.	1326	100
1869	AAY108 23	Homo sapiens	HUMA- Amino acid sequence of a human secreted protein.	183	100
1869	gi117158 4	Plasmodium falciparum	red alga1 chloroplast	72	29
1869	gi630468	Plasmodium falciparum	hypothetical protein 470 - Plasmodium falciparum >	72	29
1870	gi 143367 13	Homo sapiens	16p13.3 sequence section 3 of 8.	1867	100
1870	gi591245 9	Homo sapiens	Human DNA sequence from clone LA16-380A1 on chromosome 16 Contains two novel genes, ESTs, an STS, GSSs and five putative CpG islands, complete sequence.	1106	100
1870	gi139052 32	Mus musculus	Unknown (protein for IMAGE:3601186)	145	28

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
	82		ORF3146 polypeptide sequence SEQ ID NO:6292.		identity
1871	AAW734 00		HUMA- Human secreted protein encoded by Gene No. 4.	2454	100
1871	AAB583 40	Homo sapiens	ROSE/ Lung cancer associated polypeptide sequence SEQ ID 678.	2252	90
1872	AAB569 24	Homo sapiens	ROSE/ Human prostate cancer antigen protein sequence SEQ ID NO:1502.	2048	95
1872	AAY599 93	Homo sapiens	META- Human endometrium tumour EST encoded protein 53.	2048	95
1872	gi476122 3	Homo sapiens	NADP+-dependent isocitrate dehydrogenase (PICD) mRNA, complete cds.	2048	95
1873	AAB643 73	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA5.	1875	100
1873	AAB949 37	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16430.	1546	99
1873	gi152919 19	Drosophila melanogaster	LD31969p	1237	41
1874	AAB643 73	Homo sapiens	INCY- Amino acid sequence of human intracellular signalling molecule INTRA5.	1836	92
1874	AAB949 37	Homo sapiens	HELI- Human protein sequence SEQ ID NO:16430.	1546	99
1874	gi152919 19	Drosophila melanogaster	LD31969p	1209	39
1875	gi136235	Homo sapiens	clone MGC:12921 IMAGE:4129897, mRNA, complete cds.	590	100
1875	gi126982 16	Macaca fascicularis	hypothetical protein	589	99
1875	AAM936 16	Homo sapiens	HELI- Human polypeptide, SEQ ID NO: 3444.	584	99
1876	gi606368 8	Homo sapiens	ammecr1 gene, exon 1 and joined CDS (alternative transcripts).	968	56
1876	gi513948 2	Homo sapiens	mRNA for AMMECR1 protein.	968	56
1876	gi889465 7	Mus musculus	AMMECR1	964	53
1877	gi104402 18	Homo sapiens	cDNA: FLJ23506 fis, clone LNG03055.	2913	99
1877	AAY733 63	Homo sapiens	INCY- HTRM clone 2762174 protein sequence.	2110	100
1877	AAU162 62	Homo sapiens	HUMA- Human novel secreted protein, Seq ID 1215.	1286	98
1878	AAG671 51	Homo sapiens	INCY- Amino acid sequence of a human enzyme.	e of 1689 99	
1878	gi128562 10	128562 Mus musculus putative 1457		1457	85
878	gi312821 8	Arabidopsis thaliana	putative katanin	874	56
879	AAB600 93	Homo sapiens	INCY- Human transport protein TPPT-13.	3295	95

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1879	gi172237 24	Homo sapiens	sodium/glucose cotransporter KST1 mRNA, complete cds.	3295	95
1879	AAF8402 3_aa1	Homo sapiens	LEXI- Novel human transporter protein (NHP) encoding DNA.	3289	95
1880	AAB600 93	Homo sapiens	INCY- Human transport protein TPPT-13.	3461	99
1880	gi172237 24	Homo sapiens	sodium/glucose cotransporter KST1 mRNA, complete cds.	3461	99
1880	AAF8402 3_aa1	Homo sapiens	LEXI- Novel human transporter protein (NHP) encoding DNA.	3455	99
1881	gi 128454 75	Mus musculus	putative	1648	70
1881	gi135433 07	Homo sapiens	cargo selection protein (mannose 6 phosphate receptor binding protein), clone MGC:11117 IMAGE:3833411, mRNA, complete cds.	725	39
1881	AAY672 40	Homo sapiens	INCY- Human adipophilin-like protein (HALP) amino acid sequence.	724	39
1882	AAW469 04	Homo sapiens	ASAH A human mutant alanine aminotransferase.	1821	68
1882	gi176309 6	Homo sapiens	Human glutamate pyruvate transaminase (GPT) gene, complete cds.	1821	68
1882	gi173904 65	Homo sapiens	glutamic-pyruvate transaminase (alanine aminotransferase), clone MGC:17068 IMAGE:4179699, mRNA, complete cds.	1821	68
1883	AAD094 95_aa1	Homo sapiens	SUGE- Human SGP003 phosphatase polypeptide encoding DNA	1161	100
1883	AAE0483 7	Homo sapiens	SUGE- Human SGP003 phosphatase polypeptide.	1159	99
1883	AAB186 67	Homo sapiens	INCY- A human regulator of intracellular phosphorylation.	1021	91
1884	gi308942 7	Homo sapiens	SSC6 rearranged T cell receptor beta chain (TCRBV17) gene, complete cds.	1089	69
1884	gi300292 7	Homo sapiens	T cell receptor beta chain (TCRBV17S1-TCRBJ1S5) mRNA, complete cds.	1089	69
1884	gi298250 8	Homo sapiens	mRNA for TCR beta chain, specific for Mage 3/HLA-A2.	1089	70
1885	gi128582 21	Mus musculus	putative	1850	91
1885	gi123141 02	Homo sapiens	Human DNA sequence from clone RP3-329L24 on chromosome 6q22.1-22.33 Contains a gene for a novel protein, part of a gene for a hypothetical 23.0 KD protein, part of a gene for a protein (MCM2/3/5 family), ESTs, STSs, GSSs and a CpG island,	1405	100
1885	gi438883	Arabidopsis	complete sequence. putative DNA replication	726	41

SEC			Description	S score	Percent identity
	2	thaliana	licensing factor	 	Identity
1886	Ŏ0		clone IMAGE:3354344, mRNA, partial cds.	3001	99
1886	86	1	NEWE- Human neural cell protein marker RR/B.	673	29
1886	2		ectoderm-neural cortex-1 proteir (ENC-1) mRNA, complete eds.	673	29
1887	39		mRNA for KIAA1582 protein, partial cds.	7698	96
1887	gi165518 20		cDNA FLJ31859 fis, clone NT2RP7001231.	3076	100
1887	gi795918 1		mRNA for KIAA1460 protein, partial cds.	2840	45
1888	gi100472 39		mRNA for KIAA1582 protein, partial cds.	7800	99
1888	gi165518 20	Homo sapiens	cDNA FLJ31859 fis, clone NT2RP7001231.	2835	93
1888	gi795918	Homo sapiens	mRNA for KIAA1460 protein, partial cds.	2744	44
1889	gi100472 39	Homo sapiens	mRNA for KIAA1582 protein, partial cds.	7372	95
1889	gi795918	Homo sapiens	mRNA for KIAA1460 protein, partial cds.	2618	44
1889	gi165518 20	Homo sapiens	cDNA FLJ31859 fis, clone NT2RP7001231.	2354	81
1890	gi163072 85	Homo sapiens	clone IMAGE:3877337, mRNA, partial cds.	1627	98
1890	gi152080 51	Macaca fascicularis	hypothetical protein	1417	55
1890	AAY949 18	Homo sapiens	GEMY Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	1247	63
1891	gi278041	Homo sapiens	hBACH mRNA for brain acyl- CoA hydrolase, complete cds.	1742	100
1891	gi169243 33	Homo sapiens	cytosolic acyl coenzyme A thioester hydrolase, clone MGC:1126 IMAGE:3507488, mRNA, complete cds.	1742	100
1891	AAW748 96	Homo sapiens	HUMA- Human secreted protein encoded by gene 169 clone HPTTU11.	1715	98
1892	AAB688 74	Homo sapiens	INCY- Human RECAP polypeptide, SEQ ID NO: 4.	1266	100
1892	AAY948 90	Homo sapiens	PROT- Human protein clone HP02798.	1266	100
1892	gi144245 18	Homo sapiens	Similar to RIKEN cDNA 1190004A01 gene, clone MGC:13153 IMAGE:4302257, mRNA, complete cds.	1266	100
1893	gi145950 19	Homo sapiens	mRNA for keratin 6 irs (KRT6IRS gene).	843	77
1893	gi609207 5	Mus musculus	type II cytokeratin	836	74
893	gi128345 35	Mus musculus	putative	836	74
894	gi140291 53	Homo sapiens	microtubule-associated protein GLFND mRNA, complete cds.	2565	100

SEQ ID	Hit ID	Speicies	Description	S score	Percent identity
1894	gi131119 07	Homo sapiens	clone MGC:3213 IMAGE:3502614, mRNA, complete cds.	2565	100
1894	gi134477 59	Homo sapiens	fibronectin type 3 and SPRY domain-containing protein 1 (FSD1) mRNA, complete cds.	2562	99
1895	gi144245 91	Homo sapiens	hypothetical protein FLJ22127, clone MGC:14926 IMAGE:4123948, mRNA, complete cds.	2565	100
1895	gi104380 86	Homo sapiens	cDNA: FLJ21886 fis, clone HEP03022.	2555	99
1895	gi104384 00	Homo sapiens	cDNA: FLJ22127 fis, clone HEP19530.	1566	100
1896	gi151503 06	Homo sapiens	glycogenin-interacting protein 3 mRNA, complete cds.	1571	100
1896	gi151503 04	Homo sapiens	glycogenin-interacting protein 2 mRNA, complete cds, alternatively spliced.	1571	100
1896	gi151502 98	Homo sapiens	glycogenin-interacting protein 1 mRNA, complete cds.	1571	100

TABLE 3

SEQ ID	Database	Description	Results*
NO:	entry ID		DY 00070 A 11 02 0 500 - 00 007
950	BL00972	Ubiquitin carboxyl-terminal hydrolases	BL00972A 11.93 2.500e-20 267-
ļ]	family 2 proteins.	285 BL00972D 22.55 5.179e-17
ĺ		<u>.</u>	828-853 BL00972E 20.72 8.650e-
•		, i	13 855-877 BL00972C 16.48
			7.120e-11 411-426 BL00972B 9.45
	<u> </u>		7.923e-10 353-363
950	PR00833	POLLEN ALLERGEN POA PI	PR00833H 2.30 8.000e-10 2-17
		SIGNATURE	
950	PR00308	TYPE I ANTIFREEZE PROTEIN	PR00308A 5.90 7.671e-09 5-20
		SIGNATURE	PR00308A 5.90 9.471e-09 4-19
951	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.696e-09 331-344
951	PR00180	CELLULAR RETINALDEHYDE-	PR00180C 10.92 8.821e-09 70-92
		BINDING PROTEIN SIGNATURE	
952	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.696e-09 331-344
952	PR00180	CELLULAR RETINALDEHYDE-	PR00180C 10.92 8.821e-09 70-92
	İ	BINDING PROTEIN SIGNATURE	
953	PR00401	SH2 DOMAIN SIGNATURE	PR00401B 12.94 1.000e-08 340-
ĺ			351
954	PR00401	SH2 DOMAIN SIGNATURE	PR00401B 12.94 1.000e-08 367-
1			378
955	BL00625	Regulator of chromosome condensation	BL00625A 16.21 7.787e-16 308-
		(RCC1) proteins.	337 BL00625A 16.21 7.369e-15
}	i	1	190-219 BL00625B 17.69 1.514e-
			13 302-336 BL00625B 17.69
l			2.286e-13 184-218 BL00625B
1	1		17.69 3.957e-13 132-166
-	ł	1	BL00625A 16.21 5.690e-13 138-
1			167 BL00625A 16.21 5.731e-11
l	1		360-389 BL00625B 17.69 3.333e-
			10 354-388
L			<u> </u>

SEQ ID NO:	Database entry ID	Description	Results*
955	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633A 9.32 6.143e-09 202-219 PR00633H 15.10 6.268e-09 196- 218 PR00633F 10.03 6.354e-09 373-388 PR00633G 13.71 7.556e-
957	BL00120	Lipases, serine proteins.	09 190-209 BL00120B 11.37 9.486e-12 166-
957	PR00111	ALPHA/BETA HYDROLASE FOLD SIGNATURE	181 PR00111B 10.61 1.176e-09 170- 184
963	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.329e-10 45-93
966	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.034e-09 262-277
967	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.034e-09 74-89
968	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 804-
969	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 878-
971	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 2.080e-22 321-343 PR00380A 14.18 1.486e-21 79-101 PR00380B 12.64 6.571e-18 217- 235 PR00380C 13.18 6.927e-13 269-288
971	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 8.200e-30 320- 351 BL00411G 21.39 6.100e-28 270-312 BL00411C 15.04 7.000e- 22 79-101 BL00411F 14.77 1.273e-19 208-233 BL00411E 10.43 7.429e-12 142-161 BL00411A 11.31 4.484e-11 9-24
971	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	BL00411B 13.51 1.563e-10 45-62 PD00301A 10.24 6.400e-09 598- 609
971	DM01399	VARICELLA-ZOSTER VIRUS GENE 54 PROTEIN.	DM01399B 12.42 7.092e-09 1571- 1583

*Results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

SEQ ID NO:	Database entry ID	Description	Results*
971	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.800e-10 1350- 1361 BL00678 9.67 7.158e-09 1629-1640
971	BL00502	Polygalacturonase proteins.	BL00502A 13.44 7.341e-09 1424-
971	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 7.796e-09 568-
971	BL00226	Intermediate filaments proteins.	BL00226B 23.86 8.012e-09 930- 978
971	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 2.385e-12 1348- 1363 PR00320C 13.01 1.720e-10 1348-1363 PR00320A 16.74 4.971e-10 1348-1363 PR00320B 12.19 5.886e-10 1544-1559 PR00320A 16.74 3.415e-09 1544- 1559 PR00320C 13.01 5.500e-09 1498-1513 PR00320B 12.19 8.650e-09 1627-1642 PR00320C 13.01 9.100e-09 1627-1642

SEQ ID NO:	Database entry ID	Description	Results*
973	BL01242	Formamidopyrimidine-DNA glycosylase proteins.	BL01242F 17.92 5.300e-11 32-66
975	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 2.500e-14 46-59
975	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 7.750e-11 371- 385
976	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 99-132
977	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.250e-25 93- 115 PR00380D 9.93 4.857e-19 302-324 PR00380B 12.64 4.429e- 18 212-230 PR00380C 13.18 1.692e-16 247-266
977	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 7.750e-32 248- 290 BL00411F 14.77 1.000e-25 203-228 BL00411C 15.04 1.621e- 24 93-115 BL00411H 15.66 1.871e-24 301-332 BL00411E 10.43 6.625e-20 143-162 BL00411A 11.31 4.484e-11 5-20
977	PF00846	Hantavirus nucleocapsid protein.	PF00846H 3.96 9.182e-10 408- 445
977	BL00224	Clathrin light chain proteins.	BL00224B 16.94 7.136e-09 363- 416
978	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.368e-18 36-67
978	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 2.068e-10 36-55
980	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 9.376e-09 76- 120
982	BL00790	Receptor tyrosine kinase class V proteins.	BL00790E 29.58 1.111e-12 614- 662 BL00790E 29.58 3.111e-12 668-716 BL00790E 29.58 7.000e- 10 560-608
982	BL00279	Membrane attack complex components / perforin proteins.	BL00279E 37.11 7.632e-12 727- 775 BL00279E 37.11 2.047e-09 765-813
982	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 4.600e-11 791- 807 BL01187B 12.04 3.571e-10 829-845 BL01187B 12.04 8.714e- 10 753-769 BL01187A 9.98 4.375e-09 812-824 BL01187A 9.98 5.125e-09 774-786
982	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 5.364e-09 13-32
982	PR00764	COMPLEMENT C9 SIGNATURE	PR00764F 16.89 8.027e-10 744- 765 PR00764F 16.89 6.844e-09 782-803
982	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010A 11.79 6.192e-11 814- 826 PR00010C 11.16 5.909e-10 758-769 PR00010A 11.79 7.677e- 10 776-788 PR00010C 11.16 1.214e-09 796-807 PR00010C 11.16 8.286e-09 834-845
986	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.150e-12 126- 149
987	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 6.087e-10 93- 107 PR00019B 11.36 7.840e-09 90-104

SEQ ID NO:	Database entry ID	Description	Results*
990	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.	PD01443D 8.36 4.670e-09 815-
991	BL01101	Casein kinase II regulatory subunit proteins.	BL01101A 16.07 1.000e-40 9-54
991	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE	BL01101B 10.94 9.000e-31 72-97 PR00472C 12.38 5.154e-28 80- 102 PR00472A 8.03 7.600e-23 8- 25 PR00472B 14.84 1.000e-19
994	BL01166	RNA polymerases beta chain proteins.	25-40 BL01166G 18.10 2.500e-34 824-866 BL01166H 19.05 9.410e-30 936-986 BL01166D 17.37 4.396e-19 612-642 BL01166E 13.47 8.244e-17 682-706 BL01166C 12.21 9.357e-12 431-
995	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	456 BL00518 12.23 7.000e-09 25-34
996	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038A 13.61 6.625e-11 284- 300
996	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.	DM00984B 15.18 3.901e-09 262-
996	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009A 13.75 7.750e-09 260- 278
997	BL00905	GTP1/OBG family proteins.	BL00905D 15.00 4.214e-10 125-140
997	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 3.903e-13 63-86 PR00449A 13.20 7.750e-10 22-44
997	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.624e-10 56-96
997	BL01115	GTP-binding nuclear protein ran proteins.	BL01115B 10.81 1.505e-09 102- 146
998	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 7.300e-15 64-80
998	BL00239	Receptor tyrosine kinase class II proteins.	BI 00230F 17 14 2 602- 10 26 06
1001	BL00383	Tyrosine specific protein phosphatases proteins.	BL00239E 17.14 2.693e-10 36-86 BL00383E 10.35 5.263e-09 328- 339
1003	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 5.263e-09 246- 257
1004	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 5.263e-09 328- 339
1010	BL00226	Intermediate filaments proteins.	BL00226B 23.86 5.919e-09 560- 608
1012	PR00322	G10 PROTEIN SIGNATURE	PR00322E 6.62 1.720e-10 30-40
1012	BL00997	G10 protein.	BL00997C 6.36 3.308e-09 29-39
1013	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 110- 139 BL00269A 8.53 2.607e-20 45-65 BL00269B 19.17 5.500e-17 72-101
1014	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e-10 6-60
1015	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.846e-11 476- 493 BL00028 16.07 6.192e-11
	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	989-1006 PR00048A 10.52 6.087e-10 473- 487 PR00048A 10.52 1.000e-09 986-1000
1015	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.571e-12 464- 477 PD00066 13.92 7.000e-12 977-990 PD00066 13.92 4.600e- 09 949-962 PD00066 13.92

SEQ ID NO:	Database entry ID	Description	Results*
			7.300e-09 397-410
1019	BL00289	Pentaxin family proteins.	BL00289E 18.00 4.375e-13 22-37
1019	PR00895	PENTAXIN SIGNATURE	PR00895G 14.55 4.913e-10 19-31
1022	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 4.571e-09 140- 183
1023	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.684e-13 248- 264
1023	PR00154	AMP-BINDING SIGNATURE	PR00154A 8.88 7.375e-10 241- 253
1026	BL00421	Transmembrane 4 family proteins.	BL00421E 20.97 1.851e-09 17-47
1026	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE	PR00259D 13.50 7.097e-09 20-47
1028	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.149e-29 6-45
1028	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.692e-15 234- 247 PD00066 13.92 3.400e-14 150-163 PD00066 13.92 5.800e- 14 206-219 PD00066 13.92 8.714e-12 178-191
1028	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.350e-13 102- 119 BL00028 16.07 5.500e-11 190-207 BL00028 16.07 6.192c- 11 218-235 BL00028 16.07
<u></u>	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	1.000e-09 134-151 PR00048A 10.52 4.750e-14 215-
1028			229 PR00048A 10.52 5.500e-13 99-113 PR00048A 10.52 4.316e- 11 131-145 PR00048B 6.02 4.462e-11 115-125 PR00048A 10.52 1.391e-10 159-173 PR00048B 6.02 6.625e-10 203- 213 PR00048A 10.52 4.600e-09 187-201 PR00048B 6.02 8.579e- 09 147-157
1029	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 2.059e-10 215- 230
1029	BL00790	Receptor tyrosine kinase class V proteins.	BL00790F 15.90 2.519e-09 157- 184
1032	BL00269	Mammalian defensins proteins.	BL00269C 16.52 6.786e-26 133- 162 BL00269A 8.53 2.607e-20 68-88 BL00269B 19.17 5.500e-17 95-124
1033	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 1.231e-20 75- 128
1034	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.835e-11 326- 359
1034	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 4.150e-11 112- 126 PR00019B 11.36 8.000e-11 109-123 PR00019B 11.36 8.500e- 11 184-198 PR00019A 11.19 6.478e-10 187-201 PR00019A 11.19 7.333e-09 63-77
1034	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 9.609e-09 334- 344
1035	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 6.276e-12 358- 376
1035	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 6.459e-11 360-

SEQ ID NO:	Database entry ID	Description	Results*
			379
1038	BL00120	Lipases, serine proteins.	BL00120C 12.62 9.053e-12 95- 106
1038	PR00825	VESPID VENOM ALLERGEN PHOSPHOLIPASE A1 SIGNATURE	PR00825B 14.81 1.371e-10 83- 104
1038	PR00821	TRIACYLGLYCEROL LIPASE FAMILY SIGNATURE	PR00821E 9.64 4.896e-12 19-38 PR00821F 16.10 1.806e-09 118- 134
1044	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.500e-30 169- 212
1044	BL00032	'Homeobox' antennapedia-type protein.	BL00032C 11.28 5.179e-16 197- 215 BL00032B 10.83 3.060e-15 158-197
1044	PR00024	HOMEOBOX SIGNATURE	PR00024C 7.49 8.071e-13 201- 211 PR00024B 11.27 7.000e-12 191-202
1044	PR00026	ENGRAILED HOMEODOMAIN SIGNATURE	PR00026A 7.47 9.710e-12 153-
1044	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.724e-10 192- 209
1044	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 6.434e-10 155-
1048	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.200e-14 7-41
1048	BL00211	ABC transporters family proteins.	BL00211A 12.23 4.600e-09 9-21
1049	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 1.783e-09 211- 230 PR00014A 8.22 3.045e-09 373-383 PR00014C 15.44 6.087e- 09 309-328
1049	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 1.750e-12 642- 673 BL00790I 20.01 6.125e-12 320-351 BL00790I 20.01 6.679e- 09 222-253
1049	PR00096	GLUTAMINE AMIDOTRANSFERASE SUPERFAMILY SIGNATURE	PR00096B 9.72 9.827e-09 689-
1050	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.	DM00372C 23.69 4.919e-12 67-103
1053	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 194- 233
1053	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1057	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464A 20.47 9.591e-16 149- 170 PR00464C 18.84 1.000e-15 324-353 PR00464D 17.40 6.250e- 15 353-371 PR00464B 20.41 1.844e-12 205-224
1057	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385A 14.97 1.346e-12 335- 353 PR00385B 10.22 4.130e-11 353-367
1057	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463E 17.37 4.814e-11 344- 371
1058	PD02382	RECEPTOR CHAIN PRECURSOR TRANSME.	PD02382A 17.43 9.321e-09 99- 115
1060	BL00795	Involucrin proteins.	BL00795C 17,06 6.442e-10 905- 950
1060	BL00422	Granins proteins.	BL00422C 16.18 4.255e-10 910- 938 BL00422C 16.18 4.353e-09

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	1		913-941
1060	PF00992	Troponin.	PF00992A 16.67 2.184e-09 900- 935 PF00992A 16.67 5.382e-09 889-924
1060	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 7.429e-09 883- 934
1060	PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.326e-09 903- 938
1063	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 603- 636
1063	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.643e-10 96-111 PR00049D 0.00 2.525e-09 95-110 PR00049D 0.00 3.898e-09 114- 129 PR00049D 0.00 7.407e-09 97-112
1063	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 8.670e-09 100- 112
1064	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 137- 176
1064	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1065	BL01282	BIR repeat proteins.	BL01282B 30.49 1.000e-11 187- 226
1065	PR00544	PROGESTERONE RECEPTOR SIGNATURE	PR00544F 7.76 3.329e-09 18-35
1066	BL00218	Amino acid permeases proteins.	BL00218D 21.49 7.324e-11 226- 271 BL00218E 23.30 3.475e-09 307-347
1067	BL00994	Bacterial export FHIPEP family proteins.	BL00994A 15.15 1.086e-09 71- 118
1068	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.385e-33 6-45
1068	BL01030	RNA polymerases M / 15 Kd subunits proteins.	BL01030 23.44 7.480e-10 283- 321
1068	BL00466	TFIIS zinc ribbon domain proteins. PROTEIN ZINC-FINGER METAL-BINDI.	BL00466 25.88 5.622e-09 283- 320 PD00066 13.92 2,385e-15 271-
			284 PD00066 13.92 3.077e-15 243-256 PD00066 13.92 3.077e-15 320-333 PD00066 13.92 3.077e-15 348-361 PD00066 13.92 3.077e-15 376-389 PD00066 13.92 3.077e-15 432-445 PD00066 13.92 3.077e-15 617-630 PD00066 13.92 3.077e-15 701-714 PD00066 13.92 7.923e-15 215-228 PD00066 13.92 8.200e-14 589-602 PD00066 13.92 8.800e-14 729-742 PD00066 13.92 5.714e-12 542-555 PD00066 13.92 5.714e-12 542-555 PD00066 13.92 5.71e-12 561-574 PD00066 13.92 3.739e-11 404-417 PD00066 13.92 1.692e-10 299-312 PD00066 13.92 2.038e-10 488-501 PD00066 13.92 8.615e-10 645-658 PD00066 13.92 6.700e-

SEQ ID	Database	Description	Results*
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		Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.950e-13 388- 405 BL00028 16.07 6.400e-13 444-461 BL00028 16.07 1.692e- 11 227-244 BL00028 16.07 3.423e-11 332-349 BL00028 16.07 6.538e-11 685-702 BL00028 16.07 7.231e-11 713- 730 BL00028 16.07 7.577e-11 573-590 BL00028 16.07 4.300e- 10 601-618 BL00028 16.07 5.500e-10 171-188 BL00028 16.07 5.800e-10 255-272 BL00028 16.07 7.900e-10 657- 674 BL00028 16.07 9.700e-10 526-543 BL00028 16.07 2.029e- 09 283-300 BL00028 16.07 3.829e-09 741-758 BL00028 16.07 6.914e-09 360-377
			BL00028 16.07 7.686e-09 416-
1068	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.750e-14 570-584 PR00048A 10.52 2.929e-13 329-343 PR00048A 10.52 5.500e-13 224-238 PR00048A 10.52 1.000e-12 598-612 PR00048A 10.52 1.000e-12 598-612 PR00048A 10.52 5.735ae-12 252-266 PR00048A 10.52 5.765e-12 441-455 PR00048A 10.52 7.353e-12 385-399 PR00048A 10.52 7.353e-12 385-399 PR00048A 10.52 7.353e-12 710-724 PR00048A 10.52 7.353e-12 710-724 PR00048A 10.52 3.842e-11 357-371 PR00048A 10.52 5.263e-11 626-640 PR00048A 10.52 5.737e-11 280-294 PR00048A 10.52 7.632e-11 682-696 PR00048A 10.52 7.632e-11 682-696 PR00048A 10.52 8.579e-11 654-668 PR00048B 6.02 2.125e-10 457-467 PR00048A 10.52 2.565e-10 738-752 PR00048A 10.52 6.087e-10 523-537 PR00048B 6.02 7.188e-10 698-708 PR00048B 6.02 7.188e-10 698-708 PR00048B 6.02 7.188e-10 726-736 PR00048B 6.02 1.000e-09 240-250 PR00048A 10.52 3.520e-09 308-322 PR00048A 10.52 4.600e-09 551-565 PR00048B 6.02 1.000e-08 586-596
1069	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 1.545e-11 117- 158
1070	PF00168 PR00360	C2 DOMAIN SIGNATURE	PF00168C 27.49 1.750e-09 202- 228
		C2 DOMAIN SIGNATURE	PR00360B 13.61 2.227e-09 219- 233
	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962D 10.40 3.054e-10 178- 202
1075	PR00320	G-PROTEIN BETA WD-40 REPEAT	PR00320A 16.74 2.976e-09 181-

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		SIGNATURE	196
1078	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 2.478e-13 310- 323
1078	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09 41-52
1078	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.931e-11 214- 229 PR00320B 12.19 3.829e-10 214-229 PR00320C 13.01 3.880e- 10 214-229 PR00320C 13.01 4.900e-09 257-272
1079	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774D 10.59 8.396e-09 339- 365
1079	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.839e-09 588- 632
1080	BL00615	C-type lectin domain proteins.	BL00615A 16.68 3.160e-11 129- 147
1081	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.705e-11 47-86
1082	BL00359	Ribosomal protein L11 proteins.	BL00359B 23.07 7.462e-24 160- 201 BL00359C 22.18 6.586e-22 215-249 BL00359A 20.66 4.000e-21 124-160
1082	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 1.000e-08 144- 177
1084	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 1.220e-09 104- 139
,	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.000e-17 755- 772 BL00028 16.07 6.625e-15 699-716 BL00028 16.07 8.412e- 14 223-240 BL00028 16.07 8.941e-14 167-184 BL00028 16.07 6.850e-13 391-408 BL00028 16.07 1.783e-12 559- 576 BL00028 16.07 2.957e-12 307-324 BL00028 16.07 7.652e- 12 503-520 BL00028 16.07 7.652e-12 811-828 BL00028 16.07 8.043e-12 335-352 BL00028 16.07 1.346e-11 447- 464 BL00028 16.07 2.385e-11 867-884 BL00028 16.07 4.462e- 11 671-688 BL00028 16.07 5.846e-11 587-604 BL00028 16.07 6.192e-11 839-856 BL00028 16.07 6.192e-11 895- 912 BL00028 16.07 8.962e-11 531-548 BL00028 16.07 1.600e- 10 279-296 BL00028 16.07 1.600e-10 363-380 BL00028 16.07 6.100e-10 111-128 BL00028 16.07 6.700e-10 643- 660 BL00028 16.07 8.500e-10 251-268 BL00028 16.07 1.771e- 09 783-800 BL00028 16.07 5.886e-09 475-492
1084	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.600e-18 696- 710 PR00048A 10.52 5.091e-15 164-178 PR00048A 10.52 6.727e- 15 836-850 PR00048A 10.52

	SEQ ID	Database	Description	Dogulto*
	NO:	entry ID		Results*
	}			1.000e-14 220-234 PR00048A
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				570 PR00048A 10.52 9.250e-14
		1		388-402 PR00048A 10.52 1.643e-
		ļ		13 640-654 PR00048A 10.52 3.571e-13 304-318 PR00048A
- 1		1		10.52 3.571e-13 528-542
		1		PR00048A 10.52 8.071e-13 332-
				346 PR00048A 10.52 8.071e-13
İ				808-822 PR00048A 10.52 8.071e-
				13 864-878 PR00048A 10.52
				8.714e-13 500-514 PR00048A
-				10.52 7.353e-12 892-906
		ĺ		PR00048B 6.02 1.000e-11 292-
				302 PR00048B 6.02 1.000e-11
-				516-526 PR00048B 6.02 1.000e- 11 824-834 PR00048A 10.52
1		1		3.842e-11 276-290 PR00048A
				10.52 6.684e-11 584-598
		-		PR00048A 10.52 9.053e-11 668-
				682 PR00048A 10.52 4.130e-10
		ł		360-374 PR00048A 10.52 6.870e-
				10 752-766 PR00048B 6.02
				1.474e-09 768-778 PR00048B
1		İ		6.02 3.368e-09 236-246
1			·	PR00048B 6.02 3.368e-09 460-
-		1	·	470 PR00048B 6.02 4.789e-09
				152-162 PR00048B 6.02 4.789e- 09 376-386 PR00048B 6.02
1				4.789e-09 600-610 PR00048A
١				10.52 4.960e-09 108-122
1		ļ		PR00048A 10.52 4.960e-09 248-
1				262 PR00048B 6.02 6.211e-09
				264-274 PR00048B 6.02 6.211e-
				09 488-498 PR00048B 6.02
		. 1		6.211e-09 796-806 PR00048B
1				6.02 7.632e-09 404-414
				PR00048B 6.02 7.632e-09 712-
L				722 PR00048A 10.52 8.920e-09 780-794
1	1084	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.600e-14 295-
				308 PD00066 13.92 1.600e-14
			4	323-336 PD00066 13.92 1.600e-
ĺ				14 519-532 PD00066 13.92
				1.600e-14 547-560 PD00066
		,		13.92 1.600e-14 827-840
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		1		868 PD00066 13.92 5.200e-14
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	1	j		14 575-588 PD00066 13.92
		ĺ		8.200e-14 883-896 PD00066
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				168 PD00066 13.92 2.500e-13 155-
				379-392 PD00066 13.92 2.286e-
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L				2.286e-12 491-504 PD00066

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			13.92 2.286e-12 799-812 PD00066 13.92 2.714e-12 463- 476 PD00066 13.92 2.714e-12 715-728 PD00066 13.92 2.714e- 12 771-784 PD00066 13.92 3.571e-12 687-700 PD00066 13.92 7.000e-12 407-420 PD00066 13.92 1.000e-10 127- 140 PD00066 13.92 1.000e-08 603-616
1085	PR00679	PROHIBITIN SIGNATURE	PR00679F 8.03 6.478e-28 178- 202 PR00679C 14.44 7.677e-22 107-126 PR00679E 12.82 5.171e- 19 153-173 PR00679D 11.91 9.053e-18 130-147 PR00679G 6.13 7.882e-17 201-218 PR00679B 13.63 2.444e-10 84- 104
1086	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245E 12.40 8.286e-12 45-60
1086	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237G 19.63 5.814e-09 26-53
1087	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 6.885e-10 99- 120
1088	BL01145	Ribosomal protein L34e proteins.	BL01145A 13.73 1.000e-12 3-45
1093	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154D 12.57 7.387e-09 95- 106
1093	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE	PR00121E 13.97 9.444e-09 92- 111
1095	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e-15 439- 452 PD00066 13.92 2.800e-14 411-424 PD00066 13.92 2.800e- 14 467-480 PD00066 13.92 5.800e-14 495-508 PD00066 13.92 5.800e-14 523-536 PD00066 13.92 8.200e-14 355- 368 PD00066 13.92 5.500e-13 579-592 PD00066 13.92 3.143e- 12 551-564 PD00066 13.92 4.857e-12 383-396
1095	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.150e-13 367-384 BL00028 16.07 8.200e-13 563-580 BL00028 16.07 3.348e-12 479-496 BL00028 16.07 7.652e-12 423-440 BL00028 16.07 8.826e-12 619-636 BL00028 16.07 4.115e-11 451-468 BL00028 16.07 5.500e-11 395-412 BL00028 16.07 7.231e-11 591-608 BL00028 16.07 1.600e-10 339-356 BL00028 16.07 2.200e-10 535-552
1095	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.375e-16 560- 574 PR00048A 10.52 4.214e-13 476-490 PR00048A 10.52 6.143e- 13 364-378 PR00048B 6.02 6.400e-13 492-502 PR00048B 6.02 1.000e-11 352-362 PR00048B 6.02 1.000e-11 408-

SEQ II NO:	Database entry ID	Description	Results*
			418 PR00048B 6.02 1.692e-11 548-558 PR00048A 10.52 1.947e
			11 588-602 PR00048A 10.52 3.842e-11 420-434 PR00048B 6.02 4.462e-11 464-474
			PR00048A 10.52 6.684e-11 392- 406 PR00048A 10.52 6.684e-11 448-462 PR00048B 6.02 7.231e-
		·	11 436-446 PR00048A 10.52 5.696e-10 532-546 PR00048B
			6.02 5.263e-09 576-586 PR00048A 10.52 6.400e-09 504- 518 PR00048A 10.52 6.760e-09
		·	336-350 PR00048A 10.52 7.120e- 09 616-630
1095	PD02462	PROTEIN BOLA TRANSCRIPTION REGULATION AC.	PD02462A 22.48 9.232e-09 472- 507
1097	BL00649 PR00249	G-protein coupled receptors family 2 proteins.	426
1057	F K00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00249C 17.08 8.839e-11 402- 426 PR00249A 15.88 7.851e-09
1097	PR00248	METABOTROPIC GLUTAMATE GPCR SIGNATURE	330-355 PR00248E 17.85 9.366e-09 442- 465
1100	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.875e-09 886- 902
1101	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.655e-16 255- 273 PR00205A 14.73 1.000e-12 180-196 PR00205B 11.39 4.927e- 10 475-493 PR00205C 13.65 9.438e-10 515-530
1101	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 1.000e-40 148- 196 BL00232A 27.72 5.125e-25 54-87 BL00232B 32.79 4.286e-19 257-305 BL00232C 10.65 7.429e- 16 255-273 BL00232B 32.79 1.500e-10 372-420 BL00232C 10.65 6.538e-10 475-493 BL00232C 10.65 7.632e-09 146-
1103	BL00122	Carboxylesterases type-B serine proteins.	BL00122A 12.04 3.152e-15 86- 107 BL00122D 12.53 7.097e-14 197-213 BL00122B 16.84 1.346e- 13 148-159 BL00122C 7.91
1105	BL00018	EF-hand calcium-binding domain proteins.	9.550e-10 168-179 BL00018 7.41 2.800e-10 217-230
1105	PR00450	RECOVERIN FAMILY SIGNATURE	BL00018 7.41 8.650e-10 133-146 PR00450E 12.14 3.438e-15 174- 193 PR00450B 11.76 5.574e-13
	·		82-102 PR00450D 16.58 6.714e- 13 152-172 PR00450C 12.22 6.864e-12 128-150 PR00450G
1108	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	15.33 6.591e-09 224-245 PD00066 13.92 6.143e-12 927- 940 PD00066 13.92 7.000e-09
1108	BL00028	Zinc finger, C2H2 type, domain proteins.	343-356 BL00028 16.07 3.250e-13 911- 928 BL00028 16.07 9.100e-13

SEQ ID NO:	Database entry ID	Description	Results*
NO.	entry 1D		327-344 BL00028 16.07 3.348e- 12 939-956 BL00028 16.07 5.500e-11 270-287 BL00028
			16.07 4.000e-10 298-315 BL00028 16.07 6.700e-10 968-
			985 BL00028 16.07 9.700e-10 191-208 BL00028 16.07 9.700e- 10 355-372 BL00028 16.07
	·		4.857e-09 384-401 BL00028 16.07 7.171e-09 242-259
1108	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 6.000e-12 924- 934 PR00048A 10.52 4.522e-10
			324-338 PR00048A 10.52 4.913e- 10 908-922 PR00048A 10.52 7.652e-10 936-950 PR00048A
			10.52 4.600e-09 965-979 PR00048A 10.52 7.480e-09 352-
	1	·	366
1108	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970A 8.50 9.100e-09 910- 917
1109	DM01857	5 kw NUCLEOSIDE TRANSPORT DEPENDENT NA.	DM01857B 14.94 6.471e-19 284- 312 DM01857E 18.90 7.313e-18
			488-527 DM01857F 12.86 7.045e-15 548-575 DM01857C
			15.62 4.500e-14 312-344
			DM01857A 20.25 1.667e-13 207-
			250 DM01857D 16.80 3.165e-12 372-410
1112	DM01840	kw SPAC24B11.09 R07E5.13.	DM01840B 22.04 1.844e-40 59- 103 DM01840A 10.95 9.571e-13
	3		31-43
1114	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e-14 53-97
1114	PR00449	TRANSFORMING PROTEIN P21 RAS	PR00449A 13.20 9.308e-16 53-75
		SIGNATURE	PR00449C 17.27 8.920e-15 94- 117 PR00449B 14.34 5.680e-10 76-93
1114	PR00879	FISH ACETYLCHOLINESTERASE SIGNATURE	PR00879A 6.28 1.450e-09 37-43
1114	BL01125	ROK family proteins.	BL01125D 13.61 7.429e-09 214- 227
1115	PF00622	Domain in SPla and the RYanodine Receptor.	PF00622B 21.00 2.500e-13 265- 287
1115	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 9.571e-10 103- 112
1116	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 5.050e-11 66-80 PR00019B 11.36 6.850e-10 63-77
1116	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315G 15.85 6.362e-10 84- 120 DM00315G 15.85 3.340e-09 246-282
1117	BL00509	Ras GTPase-activating proteins.	BL00509B 10.28 5.263e-10 429- 440
1117	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.357e-10 794- 809 PR00049D 0.00 1.915e-09 793-808 PR00049D 0.00 3.593e- 09 792-807 PR00049D 0.00
1117	DM00215	PROLINE-RICH PROTEIN 3.	5.729e-09 791-806 DM00215 19.43 7.559e-09 780- 813

1117	SEQ ID		Description	Results*
1120 PR00720 MAMMALIAN LMW PHOSPHOTYROSINE PROTEIN PR00720C 12.41 1.099e-27.88-109 PR00720D 16.514 2.000e-17 28-44 PR00720C 10.01 1.342e-15 109 PR00720D 17.52 1.778e-15 109 PR00720D 17.52 1.778e-15 117-139 PR00720D 17.32 1.778e-15 117-139 PR00720D 17.32 1.778e-15 117-139 PR00720D 17.32 1.778e-15 110-127 1120 PR00719	NO:	PR00806	VINCIII IN SIGNATURE	PD000064 6 62 0 207 00 704
NAMMALIAN LMW			VALOS DA VIOLO VALORO	
PHOSPHOTYROSINE PROTEIN	1120	PR00720		
PHOSPHATASE SIGNATURE		İ	PHOSPHOTYROSINE PROTEIN	109 PR00720B 10.61 4.789e-20
117-139 PR00710 17.32 1.778e- 15 110-127 1778e- 15 110-127 1778e- 15 110-127 1778e- 15 110-127 1778e- 15 110-127 1778e- 16 110 PR00719C 14.10 5.000e-23 9-27 10 PR00719C 14.10 5.000e-13 9-27 10 PR00719C 14.10 5.000e-13 9-27 10 PR00719C 14.10 5.000e-13 9-27 10 PR00719C 14.10 5.000e-13 9-27 10 PR00719D 14.32 1.346e-15 52-69 PR00719D 17.52 9.654e-15 110-124 110 PR00719D 14.32 1.346e-15 52-69 PR00719D 17.52 9.654e-15 110-124 110 PR00719D 14.32 1.346e-15 52-69 PR00719D 17.52 9.654e-15 110-124 110 PR00719D 14.52 9.554e-19 10 PR00719D 17.52 9.654e-15 110-124 110 PR00719D 18.497 - 10 PR00719D 17.52 9.654e-15 173-152 110-124 110 PR00719D 18.497 - 10 PR00719D 17.52 9.10 10 PR00719D 18.497 - 10 PR00719D 18.4			PHOSPHATASE SIGNATURE	71-87 PR00720A 16.54 2.000e-17
1120 PR00719 LMW PHOSPHOTYROSINE PROTEIN PR007190 14.49 3.000e-23 9-27 PR007190 14.10 5.000e-18 85-101 PR007190 14.10 5.000e-18 85-101 PR007190 14.32 1.346e-15 52-69 PR007190 17.52 9.654e-15 110-124 PD00131 ATP-BINDING TRANSPORT PD00131B 34.97 7.987e-09 108-162 PR007190 17.52 9.654e-15 110-124 PD00131B 34.97 7.987e-09 108-162 PR00356 PR00358 PR00356 PR00358 PR00356 PR00358 PR00356 PR00358 PR00356 PR00358 PR00356 PR00358				28-41 PR00720E 10.01 1.342e-16
1120 PR00719 LMW PHOSPHOTYROSINE PROTEIN PR00719C 14.10 5.000e-13 9-27 PR00719C 14.10 5.000e-13 8-5 PR00719C 14.10 5.000e-18 8-5 PR00719D 17.52 9.654e-15 10-124 PD00131B 34.97 7.987e-09 108-162 PR00719D 17.52 9.654e-15 110-124 PD00131B 34.97 7.987e-09 108-162 PR00719C 17.52 9.654e-15 110-124 PD00131B 34.97 7.987e-09 108-162 PR00356 C-type lectin domain proteins. BL00615A 16.68 9.526e-13 573-591 PR00356	<u> </u>	j.,	·	117-139 PR00720D 17.32 1.778e-
PHOSPHATASE SIGNATURE	1120	PR00719	LMW PHOSPHOTYROSINE PROTEIN	
101 PR00719B 14.32 1.346c-15 52-69 PR00719D 17.52 9.654e-15 110-124 1101 PD00131			PHOSPHATASE SIGNATURE	PR00719C 14.10 5.000e-18 85-
1101	1	-		101 PR00719B 14.32 1.346e-15
1121 PD00131 ATP-BINDING TRANSPORT TRANSMEMBR. 162		1		
TRANSMEMBR	1121	PD00131	ATP-BINDING TRANSPORT	
1123 PR00356 TYPE II ANTIFREEZE PROTEIN SIGNATURE FAMILY SIGNATURE PR00439C 13.33 3.793e-10.591-609 PR00356C 13.33 3.793e-10.591-609 PR00356C 13.33 3.793e-10.591-609 PR00439C 15.32 9.217e-09.332-333 PR00439C 15.32 9.217e-09.332-333 PR00439C 15.32 9.217e-09.332-350 BL00134A 11.96.5.781e-15.493-510 BL00134B 15.99.4.194e-14 675-699 BL00021B 13.33 8.984e-12.493-510 BL00021B 13.33 8.984e-12.493-511 BL00495 Apple domain proteins. BL00021B 13.33 8.984e-12.493-511 BL00495 Apple domain proteins. BL00021B 13.33 8.984e-12.493-511 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79.5.345e-14.251-269 PR00453B 14.65 4.682e-10 290-305 PR00722C 10.87 4.273e-11 674-687 PR00722C 10.87 4.			TRANSMEMBR.	
1123 PR00356 TYPE II ANTIFREEZE PROTEIN SIGNATURE PR00356C 13.33 3.793e-10 591-609 PR00356D 13.09 5.038e-09 619-636 PR00356D 13.09 5.038e-09 619-636 PR0039C 15.32 9.217e-09 332-353 PR00439 Serine proteases, trypsin family, histidine proteins. BL00134A 11.96 5.781e-15 493-510 BL00134B 15.99 4.194e-14 675-699 BL00021B 13.33 8.984e-12 493-511 BL00495 Apple domain proteins. BL00495N 11.04 9.735e-11 667-702 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305 PR00722C 10.87 4.273e-11 674-687 PR00722C 10.87 4.273e-11 674-687 PR00722C 10.87 4.273e-11 674-687 PR00722B 12.51 4.000e-09 554-569 BL00236D 25.66 4.000e-30 64-106 BL00236D 25.66 4.000e-30 64-106 BL00236D 25.66 4.000e-30 64-106 PR00524 CHOLECYSTOKINI TYPE A RECEPTOR PR00524 F.36 7.718e-10 367-412 PR00524 CHOLECYSTOKINI TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524 CHOLECYSTOKINI TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR PR00524F 5.36 7.718e-10 367-412 PR00524F 5.36 7.	1123	BL00615	C-type lectin domain proteins.	
SIGNATURE FROU356 13.33 3.793-6.10 591-609 PRO0356D 13.09 5.038e-09 619-636	1123	PR00356	TVDE II ANTIEDEEZE DROTTER	
1123 PR00439 11-S SEED STORAGE PROTEIN FAMILY PR00439C 15.32 9.217e-09 332-353 SignATURE Serine proteases, trypsin family, histidine proteins. BL00134A 11.96 5.781e-15 493-510 BL00134B 15.99 4.194e-14 675-699 BL00021B 13.33 8.984e-12 493-511 BL0021B 13.33 8.984e-12 493-511 BL00495	1123	1100550		
1123 PR00439 I1-S SEED STORAGE PROTEIN FAMILY PR00439C 15.32 9.217e-09 332-353 353 353 353 353 350 3				
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1127 BL00021 Kringle domain proteins. BL00021B 13.33 8.984e-12 493-511 1127 BL00495 Apple domain proteins. BL000495N 11.04 9.735e-11 667-702 1127 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305 1127 PR00722 CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE PR00722A 12.27 9.129e-13 494-510 PR00722C 10.87 4.273e-11 674-687 PR00722B 12.51 4.000e-09 554-569 1128 BL00236 Neurotransmitter-gated ion-channels proteins. BL00236D 25.66 4.000e-30 64-106 1128 PR00252 NEUROTRANSMITTER-GATED ION CHANNEL FAMILY SIGNATURE BL00604F 5.96 7.718e-10 367-412 1129 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.000e-11 31-58 BL01113A 17.99 1.000e-11 31-58 BL01113A 17.99 1.015e-11 31-58 BL01113A 17.99 5.001e-11 167-194 BL01113A 17.99 5.001e-11 167-19	112/	BL00134	Serine proteases, trypsin family, histidine	BL00134A 11.96 5.781e-15 493-
BL00021 Kringle domain proteins. BL00021B 13.33 8.984e-12 493-511			protonis.	510 BL00134B 15.99 4.194e-14
1127 BL00495 Apple domain proteins. BL00495N 11.04 9.735e-11 667-702 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305 PR00722A 12.27 9.129e-13 494-510 PR00722	1127	BL00021	Kringle domain proteins.	BL00021B 13 33 8 984e-12 403
1127 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305 PR00722A 12.27 9.129e-13 494-510 PR00722 CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE PR00722A 12.27 9.129e-13 494-510 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR0072B 1	1107			511
1127 PR00453 VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE PR00453A 12.79 5.345e-14 251-269 PR00453B 14.65 4.682e-10 290-305 PR00722 CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE PR00722A 12.27 9.129e-13 494-510 PR00722C 10.87 4.273e-11 674-687 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-09 554-569 PR00722B 12.51 4.000e-30 64-106 PR0072B 12.51 4.000e-30 64-106 PR0072B 12.29 7.097e-10 71-84 PR0072B 12.51 4.000e-30 64-106 PR0072B 12.29 7.097e-10 71-84 PR0072B 12.29 7.09	1127	BL00495		
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1127 PR00722 CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE PR00722A 12.27 9.129e-13 494-510 PR00722C 10.87 4.273e-11 674-687 PR00722B 12.51 4.000e-09 554-569 BL01253 I1.34 5.348e-09.674-688 BL00236 Neurotransmitter-gated ion-channels proteins. BL00236D 25.66 4.000e-30 64-106 BL00236D NEUROTRANSMITTER-GATED ION CHANNEL FAMILY SIGNATURE PR00252D 12.29 7.097e-10 71-84 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE PR00524F 5.36 7.415e-09 208-222 S1031134 17.99 6.455e-14 158-185 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.614e-11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01114B 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180-1148 180			DOMAIN SIGNATURE	269 PR00453R 14 65 4 6922 10
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1127 BL01253 Type I fibronectin domain proteins. BL01253G 11.34 5.348e-09.674-688 1128 BL00236 Neurotransmitter-gated ion-channels proteins. BL00236D 25.66 4.000e-30 64-106 1128 PR00252 NEUROTRANSMITTER-GATED ION CHANNEL FAMILY SIGNATURE CHANNEL FAMILY SIGNATURE 1129 BL00604 Synaptophysin / synaptoporin proteins. BL00604F 5.96 7.718e-10 367-412 1129 PR00524 CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE C1q domain proteins. BL01113A 17.99 6.455e-14 158-185 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 1.923e-12 393-420 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.000e-11 284-311 BL01113A 17.99 1.000e-11 31-58 BL01113A 17.99 1.014e-11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A 17.99 5.091e-11 167-194 BL01113A			FAMILY (SI) SIGNATURE	510 PR00722C 10.87 4.273e-11
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PR00252 NEUROTRANSMITTER-GATED ION CHANNEL FAMILY SIGNATURE	1128	BL00236	Neurotransmitter-gated ion-channels proteins.	
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PR00524 CHOLECYSTOKININ TYPE A RECEPTOR PR00524F 5.36 7.415e-09 208-222	1129	BL00604	Synaptophysin / synaptoporin proteins.	BL00604F 5.96 7.718e-10 367-
SIGNATURE SIGNATURE 222 BL01113 C1q domain proteins. BL01113A 17.99 6.455e-14 158- 185 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 1.923e- 12 393-420 BL01113A 17.99 4.462e-12 230-257 BL01113A 17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.000e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A	1120	DD00524	CYTOX P.CYCOTO VID.	412
BL01113 C1q domain proteins. BL01113A 17.99 6.455e-14 158- 185 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 1.923e- 12 393-420 BL01113A 17.99 4.462e-12 230-257 BL01113A 17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A	1129	PK00524	SIGNATURE	
185 BL01113A 17.99 5.622e-13 28-55 BL01113A 17.99 1.923e- 12 393-420 BL01113A 17.99 4.462e-12 230-257 BL01113A 17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A	1129	BL01113		
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12 393-420 BL01113A 17.99 4.462e-12 230-257 BL01113A 17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A				28-55 BL01113A 17.99 1.923e-
17.99 6.538e-12 34-61 BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A				12 393-420 BL01113A 17.99
BL01113A 17.99 1.000e-11 284- 311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A	1			4.462e-12 230-257 BL01113A
311 BL01113A 17.99 1.205e-11 31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A	l		,	
31-58 BL01113A 17.99 1.614e- 11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A]			311 BL01113A 17.99 1 205e_11
11 170-197 BL01113A 17.99 5.091e-11 167-194 BL01113A				31-58 BL01113A 17.99 1.614e-
5.091e-11 167-194 BL01113A	j			11 170-197 BL01113A 17.99
	}			5.091e-11 167-194 BL01113A 17.99 6.523e-11 456-483

SEQ ID	Database	Description	Results*
NO:	entry ID		BL01113A 17.99 7.341e-11 411-
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			BL01113A 17.99 7.319e-10 293-
		·	320 BL01113A 17.99 8.085e-10
'			164-191 BL01113A 17.99
		<u> </u>	8.660e-10 305-332 BL01113A
		•	17.99 2.038e-09 272-299
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			86-113 BL01113A 17.99 2.731e-
			09 149-176 BL01113A 17.99
	}		2.904e-09 453-480 BL01113A
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			335 BL01113A 17.99 3.769e-09
	<u> </u>		396-423 BL01113A 17.99
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	ì		BL01113A 17.99 3.942e-09 173-
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]	347 BL01113A 17.99 6.192e-09
		1	143-170 BL01113A 17.99
			7.231e-09 224-251 BL01113A 17.99 8.269e-09 245-272
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1129	BL00420	Speract receptor repeat proteins domain	BL00420A 20.42 9.082e-13 113-
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1		İ	311-340 BL00420A 20.42
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}		1	20.42 4.541e-10 158-187
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	Ĭ		49-78 BL00420A 20.42 6.902e-
[10 266-295 BL00420A 20.42
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	1		20.42 8.082e-10 25-54
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			196 BL00420A 20.42 2.800e-09
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SEQ ID NO:	Database entry ID	Description	Results*
1132	PR00042	FOS TRANSFORMING PROTEIN	DD00042E 0 60 7 652- 00 724
		SIGNATURE	PR00042E 9.69 7.652e-09 234- 258
1135	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 9.400e-14 365-
1			378 PD00066 13.92 6.143e-12
	1		335-348 PD00066 13.92 2.174e-
1135	BL00970	Nivelentary iting and in 2 and i	11 395-408
1135	PR00049	Nuclear transition protein 2 proteins. WILM'S TUMOUR PROTEIN SIGNATURE	BL00970B 10.09 3.069e-10 55-81
1	1100043	WIEMS TOMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.746e-09 223- 238 PR00049D 0.00 3.746e-09
		,	224-239 PR00049D 0.00 3.898e-
<u>L</u>			09 220-235
1135	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.885e-11 349-
1			366 BL00028 16.07 5.886e-09
			379-396
1135	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 6.211e-09 362-
1105			372
1135	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 8.169e-09 221-
1136	BL00962	Dihaamal mat in CO.	254
1130	BL00902	Ribosomal protein S2 proteins.	BL00962D 22.51 5.500e-35 131-
-			175 BL00962C 15.90 9.591e-17 106-124 BL00962B 36.15 9.060e-
			15 40-94
1136	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE	PR00395C 16.17 1.000e-17 106-
Ì			124 PR00395D 13.04 7.000e-17
	ŀ		131-149 PR00395F 10.56 6.400e-
	ł		16 169-184 PR00395E 14.46
1100	7100110		4.103e-11 148-160
1137	BL00152	ATP synthase alpha and beta subunits	BL00152A 15.38 5.109e-14 128-
1139	BL00152	proteins. ATP synthase alpha and beta subunits	154 DY 00150D 01 40 4 070 07 10
	DD00132	proteins.	BL00152B 21.40 4.273e-37 124- 162 BL00152A 15.38 8.364e-23
		proteins.	67-93
1139	PR00449	TRANSFORMING PROTEIN P21 RAS	PR00449A 13.20 2.862e-09 139-
		SIGNATURE	161
1140	BL00152	ATP synthase alpha and beta subunits	BL00152B 21.40 2.000e-32 185-
		proteins.	223 BL00152A 15.38 8.364e-23
1140	DD 00440	MD 12 Yeb Co.	128-154
1140	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.672e-09 200-
1141	PR00493	BREAST CANCER TYPE I	PR00493G 7.57 1.184e-10 652-
••••	1100475	SUSCEPTIBILITY PROTEIN SIGNATURE	673
1141	PD00078	REPEAT PROTEIN ANK NUCLEAR	PD00078B 13.14 3.700e-10 494-
		ANKYR.	507
1141	BL00518	Zinc finger, C3HC4 type (RING finger),	BL00518 12.23 3.667e-09 102-
		proteins.	111
1141	PF00791	Domain present in ZO-1 and Unc5-like netrin	PF00791B 28.49 9.047e-15 501-
ļ		receptors.	556 PF00791B 28.49 9.386e-14
			468-523 PF00791C 20.98 9.814e-
			10 515-554 PF00791C 20.98
1141	PF00023	Ank repeat proteins.	7.618e-09 482-521
44	* * ^^^	Ana Topeat proteins.	PF00023A 16.03 3.500e-12 534- 550 PF00023A 16.03 7.857e-11
			501-517 PF00023B 14.20 9.591e-
			09 497-507
1143	BL00301	GTP-binding elongation factors proteins.	BL00301A 12.41 1.750e-12 72-84
1143	PR00315	GTP-BINDING ELONGATION FACTOR	PR00315A 11.81 4.000e-14 72-86
		SIGNATURE	PR00315B 11.66 7.600e-10 118-

SEQ ID NO:	Database entry ID	Description	Results*
NO:	entry ID		127
1145	BL00745	Prokaryotic-type class I peptide chain release factors signat.	BL00745C 13.66 7.398e-18 59- 106
1146	BL00745	Prokaryotic-type class I peptide chain release factors signat.	BL00745C 13.66 4.706e-12 59- 106
1149	BL00660	Band 4.1 family domain proteins.	BL00660B 17.33 4.800e-27 136- 176 BL00660A 31.50 7.911e-20 52-105 BL00660C 23.36 2.241e-
			19 215-259 BL00660E 23.41 9.647e-13 301-324
1149	PR00935	BAND 4.1 PROTEIN FAMILY SIGNATURE	PR00935C 11.98 4.300e-17 154- 175 PR00935D 10.20 1.281e-14 215-232 PR00935B 10.58 6.108e- 12 141-155 PR00935A 10.16 3.605e-10 76-89
1149	PR00661	ERM FAMILY SIGNATURE	PR00661C 9.53 3.616e-10 150- 172
1153	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 1.882e-12 155- 174
1153	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 1.818e-15 155- 186 BL00107B 13.31 8.714e-11 221-237
1153	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 1.774e-09 90- 138
1153	BL00240	Receptor tyrosine kinase class III proteins.	BL00240E 11.56 6.657e-09 141-
1153	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 9.000e-09 200- 213
1155	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 4.064e-11 155- 172 PR00837A 14.77 4.960e-10 78-97 PR00837B 11.64 1.310e-09 133-147
1155	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 8.759e-12 156- 177 BL01009C 10.54 1.730e-09 133-147
1155	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199F 16.19 9.483e-09 113- 140
1156	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 8.909e-13 4-48
1156	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 2.059e-19 4-26 PR00449C 17.27 1.000e-18 44-67 PR00449B 14.34 6.727e-11 27-44
1159	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175D 27.67 4.000e-40 367- 419 BL00175C 23.75 6.870e-28 316-348 BL00175A 15.42 8.200e-19 252-272 BL00175B 12.60 8.714e-17 299-312
1159	BL00300	SRP54-type proteins GTP-binding domain proteins.	BL00300B 20.56 7.554e-11 38-84
1160	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 1.000e-14 547-560 PD00066 13.92 2.200e-14 353-366 PD00066 13.92 3.400e-14 241-254 PD00066 13.92 6.400e-14 325-338 PD00066 13.92 1.500e-13 297-310 PD00066 13.92 6.500e-13 465-478 PD00066 13.92 7.500e-13 437-450 PD00066 13.92 8.500e-13 409-422 PD00066 13.92

13. PD	
13. PD	.92 3.571e-12 381-394 000066 13.92 7.577e-10 519- 2
	00000 1000 2000 14 505
130 mgs, 5212 type, domain proteins. 544 309 13 7.7 166. BL 242 421 122. 2.00 166. BL665 503	-00028 16.07 3.647e-14 531-8 BL00028 16.07 9.471e-14 9-326 BL00028 16.07 1.900e-559-576 BL00028 16.07 1.900e-559-576 BL00028 16.07 2.174e-12 337-354 2.0028 16.07 6.478e-12 225-2 BL00028 16.07 8.043e-12 1-438 BL00028 16.07 9.217e-365-382 BL00028 16.07 9.217e-365-382 BL00028 16.07 9.217e-365-382 BL00028 16.07 9.217e-38e-11 253-270 BL00028 07 7.231e-11 281-298 2.00028 16.07 6.100e-10 449-36 BL00028 16.07 8.800e-10 3-520 BL00028 16.07 5.371e-393-410
PR00048 C2H2-TYPE ZINC FINGER SIGNATURE PRO 432 362	00048A 10.52 7.429e-13 418- 2 PR00048A 10.52 2.588e-12 2-376 PR00048A 10.52 3.647e- 556-570 PR00048A 10.52
8.41 10.5 PRO	12e-12 474-488 PR00048A 52 9.471e-12 222-236 00048A 10.52 2.421e-11 306-
350- 11 2 7-63 10.5 PR0 460 544- 11 5	PR00048B 6.02 4.462e-11 -360 PR00048A 10.52 5.737e- 250-264 PR00048A 10.52 32e-11 528-542 PR00048A 52 8.579e-11 278-292 00048A 10.52 9.053e-11 446- PR00048B 6.02 9.308e-11 -554 PR00048B 6.02 9.308e- 572-582 PR00048B 6.02
10.5: PR00 388 390- 10 2: 1.94	2 2.565e-10 334-348 0048B 6.02 4.938e-10 378- PR00048A 10.52 5.304e-10 404 PR00048B 6.02 8.313e- 38-248 PR00048B 6.02 7e-09 434-444 PR00048B
PR00 332 266- 09 29	2.421e-09 462-472 0048B 6.02 3.368e-09 322- PR00048B 6.02 3.842e-09 276 PR00048B 6.02 6.211e- 94-304
PD02331 CYCLIN CELL CYCLE DIVISION PROTE. PD02	2331C 13.84 1.913e-11 9-36
Protamine P1 proteins. BL00	0048 6.39 3.700e-09 165-192
PROTEIN. CORONAVIRUS NUCLEOCAPSID PROTEIN. 189 1 248-2 7.781	0048 6.39 4.938e-09 281-308 01206B 10.69 9.328e-11 169- DM01206B 10.69 1.247e-10 268 DM01206B 10.69 1e-10 200-220 DM01206B
1163 BL00239 Receptor tyrosine kinase class II proteins. BL00 148	9 6.582e-09 246-266 0239B 25.15 3.915e-15 100-

SEQ ID	Database	Description	Results*
NO: 1163	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 6.362e-13 165- 184
1163	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 1.000e-10 208- 221
1163	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 165- 196 BL00107B 13.31 3.647e-09 230-246
1164	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.135e-22 501- 545 BL01013A 25.14 4.600e-14 220-256 BL01013C 9.97 4.906e- 12 330-340 BL01013B 11.33 3.017e-11 287-298
1167	BL00289	Pentaxin family proteins.	BL00289A 30.36 6.850e-26 25-56 BL00289E 18.00 6.684e-14 78-93
1167	PR00895	PENTAXIN SIGNATURE	PR00895A 14.53 1.563e-15 48-63 PR00895G 14.55 5.846e-12 75-87
1167	PR00468	PLANT LIPOXYGENASE SIGNATURE	PR00468I 13.42 9.870e-09 59-74
1168	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 7.527e-09 547- 563
1169	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE	PR00756D 10.58 1.529e-21 367- 383 PR00756B 14.06 5.737e-16 253-269 PR00756A 12.90 1.237e- 13 205-221 PR00756E 11.91 4.094e-13 386-399 PR00756C 11.60 6.108e-11 331-342
1169	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 5.500e-10 367-378
1170	DM01688	2 POLY-IG RECEPTOR.	DM01688I 14.97 6.279e-09 75- 123
1172	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 2.523e-10 40-50 PR00308C 3.83 8.892e-10 41-51 PR00308C 3.83 8.892e-10 42-52 PR00308B 4.28 6.671e-09 40-52
1172	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 7.115e-09 30-45
1179	BL00300	SRP54-type proteins GTP-binding domain proteins.	BL00300C 25.57 6.000e-09 215- 269
1180	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 9.463e-19 233- 270 BL00514E 14.28 7.750e-12 293-310 BL00514D 15.35 9.824e-11 274-287 BL00514G 15.98 4.273e-10 356-386 BL00514H 14.95 6.217e-09 391- 416
1181	BL01158	Macrophage migration inhibitory factor family proteins.	BL01158A 21.81 4.130e-30 2-47 BL01158B 17.07 4.316e-29 47-74
1182	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 6.250e-40 46- 101 BL00456C 24.55 6.586e-40 184-239 BL00456B 18.94 8.125e- 25 122-152 BL00456D 6.92 5.500e-10 476-486
1185	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 4.780e-14 241- 261
1185	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 1.976e-10 231- 252 PR00918A 13.76 2.084e-10 495-516
1185	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-	PR00300A 9.56 5.857e-12 237-

SEQ ID	Database	Description	Results*
NO:	entry ID	Drawn of the state	<u> </u>
		BINDING SUBUNIT SIGNATURE	256 PR00300A 9.56 5.909e-09 501-520
1185	BL00370	PEP-utilizing enzymes phosphorylation site proteins proteins.	BL00370A 5.71 6.294e-09 79-87
1185	BL00113	Adenylate kinase proteins.	BL00113A 12.74 7.231e-09 502- 519
1185	BL00674	AAA-protein family proteins.	BL00674D 23.41 2.286e-30 324-371 BL00674B 4.46 1.205e-17 234-256 BL00674C 22.60 2.059e-17 531-574 BL00674B 4.46 4.886e-17 498-520 BL00674E 15.24 2.800e-15 402-422 BL00674C 22.60 7.600e-09 270-313
1185	BL00870	Chaperonins clpA/B proteins.	BL00870A 11.78 9.534e-09 210- 257
1185	BL00675	Sigma-54 interaction domain proteins ATP-	BL00675A 24.86 9.775e-09 237-
		binding region A proteins.	281
1186	PR00165	ANION EXCHANGER SIGNATURE	PR001651 10.02 8.412e-14 829- 849 PR00165A 9.84 6.423e-13 495-518 PR00165B 15.26 9.090e- 11 520-541 PR00165F 10.39 6.663e-10 639-658
1186	BL00291	Prion protein.	BL00291A 4.49 9.675e-10 436- 471
1186	BL00219 PD01168	Anion exchangers family proteins. SYNTHETASE LIGASE PROTEIN	BL00219B 14.47 2.707e-24 296-340 BL00219C 17.29 5.426e-23 341-380 BL00219K 12.73 9.100e-23 831-873 BL00219M 9.98 9.299e-23 916-962 BL00219H 10.06 5.705e-21 618-666 BL00219I 6.16 4.968e-20 741-795 BL00219A 17.13 7.833e-19 122-154 BL00219E 11.63 2.988e-16 485-525 BL00219F 10.52 8.953e-14 525-549 BL00219G 12.86 8.163e-13 578-617 BL00219L 18.71 8.423e-13 873-912 BL00219N 10.66 6.942e-12 978-1022 BL00219D 15.15 5.286e-11 380-416 BL00219O 14.02 3.377e-09 1023-1063
		ALANYL.	PD01168L 9.47 7.833e-09 452- 467
1186	DM01724	kw ALLERGEN POLLEN CIMI HOL-LI.	DM01724 8.14 4.296e-10 446-466 DM01724 8.14 6.447e-09 442-462 DM01724 8.14 7.987e-09 438-458
	BL00027	'Homeobox' domain proteins.	BL00027 26.43 7.943e-14 65-108
	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 4.000e-11 51-67
	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 7.660e-10 54-93
	PR00028	POU DOMAIN SIGNATURE	PR00028D 17.92 2.286e-09 49-70
	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 2.047e-10 469- 518
	BL01215	Mrp family proteins.	BL01215A 9.75 2.436e-09 466- 493
192	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 5.757e-09 470-
		·	

SEQ ID NO:	Database entry ID	Description	Results*
110.	entry in		489
1192	PR00364	DISEASE RESISTANCE PROTEIN	PR00364A 8.19 7.341e-09 470-
		SIGNATURE	486
1192	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.062e-09 472- 489
1193	PR00303	PREPROTEIN TRANSLOCASE SECY SUBUNIT SIGNATURE	PR00303G 10.45 8.759e-09 88-
1197	PF00429	ENV polyprotein (coat polyprotein).	PF00429 31.08 8.015e-16 415-465
1198	BL00415	Synapsins proteins.	BL00415N 4.29 7.115e-10 224- 268
1198	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 1.307e-09 253- 265
1198	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 7.537e-12 245-
1170	1100211		266 PR00211B 0.86 2.644e-10 251-272 PR00211B 0.86 4.083e- 09 233-254 PR00211B 0.86 7.583e-09 239-260
1198	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.688e-12 227- 260 DM00215 19.43 6.250e-12 225-258 DM00215 19.43 5.235e- 11 232-265 DM00215 19.43 5.941e-11 242-275 DM00215 19.43 4.375e-10 236-269 DM00215 19.43 4.857e-10 222- 255 DM00215 19.43 5.179e-10 230-263 DM00215 19.43 8.554e-
			10 237-270 DM00215 19.43 2.068e-09 215-248 DM00215 19.43 3.898e-09 235-268 DM00215 19.43 4.508e-09 240- 273 DM00215 19.43 5.576e-09 231-264 DM00215 19.43 6.339e- 09 220-253 DM00215 19.43 9.847e-09 218-251
1200	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 4.326e-22 81-129
1202	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.214e-16 108- 148 BL00237C 13.19 3.323e-11 245-272 BL00237B 5.28 2.227e- 09 182-194
1202	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 4.600e-13 250- 275 PR00237E 13.03 1.000e-12 174-198 PR00237G 19.63 7.469e- 12 288-315 PR00237B 13.50 7.207e-11 75-97 PR00237C 15.69 7.750e-09 122-145
1203	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 4.214e-16 108- 148 BL00237C 13.19 3.323e-11 280-307 BL00237B 5.28 2.227e- 09 217-229
1203	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 4.600e-13 285- 310 PR00237E 13.03 1.000e-12 209-233 PR00237G 19.63 7.469e- 12 323-350 PR00237B 13.50 7.207e-11 75-97 PR00237C 15.69 7.750e-09 122-145
1207	PR00259	TRANSMEMBRANE FOUR FAMILY	PR00259B 14.81 3.769e-21 50-77

SEQ ID	Database	Description	Results*
NO:	entry ID		
1207	BL00421	Transmembrane 4 family proteins.	12-36
1.207	BB00421	Transmentorane 4 faithly proteins.	BL00421B 17.62 7.261e-36 56-95 BL00421A 11.79 8.313e-16 8-27
1207	PR00164	ABC-2 TYPE TRANSPORT SYSTEM	PR00164D 13.90 1.486e-09 9-34
		MEMBRANE PROTEIN SIGNATURE	1110010 12 10150 111000-05 5-54
1208	BL00282	Kazal serine protease inhibitors family	BL00282 16.88 7.207e-14 562-
1000	1	proteins.	585
1208	BL00216	Sugar transport proteins.	BL00216B 27.64 3.250e-10 267-
1209	PF00922	Vesiculovirus phosphoprotein.	317
	110032	vesiculovitus phosphoprotein.	PF00922A 19.17 7.724e-09 88-
1214	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.143e-10 17-32
1214	PD01351	PROTEIN REPEAT NEUROFILAMENT	PD01351B 13.72 9.518e-10 18-44
		TRIPL.	PD01351B 13.72 3.758e-09 24-50
1214	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 5.576e-09 5-38
1214	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 7.857e-09 17-30
1215	BL00612	SIGNATURE Osteonectin domain proteins.	Di cocion de de company
1213	BLOODIZ	Osteonecun domain proteins.	BL00612E 13.12 3.947e-11 379- 424
1215	BL00484	Thyroglobulin type-1 repeat proteins proteins.	BL00484C 17.01 3.854e-11 131-
			146 BL00484B 9.04 1.491e-10
		,	238-252 BL00484C 17.01 8.560e-
	ļ		10 258-273 BL00484B 9.04
1216	BL00223		3.850e-09 111-125
1210	BL00223	Annexins repeat proteins domain proteins.	BL00223A 15.59 1.000e-33 147-
	1		181 BL00223A 15.59 1.435e-16
	,		75-109 BL00223C 24.79 3.928e- 15 134-189
1216	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196C 10.36 3.571e-25 151-
			173 PR00196A 11.16 7.300e-24
,			84-107 PR00196B 10.68 4.808e-
			16 124-141 PR00196A 11.16
			6.236e-14 156-179 PR00196E 9.19 1.000e-12 155-176
			PR00196G 11.72 5.829e-11 199-
	į		213 PR00196C 10.36 7.913e-11
			79-101
1216	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201D 10.49 8.729e-14 151-
			173 PR00201A 6.05 1.976e-13
	·		84-107 PR00201G 11.02 3.847e-
			12 155-182 PR00201A 6.05 8.241e-12 156-179 PR00201H
			12.04 4.889e-10 199-213
1216	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198D 7.65 7.787e-21 151-
			173 PR00198B 8.71 3.880e-17
			84-107 PR00198C 14.32 2.688e-
		ļ	11 124-141 PR00198G 8.09
1216	PR00200	ANNEXIN TYPE IV SIGNATURE	7.033e-10 155-176
.2.0	1100200	AMINDAIN THE IN SIGNATURE	PR00200E 10.00 5.030e-19 151- 173 PR00200G 9.43 5.546e-14
			155-182 PR00200B 7.39 4.653e-
			11 156-179 PR00200B 7.39
		,	4.857e-10 84-107 PR00200H
			13.68 9.663e-10 199-213
1216	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 151-
			173 PR00202G 8.01 5.545e-13
			155-182 PR00202B 11.44 2.782e-
			10 155-179 PR00202B 11.44

SEQ ID	Database	Description	Results*
NO:	entry ID		
.,,,,			5.206e-09 83-107
1216	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197B 7.56 4.960e-29 84-107
			PR00197D 7.50 3.000e-26 151- 173 PR00197A 8.68 7.577e-20
			35-51 PR00197A 8.68 7.577e-20
			124-141 PR00197F 9.03 7.128e-
	Į.	}	10 155-176 PR00197P 7.50
	1		6.250e-09 79-101
		THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRE	PR00199D 5.65 9.297e-17 151-
1216	PR00199	ANNEXIN TYPE III SIGNATURE	173 PR00199B 6.86 2.915e-13
)		84-107 PR00199B 6.86 1.265e-11
			156-179 PR00199G 9.09 4.351e-
ļ	1		11 156-182 PR00199D 5.65
Ì	j		3.641e-09 79-101 PR00199C
[13.84 9.571e-09 124-141
1017	BL00223	Annexins repeat proteins domain proteins.	BL00223B 28.47 1.000e-40 188-
1217	DLUU223	Aimoxina repeat proteins demant proteins	238 BL00223A 15.59 1.000e-33
İ			119-153 BL00223A 15.59
(1.435e-16 47-81 BL00223C 24.79
	1		3.928e-15 106-161
1217	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201D 10.49 8.729e-14 123-
1217	1100201		145 PR00201A 6.05 1.976e-13
ļ			56-79 PR00201G 11.02 3.847e-12
			127-154 PR00201A 6.05 8.241e-
· I			12 128-151 PR00201E 12.37
]	1		3.317e-11 206-233 PR00201H
			12.04 4.889e-10 171-185
1217	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198D 7.65 7.787e-21 123-
1	}		145 PR00198B 8.71 3.880e-17 56-79 PR00198E 14.67 5.286e-15
1			206-233 PR00198C 14.32 2.688e-
1			11 96-113 PR00198G 8.09
1	1		7.033e-10 127-148
		AND THE PARTY OF T	PR00196D 21.86 1.000e-27 206-
1217	PR00196	ANNEXIN FAMILY SIGNATURE	233 PR00196C 10.36 3.571e-25
1			123-145 PR00196A 11.16 7.300e-
			24 56-79 PR00196B 10.68
1			4.808e-16 96-113 PR00196A
			11.16 6.236e-14 128-151
1			PR00196E 9.19 1.000e-12 127-
			148 PR00196G 11.72 5.829e-11
			171-185 PR00196C 10.36 7.913e-
1	ł		11 51-73 PR00196C 10.36
			8.750e-10 282-304
1217	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 123-
			145 PR00202G 8.01 5.545e-13
	j	j	127-154 PR00202E 13.00 8.740e-
			11 206-233 PR00202B 11.44
			2.782e-10 127-151 PR00202B
			11.44 5.206e-09 55-79
1217	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197E 11.89 1.794e-32 206-
1			233 PR00197B 7.56 4.960e-29
-			56-79 PR00197D 7.50 3.000e-26 123-145 PR00197A 8.68 7.577e-
			123-145 PR00197A 8.68 7.57/e- 20 7-23 PR00197C 7.50 1.000e-
	1		19 96-113 PR00197C 7.50 1.000e-
			7.128e-10 127-148 PR00197D
			7.128e-10 127-148 PR00197D
]		1.30 0.2305-03 31-13

SEQ ID	Database	Description	Results*
NO:	entry ID	<u>-</u>	Results
1217	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200E 10.00 5.030e-19 123- 145 PR00200G 9.43 5.546e-14 127-154 PR00200B 7.39 4.653e- 11 128-151 PR00200F 13.72 7.094e-11 206-233 PR00200B 7.39 4.857e-10 56-79 PR00200H 13.66 9.663e-10 171-185 PR00200E 10.00 8.842e-09 282- 304
1217	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199D 5.65 9.297e-17 123- 145 PR00199F 16.19 4.391e-15 206-233 PR00199B 6.86 2.915e- 13 56-79 PR00199B 6.86 1.265e- 11 128-151 PR00199G 9.09 4.351e-11 128-154 PR00199D 5.65 3.641e-09 51-73 PR00199C 13.84 9.571e-09 96-113
1218	BL00223	Annexins repeat proteins domain proteins.	BL00223A 15.59 1.000e-33 119- 153 BL00223A 15.59 1.435e-16 47-81 BL00223C 24.79 3.928e-15 106-161
1218	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196C 10.36 3.571e-25 123- 145 PR00196A 11.16 7.300e-24 56-79 PR00196B 10.68 4.808e-16 96-113 PR00196A 11.16 6.236e- 14 128-151 PR00196E 9.19 1.000e-12 127-148 PR00196G 11.72 5.829e-11 171-185
1218	PR00201	ANNEXIN TYPE V SIGNATURE	PR00196C 10.36 7.913e-11 51-73 PR00201D 10.49 8.729e-14 123-145 PR00201A 6.05 1.976e-13 56-79 PR00201G 11.02 3.847e-12 127-154 PR00201A 6.05 8.241e-12 128-151 PR00201H 12.04
1218	PR00198	ANNEXIN TYPE II SIGNATURE	4.889e-10 171-185 PR00198D 7.65 7.787e-21 123- 145 PR00198B 8.71 3.880e-17 56-79 PR00198C 14.32 2.688e-11 96-113 PR00198G 8.09 7.033e-10 127-148
1218	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200E 10.00 5.030e-19 123- 145 PR00200G 9.43 5.546e-14 127-154 PR00200B 7.39 4.653e- 11 128-151 PR00200B 7.39 4.857e-10 56-79 PR00200H 13.68 9.663e-10 171-185
1218	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202D 5.58 6.793e-14 123- 145 PR00202G 8.01 5.545e-13 127-154 PR00202B 11.44 2.782e- 10 127-151 PR00202B 11.44 5.206e-09 55-79
1218	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197B 7.56 4.960e-29 56-79 PR00197D 7.50 3.000e-26 123- 145 PR00197A 8.68 7.577e-20 7- 23 PR00197C 7.50 1.000e-19 96- 113 PR00197F 9.03 7.128e-10 127-148 PR00197D 7.50 6.250e- 09 51-73

SEQ ID NO:	Database entry ID	Description	Results*
1218	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199D 5.65 9.297e-17 123- 145 PR00199B 6.86 2.915e-13 56-79 PR00199B 6.86 1.265e-11 128-151 PR00199G 9.09 4.351e- 11 128-154 PR00199D 5.65 3.641e-09 51-73 PR00199C 13.84 9.571e-09 96-113
1221	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.	BL00086 20.87 8.615e-27 423- 455
1221	PR00465	E-CLASS P450 GROUP IV SIGNATURE	PR00465F 13.37 8.468e-12 393- 412
1221	PR00359	B-CLASS P450 SIGNATURE	PR00359I 11.13 7.261e-11 433- 445
1221	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463I 15.02 9.571e-21 433- 457 PR00463G 18.24 6.760e-19 388-413 PR00463E 17.37 6.595e- 17 304-331 PR00463F 17.63 7.568e-12 347-366 PR00463B 17.50 7.692e-12 79-101 PR00463D 14.02 8.875e-11 284- 302 PR00463C 12.85 6.932e-10 171-190
1221	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464G 12.41 2.588e-12 398- 414 PR00464E 18.28 3.077e-10 342-363 PR00464I 14.64 3.106e- 10 433-457 PR00464H 13.32 4.635e-09 420-434 PR00464D 17.40 5.787e-09 313-331 PR00464C 18.84 5.808e-09 284- 313
1221	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385E 12.66 9.100e-14 433- 445 PR00385A 14.97 5.696e-13 295-313 PR00385B 10.22 6.400e- 09 313-327
1221	PR00408	MITOCHONDRIAL P450 SIGNATURE	PR00408D 15.44 6.831e-09 295- 313
1222	PR00385	P450 SUPERFAMILY SIGNATURE	PR00385A 14.97 5.696e-13 295- 313
1222	PR00463	E-CLASS P450 GROUP I SIGNATURE	PR00463B 17.50 7.692e-12 79- 101 PR00463D 14.02 8.875e-11 284-302 PR00463C 12.85 6.932e- 10 171-190
1222	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464C 18.84 5.808e-09 284- 313
1222	PR00408	MITOCHONDRIAL P450 SIGNATURE	PR00408D 15.44 6.831e-09 295- 313
1223	BL00477	Alpha-2-macroglobulin family thiolester region proteins.	BL00477A 13.50 9.182e-19 70-99
1225	BL00500	Thymosin beta-4 family proteins.	BL00500 9.77 2.565e-28 2-42
1227	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.971e-10 231- 246 PR00320C 13.01 8.200e-10 231-246 PR00320B 12.19 9.486e- 10 231-246 PR00320B 12.19 3.475e-09 188-203 PR00320B 12.19 4.600e-09 315-330 PR00320C 13.01 4.900e-09 315- 330
1227	PR00319	BETA G-PROTEIN (TRANSDUCIN)	PR00319B 11.47 9.143e-09 315-

SEQ ID NO:	Database entry ID	Description	Results*
	1	SIGNATURE	330
1227	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.600e-10 233-244 BL00678 9.67 1.000e-08 317-328
1236	PF00580	UvrD/REP helicase.	PF00580D 13.15 8.920e-13 670- 684 PF00580E 13.89 2.800e-11 867-886 PF00580F 8.62 9.438e- 10 913-926
1237	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.000e-09 64-78 PR00019A 11.19 8.000e-09 90- 104
1238	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-10 229- 250
1243	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 4.759e-09 464-
1243	BL00315	Dehydrins proteins.	BL00315A 9.35 1.000e-08 389-
1245	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.054e-15 191- 209
1246	PF00023	Ank repeat proteins.	PF00023A 16.03 9.500e-12 347- 363 PF00023A 16.03 8.500e-10 283-299 PF00023A 16.03 8.875e- 10 184-200
1246	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 1.989e-13 217- 272 PF00791B 28.49 6.044e-13 117-172 PF00791B 28.49 4.316e- 12 184-239 PF00791B 28.49 9.432e-12 250-305 PF00791B 28.49 6.243e-10 84-139 PF00791C 20.98 4.971e-09 98- 137
1246	BL00906	Uroporphyrinogen decarboxylase proteins.	BL00906D 24.33 7.750e-09 212- 256
1248	BL00415	Synapsins proteins.	BL00415Q 2.23 8.297e-09 13-49
1250	BL01113	Clq domain proteins.	BL01113B 18.26 2.500e-13 841-
1252	BL01248	Laminin-type EGF-like (LE) domain proteins.	BL01248 11.02 7.171e-12 258- 271 BL01248 11.02 7.943e-12 325-338
1252	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 7.000e-17 376- 395 PR00011A 14.06 1.000e-14 376-395 PR00011B 13.08 5.167e- 14 376-395 PR00011C 24.25 8.468e-14 395-424 PR00011D 14.03 9.739e-09 249-268
1253	BL00164	Enolase proteins.	BL00164A 11.58 2.800e-28 41-64
1253	PR00148	ENOLASE SIGNATURE	PR00148A 10.11 1.783e-18 44-59
1255	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 8.322e-14 102- 128 BL01153C 13.67 6.507e-10
1256	BL00892	HIT family proteins.	51-65 BL00892B 16.86 1.000e-20 130- 154 BL00892A 18.17 6.657e-20 64-95
1256	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE	PR00332B 13.62 3.000e-16 76-95 PR00332C 7.37 4.600e-14 143- 154 PR00332A 10.15 7.375e-12 55-72
1257	PF00791	Domain present in ZO-1 and Unc5-like netrin	PF00791B 28.49 4.146e-10 73-

SEQ ID NO:	Database entry ID	Description	Results*
1,0.	0225	receptors.	128
1258	BL00615	C-type lectin domain proteins.	BL00615B 12.25 5.200e-12 166- 180
1259	BL00071	Glyceraldehyde 3-phosphate dehydrogenase proteins.	BL00071B 21.70 1.000e-40 80- 126 BL00071C 11.81 1.000e-40 146-181 BL00071D 19.39 3.118e-25 184-239 BL00071E 11.48 4.600e-24 308-329
1259	PR00078	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE SIGNATURE	BL00071A 5.81 2.607e-14 5-17 PR00078B 7.45 3.250e-24 146- 165 PR00078D 11.49 2.800e-21 231-249 PR00078E 10.50 6.211e- 16 271-287 PR00078A 10.38 1.000e-15 111-125 PR00078C 15.99 6.211e-11 173-190
1262	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 2.688e-10 15-38 PR00926D 10.53 6.625e-10 21-40
1262	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR I SIGNATURE	PR00927E 14.93 6.143e-10 44-66 PR00927B 14.66 9.870e-10 265- 287 PR00927B 14.66 5.685e-09 46-68
1262	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 6.250e-17 13-38 BL00215A 15.82 1.600e-15 230- 255 BL00215A 15.82 5.974e-13 108-133 BL00215B 10.44 7.600e- 09 275-288
1263	PR00654	ANGIOTENSINOGEN SIGNATURE	PR00654A 15.64 1.540e-26 23-44 PR00654D 10.48 3.538e-26 153- 175 PR00654F 15.16 8.071e-26 255-275 PR00654E 9.81 2.241e- 25 194-215 PR00654C 9.50 5.500e-21 115-135
1263	BL00284	Serpins proteins.	BL00284C 28.56 9.514e-21 254- 296 BL00284E 19.15 9.710e-16 439-464 BL00284A 15.64 8.147e-14 113-137 BL00284D 16.34 1.837e-12 361-388 BL00284B 17.99 7.500e-11 229- 250
1264	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.071e-17 34-57
1265	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.600e-16 34-57
1266	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 2.800e-16 31-54
1267	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 9.400e-16 34-57
1268	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 4.000e-21 282- 300 BL00290A 20.89 4.600e-16 34-57 BL00290A 20.89 2.421e- 13 225-248
1269	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-16 34-57
1271	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 8.071e-17 34-57
1272	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.600e-16 34-57
1273	BL00290	Immunoglobulins and major	BL00290A 20.89 4.600e-16 34-57

SEQ ID NO:	Database entry ID	Description	Results*
		histocompatibility complex proteins.	
1274	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 2.500e-14 46-59
1274	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 6.063e-09 300- 310
1274	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 7.750e-11 472- 486 PR00501A 8.25 7.955e-09 328-342
1281	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 3.919e-15 101- 119 BL00972B 9.45 7.577e-10 180-190
1285	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 5.941e-09 213- 234
1286	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 5.941e-09 259- 280
1287	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 3.000e-19 19-39 PR00625B 13.48 2.756e-17 47-68
1287	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 7.600e-19 23-40 BL00636B 15.11 6.870e-15 47-68
1288	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.714e-10 24-33
1289	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500I 9.22 1.107e-31 2810- 2833 PR00500G 3.68 1.087e-30 2525-2548 PR00500H 17.80 1.107e-29 2662-2684 PR00500E 6.99 1.106e-27 2350-2370 PR00500F 9.44 1.108e-26 2483-
1289	PF00801	PKD domain proteins.	2503 PF00801B 23.63 9.217e-26 1055- 1083 PF00801A 13.49 6.276e-11 222-235 PF00801B 23.63 3.087e- 10 719-747 PF00801B 23.63
1291	BL00415	Synapsins proteins.	6.609e-10 1652-1680 BL00415N 4.29 5.401e-09 136- 180
1292	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 2.800e-23 229- 270 PD00930A 25.62 5.021e-12 125-151
1292	PF00620	GTPase-activator protein for Rho-like GTPases.	PF00620B 14.20 7.000e-12 178-
1293	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.043e-34 281- 318 BL00023 24.31 5.320e-32 223-260 BL00023 24.31 5.800e- 29 340-377
1293	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 1.000e-12 398-409
1293	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 5.500e-30 398- 424 PR00138C 16.41 1.000e-29 164-193 PR00138B 15.82 5.875e- 16 141-157 PR00138A 15.14 1.000e-15 94-108 PR00138E 6.01
1293	BL00024	Hemopexin domain proteins.	8.472e-11 431-445 BL00024C 22.98 1.000e-40 163- 212 BL00024D 17.28 4.316e-36 392-424 BL00024B 21.53 7.545e- 33 115-149 BL00024F 11.30 2.895e-18 486-507 BL00024A 11.49 3.667e-12 94-105

SEQ ID NO:	Database entry ID	Description	Results*
			BL00024G 13.31 4.857e-12 525- 538 BL00024E 7.58 2.263e-10 431-445
1293	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 1.771e-09 393- 412
1293	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE	PR00013C 12.29 7.136e-19 372-388 PR00013C 12.29 6.464e-18 313-329 PR00013C 12.29 5.500e-16 255-271 PR00013B 14.75 4.375e-12 355-368 PR00013A 12.26 1.973e-11 344-354 PR00013A 12.26 6.595e-11 227-237 PR00013B 14.75 8.568e-10 296-309 PR00013A 12.26 2.167e-09 285-295 PR00013B 14.75 2.588e-09 238-251
1293	BL00546	Matrixins cysteine switch.	BL00546B 20.11 3.368e-40 164- 208 BL00546C 16.41 6.400e-31 392-424 BL00546A 19.62 6.523e-19 74-104 BL00546E 10.23 7.947e-13 486-507 BL00546F 12.40 5.339e-09 525- 538
1294	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.043e-34 281- 318 BL00023 24.31 5.320e-32 223-260 BL00023 24.31 5.800e- 29 340-377
1294	BL00546	Matrixins cysteine switch.	BL00546B 20.11 3.368e-40 164- 208 BL00546C 16.41 6.400e-31 392-424 BL00546A 19.62 6.523e-19 74-104
1294	PR00138	MATRIXIN SIGNATURE	PR00138D 16.56 5.500e-30 398- 424 PR00138C 16.41 1.000e-29 164-193 PR00138B 15.82 5.875e- 16 141-157 PR00138A 15.14 1.000e-15 94-108
1294	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 1.000e-12 398-409
1294	BL00024	Hemopexin domain proteins.	BL00024C 22.98 1.000e-40 163- 212 BL00024D 17.28 4.316e-36 392-424 BL00024B 21.53 7.545e- 33 115-149 BL00024A 11.49 3.667e-12 94-105
1294	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 1.771e-09 393-
1294	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE	PR00013C 12.29 7.136e-19 372-388 PR00013C 12.29 6.464e-18 313-329 PR00013C 12.29 5.500e-16 255-271 PR00013B 14.75 4.375e-12 355-368 PR00013A 12.26 1.973e-11 344-354 PR00013A 12.26 6.595e-11 227-237 PR00013B 14.75 8.568e-10 296-309 PR00013A 12.26 2.167e-09 285-295 PR00013B 14.75 2.588e-09 238-251
1298	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354R 8.50 2.969e-22 2115- 2145 DM01354S 11.61 1.692e-14

SEQ ID NO:	Database entry ID	Description	Results*
			2145-2166
1298	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 8.244e-09
1000			1714-1737
1298	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.737e-10 1807-
		·	1817 DM00179 13.97 7.158e-10
	1		1077-1087 DM00179 13.97
1			9.053e-10 759-769 DM00179
			13.97 9.053e-10 1328-1338
		1	DM00179 13.97 4.130e-09 574- 584 DM00179 13.97 4.130e-09
	1		1431-1441 DM00179 13.97
!			6.870e-09 1713-1723 DM00179
			13.97 7.652e-09 850-860
	1		DM00179 13.97 8.435e-09 2089-
1298	DI 00040		2099
1270	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.909e-13 623-
	1		647 BL00240B 24.70 1.209e-10
			1126-1150 BL00240B 24.70
	l		4.558e-10 124-148 BL00240B 24.70 6.442e-10 529-553
			BL00240B 24.70 4.255e-09 1222-
	ł		1246 BL00240B 24.70 8.468e-09
1000			995-1019
1298	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR	13.0 . 0.03.20 03 1120
		IMMUNOGLO.	1148 PD02327B 19.84 9.318e-09
1298	PD02870	DECERTOR DITERLEMENT	1222-1244
1270	1 502870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 1.200e-10 1610-
		TADEONSON.	1643 PD02870B 18.83 7.400e-10
4			2081-2114 PD02870B 18.83 7.800e-10 1069-1102 PD02870B
			18.83 5.213e-09 1423-1456
			PD02870B 18.83 6.649e-09 67-
		İ	100 PD02870B 18.83 7.989e-09
			1518-1551 PD02870D 15.74
			8.564e-09 566-601 PD02870B
			18.83 9.521e-09 286-319
			PD02870B 18.83 9.904e-09 1258- 1291
1299	BL00888	Cyclic nucleotide-binding domain proteins.	BL00888B 14.79 4.706e-18 372-
		, and a second processing	396 BL00888A 18.03 1.000e-08
			354-371
1301	PF00615	Regulator of G protein signalling domain	PF00615B 16.25 9.625e-16 73-90
		proteins.	PF00615C 10.06 9.206e-12 150-
1302	BL00766	Tetrahydrofolate	164
1302	DE00700	dehydrogenase/cyclohydrolase proteins.	BL00766E 13.78 9.625e-39 191-
		denydrogenase/cyclonydrolase proteins.	228 BL00766C 25.86 4.375e-31
			77-125 BL00766D 17.05 5.966e- 25 152-182
1302	PR00085	TETRAHYDROFOLATE	PR00085E 15.79 7.000e-26 151-
į		DEHYDROGENASE/CYCLOHYDROLASE	181 PR00085G 10.74 1.865e-22
[FAMILY SIGNATURE	208-227 PR00085C 15.23 6.182e-
1			21 47-69 PR00085D 15.02
			2.688e-20 92-113 PR00085F 9.77
1303	DI 00100	Olateria	6.595e-15 191-208
202	BL00180	Glutamine synthetase proteins.	BL00180E 17.60 1.000e-40 154-
			206 BL00180D 13.26 2.174e-24
			119-141 BL00180F 10.05 6.211e-
			17 218-231 BL00180G 10.20

SEQ ID NO:	Database entry ID	Description	Results*
NO.	entry ID		8.435e-17 307-322 BL00180C 12.14 4.600e-14 102-112 BL00180B 18.03 4.971e-14 68-87 BL00180A 13.20 5.065e-14 32-45
1304	BL00180	Glutamine synthetase proteins.	BL00180F 10.05 6.750e-15 49-62
1306	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 1.000e-08 77- 123
1308	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 5.440e-09 36-49
1309	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191A 8.16 5.440e-09 61-74
1310	PF00606	Herpesviral Glycoprotein B.	PF00606I 20.74 7.894e-09 264- 316
1310	BL01219	Ammonium transporters proteins.	BL01219D 11.63 2.957e-10 217- 241 BL01219F 15.24 8.809e-09 335-360
1310	PR00342	RHESUS BLOOD GROUP PROTEIN SIGNATURE	PR00342G 8.18 1.458e-19 220- 239 PR00342B 11.09 8.657e-13 61-79 PR00342D 8.46 2.857e-12 128-145 PR00342I 4.99 6.016e- 12 285-299 PR00342H 7.61 6.927e-11 250-273 PR00342C 10.10 4.770e-10 90-108 PR00342E 14.49 5.950e-10 151- 175 PR00342F 7.02 1.556e-09 185-201 PR00342J 8.97 7.940e- 09 308-327 PR00342L 7.61 9.600e-09 398-424
1311	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 9.080e-11 80-99 PR00209B 4.88 6.967e-10 86-105
1311	DM00406	GLIADIN.	DM00406 7.73 1.400e-09 86-99
1311	PR00501	KELCH REPEAT SIGNATURE	PR00501B 18.88 8.342e-09 440- 455
1312	PR00528	GLUCOCORTICOID RECEPTOR SIGNATURE	PR00528F 9.13 9.063e-09 31-51
1313	PF00622	Domain in SPla and the RYanodine Receptor.	PF00622C 12.62 6.625e-13 759- 773
1313	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39 BL00518 12.23 1.667e-09 356- 365
1314	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 2.824e-25 37-92 BL00420C 11.90 9.250e-12 122- 133
1314	PR00258	SPERACT RECEPTOR SIGNATURE	PR00258D 14.41 6.333e-11 98- 113 PR00258B 9.63 7.474e-11 52-64 PR00258E 13.33 1.750e-09 121-134 PR00258C 9.05 5.167e- 09 67-78
1315	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 8.548e-10 122- 134
1315	BL00766	Tetrahydrofolate dehydrogenase/cyclohydrolase proteins.	BL00766C 25.86 7.632e-09 20-68
1315	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 2.452e-13 41-59 PR00081C 15.13 9.229e-09 167- 184
1317	BL00263	Natriuretic peptides proteins.	BL00263 11.87 5.909e-22 129- 147

1317 1317 1318	PR00711 PR00713 PR00710 PR00712 BL00609	ATRIAL NATRIURETIC PEPTIDE SIGNATURE C-TYPE NATRIURETIC PEPTIDE SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	PR00711G 11.75 1.113e-30 128-151 PR00711B 10.71 7.545e-24 32-51 PR00711D 7.91 1.000e-22 72-90 PR00711F 3.17 2.463e-22 109-128 PR00711C 5.66 7.818e-22 51-70 PR00711E 6.39 1.000e-21 92-109 PR00711A 12.00 9.769e-20 11-30 PR00713C 14.14 1.370e-13 130-146 PR00710A 10.90 3.250e-14 127-137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128-139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	C-TYPE NATRIURETIC PEPTIDE SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	32-51 PR00711D 7.91 1.000e-22 72-90 PR00711F 3.17 2.463e-22 109-128 PR00711C 5.66 7.818e- 22 51-70 PR00711E 6.39 1.000e- 21 92-109 PR00711A 12.00 9.769e-20 11-30 PR00713C 14.14 1.370e-13 130- 146 PR00710A 10.90 3.250e-14 127- 137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	72-90 PR00711F 3.17 2.463e-22 109-128 PR00711C 5.66 7.818e- 22 51-70 PR00711E 6.39 1.000e- 21 92-109 PR00711A 12.00 9.769e-20 11-30 PR00713C 14.14 1.370e-13 130- 146 PR00710A 10.90 3.250e-14 127- 137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	22 51-70 PR00711E 6.39 1.000e- 21 92-109 PR00711A 12.00 9.769e-20 11-30 PR00713C 14.14 1.370e-13 130- 146 PR00710A 10.90 3.250e-14 127- 137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	21 92-109 PR00711A 12.00 9.769e-20 11-30 PR00713C 14.14 1.370e-13 130-146 PR00710A 10.90 3.250e-14 127-137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128-139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	9.769e-20 11-30 PR00713C 14.14 1.370e-13 130-146 PR00710A 10.90 3.250e-14 127-137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128-139 PR00712E 10.62 7.231e-10
1317 1317 1318	PR00710 PR00712	SIGNATURE NATRIURETIC PEPTIDE FAMILY SIGNATURE BRAIN NATRIURETIC PEPTIDE SIGNATURE	146 PR00710A 10.90 3.250e-14 127- 137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1317	PR00712	BRAIN NATRIURETIC PEPTIDE SIGNATURE	137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1318		BRAIN NATRIURETIC PEPTIDE SIGNATURE	137 PR00710B 11.08 1.391e-12 136-146 PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1318		SIGNATURE	PR00712D 10.52 4.109e-12 128- 139 PR00712E 10.62 7.231e-10
1318		SIGNATURE	139 PR00712E 10.62 7.231e-10
	BL00609	Chronyl hydrol	
	BL00609	Glyppoul budget C 11 55	138-152
1318		Glycosyl hydrolases family 32 proteins.	BL00609C 13.27 9.270e-11 249-
	BL01187	Calcium-binding EGF-like domain proteins	261
: !	DEGLIGA	pattern proteins.	BL01187B 12.04 6.538e-16 757- 773 BL01187B 12.04 7.750e-14
	•		610-626 BL01187B 12.04 8.200e-
		·	14 651-667 BL01187B 12.04
			2.029e-10 523-539 BL01187A
1318	PR00907	THROMBOMODULIN SIGNATURE	9.98 7.429e-10 591-603
		THE OWN OWN OF THE PROPERTY OF	PR00907B 11.29 6.301e-11 753- 770 PR00907B 11.29 2.636e-10
			647-664 PR00907B 11.29 3.524e-
			09 519-536 PR00907G 11.63
1318 I	BL01177	Anaphylatoxin domain proteins.	4.243e-09 651-678
		•	BL01177C 17.39 8.286e-09 517-
1318 F	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 1.429e-09 762-
			773 PR00010C 11.16 8.500e-09
1318 E	BL00022	EGF-like domain proteins.	528-539
			BL00022B 7.54 1.000e-08 619- 626
1319 P	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 4.000e-10 26-50
1320 E	BL00125	Serine/threonine specific protein	BL00125D 33.11 9.719e-35 23-78
1000		phosphatases proteins.	25.78
1320 P	PR00114	SERINE/THREONINE PHOSPHATASE	PR00114F 17.51 4.706e-16 39-60
1321 B	3L00453	FAMILY SIGNATURE FKBP-type peptidyl-prolyl cis-trans	PR00114G 17.20 5.421e-12 61-78
	32500433	isomerase proteins.	BL00453B 23.86 6.538e-26 281-
		p. comb	315 BL00453A 15.57 8.364e-12 249-264 BL00453C 9.72 3.250e-
1201	200000		11 323-336
1321 P	R00280	CHANNEL FORMING COLICIN SIGNATURE	PR00280A 11.09 8.227e-09 284-
1322 P		NEUTROPHIL CYTOSOL FACTOR P40	300 PR00497A 6.92 8.261e-09 310-
1000		SIGNATURE	328
1322 B	L50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 9.500e-09 45-59
1323 PI		TRANSFORMING PROTEIN P21 RAS	DR0040A 12 20 9 200- 10 2
		SIGNATURE	PR00449A 13.20 8.269e-16 34-56
	L01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 2.474e-09 34-78
1323 PI	R00300	ATP-DEPENDENT CLP PROTEASE ATP- BINDING SUBUNIT SIGNATURE	PR00300A 9.56 6.260e-09 36-55

SEQ ID NO:	Database entry ID	Description	Results*
1323	BL00567	Phosphoribulokinase proteins.	BL00567A 10.66 9.100e-09 35-54
1324	PR00109	TYROSINE KINASE CATALYTIC	PR00109B 12.27 9.847e-10 314-
1321	1 110010	DOMAIN SIGNATURE	333
1324	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242G 13.52 6.276e-09 748-788
1324	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 381- 397 BL00107A 18.39 8.091e-09 314-345
1325	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.847e-10 314- 333
1325	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242G 13.52 6.276e-09 721- 761
1325	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 381- 397 BL00107A 18.39 8.091e-09 314-345
1326	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signatur.	BL00472C 20.76 8.225e-09 50-87
1327	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 8.667e-13 114- 130 PR00705B 10.22 2.385e-10 293-304
1327	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 8.125e-17 312- 329 BL00139C 9.23 2.800e-10 292-302 BL00139B 10.19 7.600e- 10 157-166 BL00139A 10.29 2.723e-09 114-124
1328	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE	PR00705A 10.55 8.667e-13 155- 171 PR00705B 10.22 2.385e-10 334-345
1328	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.	BL00139D 9.24 8.125e-17 353- 370 BL00139C 9.23 2.800e-10 333-343 BL00139B 10.19 7.600e- 10 198-207 BL00139A 10.29 2.723e-09 155-165
1330	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 7.443e-10 129- 169 PD01270A 17.22 7.387e-09 36-76
1332	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.772e-10 250- 301
1332	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.068e-09 751- 784
1333	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 8.594e-35 151- 199 BL00232B 32.79 5.579e-22 260-308 BL00232A 27.72 1.000e-20 57-90 BL00232C 10.65 3.613e-14 258-276 BL00232B 32.79 4.872e-11 377-425 BL00232C 10.65 3.211e-09 480- 498
1333	DM01724	kw ALLERGEN POLLEN CIMI HOL-LI.	DM01724 8.14 9.113e-10 698-718 DM01724 8.14 6.803e-09 694-714
1333	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 4.545e-15 258- 276 PR00205A 14.73 5.600e-09 183-199 PR00205B 11.39 8.017e- 09 480-498
1335	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 9.000e-29 47-92 BL00214A 21.17 1.000e-24 6-32
1335	PR00178	FATTY ACID-BINDING PROTEIN	PR00178C 20.54 3.864e-25 65-93

SEQ ID NO:	Database entry ID	Description	Results*
		SIGNATURE	PR00178A 15.07 7.188e-23 7-28 PR00178D 13.52 6.170e-12 111- 130
1336	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 8.250e-09 509- 525
1338	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.759e-17 112- 130 BL00972D 22.55 8.116e-12 354-379 BL00972B 9.45 7.088e- 09 193-203
1340	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.155e-09 1-44
1340	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633E 12.18 4.682e-10 182- 199 PR00633G 13.71 1.667e-09 185-204 PR00633H 15.10 3.963e- 09 244-266
1340	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625B 17.69 5.219e-15 179- 213 BL00625B 17.69 9.194e-14 343-377 BL00625A 16.21 4.405e-12 185-214 BL00625A 16.21 5.500e-12 129-158 BL00625A 16.21 7.203e-12 349- 378 BL00625B 17.69 5.778e-10 123-157 BL00625B 17.69 5.034e- 09 285-319
1342	BL00476	Fatty acid desaturases family 1 proteins.	BL00476F 12.75 6.551e-09 45-90
1345	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.690e-11 292- 307 PR00320B 12.19 4.343e-10 292-307 PR00320C 13.01 7.840e- 10 292-307
1345	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.000e-09 294-305
1345	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.	BL00225B 18.06 7.273e-22 6-41 BL00225B 18.06 5.673e-14 97- 132 BL00225A 13.82 7.218e-09 61-82
1350	PD01823	PROTEIN INTERGENIC REGION ABC1 PRECURSOR MITOCHONDRION T.	PD01823D 16.66 3.093e-15 21-42 PD01823E 9.30 5.909e-15 75-88
1352	BL00540	Ferritin iron-binding regions proteins.	BL00540A 15.06 1.000e-40 9-50 BL00540B 18.82 1.000e-40 100- 155 BL00540C 13.00 7.500e-15 165-177
1353	PR00294	STREPTOMYCES SUBTILISIN INHIBITOR SIGNATURE	PR00294A 10.44 6.444e-10 159- 186
1353	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 7.167e-10 206- 245
1356	BL00428	Cell cycle proteins ftsW / rodA / spoVE proteins.	BL00428A 14.30 3.613e-09 91- 110
1359	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.	BL00142 8.38 7.188e-10 389-400
1359	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 7.983e-16 550- 578 PD01719B 9.30 1.750e-09 877-885 PD01719A 12.89 3.000e-09 1006-1034
1359	PR00480	ASTACIN FAMILY SIGNATURE	PR00480B 15.41 3.186e-09 384- 403
1360	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.	DM00191D 13.94 6.330e-11 232- 271 DM00191D 13.94 7.728e-11 48-87 DM00191D 13.94 5.000e- 10 112-151 DM00191D 13.94

SEQ ID NO:	Database entry ID	Description	Results*
1101	ondy Ho		5.667e-10 59-98 DM00191D 13.94 5.667e-10 123-162 DM00191D 13.94 6.583e-10 56- 95 DM00191D 13.94 8.417e-10
·	•		280-319 DM00191D 13.94 8.917e-10 192-231 DM00191D
·			13.94 1.391e-09 224-263 DM00191D 13.94 2.409e-09 208- 247 DM00191D 13.94 4.835e-09
			120-159 DM00191D 13.94 5.304e-09 149-188 DM00191D 13.94 5.461e-09 211-250
			DM00191D 13.94 6.322e-09 80- 119 DM00191D 13.94 7.652e-09 243-282 DM00191D 13.94 8.513e-09 216-255 DM00191D
1000	PE00624	Flocculin repeat proteins.	13.94 9.452e-09 177-216 PF00624J 6.21 3.496e-11 237-292
1360	PF00624	Procedim repeat proteins.	PF00624J 6.21 6.597e-11 53-108 PF00624J 6.21 4.121e-10 253-308 PF00624J 6.21 5.718e-10 141-196 PF00624F 11.04 1.508e-09 50-86 PF00624J 6.21 3.163e-09 101-156 PF00624J 6.21 3.233e-09 165-220 PF00624I 9.10 5.181e-09 140-170
			PF00624F 11.04 6.008e-09 130- 166 PF00624J 6.21 6.093e-09 125-180 PF00624J 6.21 6.163e- 09 221-276 PF00624G 10.91
			6.806e-09 45-100 PF00624G 10.91 7.169e-09 181-236 PF00624G 10.91 7.387e-09 221- 276 PF00624J 6.21 8.674e-09 197-252 PF00624J 6.21 8.884e- 09 117-172 PF00624J 6.21 8.884e-09 213-268 PF00624J 6.21 9.512e-09 55-110
1360	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 6.163e-10 22-71 BL00115Z 3.12 7.618e-09 36-85 BL00115Z 3.12 9.603e-09 241- 290
1363	PF00023	Ank repeat proteins.	PF00023A 16.03 1.321e-09 110- 126
1363	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.527e-13 110- 165 PF00791B 28.49 6.119e-09 77-132 PF00791C 20.98 7.529e- 09 91-130
1366	PF00168	C2 domain proteins.	PF00168C 27.49 9.250e-17 320- 346
1366	PR00399	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 1.844e-14 148- 164 PR00399C 12.82 8.071e-14 218-234 PR00399B 14.27 2.853e- 13 163-177 PR00399D 14.48 1.871e-11 238-249
1366	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.759e-12 337- 351 PR00360A 14.59 3.903e-10 308-321 PR00360B 13.61 4.789e- 10 203-217

NO: entry ID 1367 PF00168 C2 domain proteins. PF00168C 27.49 9.25 346 1367 PR00399 SYNAPTOTAGMIN SIGNATURE PR00399A 9.52 1.84 164 PR.00399C 12.8 218-234 PR00399B 13 163-177 PR00399 1.871e-11 238-249 PR00360B 13.618.75 351 PR00360B 13.618.75 308-321 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00360B 1.0 203-217 PR00464E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00463E 1.0 203-217 PR00	le-14 148- 8.071e-14 14.27 2.853e- D 14.48 19e-12 337- 13.903e-10 3.61 4.789e- 16-17 454-
1367 PR00399 SYNAPTOTAGMIN SIGNATURE PR00399A 9.52 1.84 164 PR00399C 12.82 218-234 PR00399B 13 163-177 PR00399 1.871e-11 238-249 PR00360B 13.61 8.75 351 PR00360B 13.61 8.75 308-321 PR00360B 1 10 203-217 1368 BL00086 Cytochrome P450 cysteine heme-iron ligand proteins. 1368 PR00464 E-CLASS P450 GROUP II SIGNATURE PR00464I 14.64 4.375 478 PR00464	8 8.071e-14 4.27 2.853e- D 14.48 9e-12 337- 9 3.903e-10 3.61 4.789e- e-20 444- ie-17 454-
1367 PR00360 C2 DOMAIN SIGNATURE PR00360B 13.61 8.75	14.27 2.853e- D 14.48 19e-12 337- 2 3.903e-10 3.61 4.789e- e-20 444- ie-17 454-
1.871e-11 238-249 PR00360B 13.61 8.75 351 PR00360B 13.61 8.75 351 PR00360B 13.61 8.75 363-321 PR00360B 14.55 308-321 PR00360B 1	9e-12 337- 3.903e-10 3.61 4.789e- e-20 444- 6e-17 454-
1368 BL00086 Cytochrome P450 cysteine heme-iron ligand proteins. 10 203-217	3.903e-10 3.61 4.789e- e-20 444- 6e-17 454-
308-321 PR00360B 1 10 203-217 10 203-217	3.61 4.789e- e-20 444- 6e-17 454-
1368 BL00086 Cytochrome P450 cysteine heme-iron ligand proteins. 476 H76 PR00464 E-CLASS P450 GROUP II SIGNATURE PR00464I 14.64 4.375 478 PR00464A 20.47 130-151 PR00464C 1 15 305-334 PR00464C 1 15 305-334 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 12 363-384 PR00464E 13 368 PR00385 P450 SUPERFAMILY SIGNATURE PR00465H 17.76 6.58 473 1368 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.344 334 PR00385B 10.22 334-348 PR00385B 10.22	ie-17 454-
PR00464 E-CLASS P450 GROUP II SIGNATURE PR00464I 14.64 4.375	
1368 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.3468 PR00385 PA50 GROUP I SIGNATURE PR00385A 14.97 1.3468 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00385A 14.97 1.3468 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00385A 14.97 1.34634 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385B 10.22 334-348 PR00385B 1: 10 445-455 PR00385B 1:	
130-151 PR00464C 1 15 305-334 PR00464C 1 15 305-334 PR00464C 1 15 305-334 PR00464C 1 15 305-334 PR00464E 13.32 8.941e-15 441-4 PR00464F 15.23 9.65c 419 PR00464B 20.41 186-205 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00465E 12 363-384 PR00465E 17.76 6.58c 473 473 473 473 473 473 473 473 474 473 473 474 475	
15 305-334 PR00464 6.250e-15 334-352 PI 13.32 8.941e-15 441-4 PR00464F 15.23 9.656 419 PR00464B 20.41 186-205 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 12 363-384 PR00464E 1 13 368 PR00385 P450 GROUP IV SIGNATURE PR00465H 17.76 6.58 473 PR00385A 14.97 1.346 334 PR00385B 10.22 334-348 PR00385D 1 10 445-455 PR00385B 10.22 334-348 PR00385D 1 10 445-455 PR00385B 9.438e-10 454-466 434 PR00463E 17.37 325-352 PR00463I 15.	8.84 1.000e.
13.32 8.941e-15 441-4 PR00464F 15.23 9.65c 419 PR00464B 20.41 186-205 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00465E 12 363-384 PR00465H 17.76 6.58c 473 1368 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.34c 334 PR00385B 10.22 334-348 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385E 9.438e-10 454-466 1368 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.605 434 PR00463E 17.37 325-352 PR00463I 15.	
PR00464F 15.23 9.65- 419 PR00464B 20.41 186-205 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00464E 1. 12 363-384 PR00465H 17.76 6.58 473 PR00465H 17.76 6.58 473 PR00385A 14.97 1.34 334 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385D 1: 10 445-455 PR00385B 9.438e-10 454-466 PR00463E 17.37 325-352 PR00463I 15.	
1368 PR00465 E-CLASS P450 GROUP IV SIGNATURE PR00465H 17.76 6.58 473 1368 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.344 334 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385D 1: 10 445-455 PR00385B 10.22 348-10 454-466 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.60: 434 PR00463E 17.37 325-352 PR00463I 15.	
186-205 PR00464	le-13 403-
12 363-384 PR004644 8.412e-12 419-435 1368 PR00465 E-CLASS P450 GROUP IV SIGNATURE PR00465H 17.76 6.58 473 473 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.344 334 PR00385B 10.22 334-348 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385E 1368 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.60: 434 PR00463E 17.37 325-352 PR004631 15.	
1368 PR00465 E-CLASS P450 GROUP IV SIGNATURE PR00465H 17.76 6.58 473	3.20 /.9U/E- 3.12 //1
1368 PR00465 E-CLASS P450 GROUP IV SIGNATURE PR00465H 17.76 6.58 473	J 14.71
1368 PR00385 P450 SUPERFAMILY SIGNATURE PR00385A 14.97 1.344 334 PR00385B 10.22 334-348 PR00385D 1: 10 445-455 PR00385E 9.438e-10 454-466 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.603 434 PR00463E 17.37 325-352 PR004631 15	5e-10 454-
1368 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.603 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.603 434 PR00463E 17.37 325-352 PR004631 15	
334-348 PR00385D 1: 10 445-455 PR00385D 1: 10 445-455 PR00385E 9.438e-10 454-466 1368 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.60: 434 PR00463E 17.37 325-352 PR00463I 15.	5e-12 316-
1368 PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.60: 434 PR00463E 17.37 325-352 PR004631 15	
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PR00463 E-CLASS P450 GROUP I SIGNATURE PR00463G 18.24 3.603 434 PR00463E 17.37 325-352 PR004631 15	, 12.00
325-352 PR00463I 15	ie-14 409-
	4.814e-11
09 454-478 PR00463F 7.158e-09 444-455	1 12.41
1370 BL00218 Amino acid permeases proteins. BL00218D 21.49 9.757	le 11 262
308	C-11 203-
1371 PR00049 WILM'S TUMOUR PROTEIN SIGNATURE PR00049D 0.00 3.288e	-09 35-50
1372 PR00380 KINESIN HEAVY CHAIN SIGNATURE PR00380A 14.18 4.086	e-22 84-
106 PR00380C 13.18	.286e-17
240-259 PR00380D 9.	
17 290-312 PR00380B 7.805e-14 207-225	1264
1372 BL00411 Kinesin motor domain proteins. BL00411G 21.39 7.750	A A. UT
283 BL00411C 15.04 2	
84-106 BL00411H 15.	e-25 241-
16 289-320 BL00411E	e-25 241- 2.500e-22 66 8.235e-
9.129e-16 135-154 BL	e-25 241- 2.500e-22 66 8.235e- 10.43
14.77 9.795e-16 198-22 BL00411D 12.13 5.909	e-25 241- 2.500e-22 66 8.235e- 10.43
	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F
1373 PR00049 WILM'S TUMOUR PROTEIN SIGNATURE PR00049D 0.00 1.915e-	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F
1073 605	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F 3 e-09 114-
1373 PR00019 LEUCINE-RICH REPEAT SIGNATURE PR00019A 11.19 5.8000	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F 3 e-09 114- 09 590-
172 PR00019B 11.36 1	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F 3 e-09 114- 09 590-
130-144 PR00019A 11. 10 133-147 PR00019B	e-25 241- 2.500e-22 66 8.235e- 10.43 00411F 3 e-09 114- 09 590- e-12 158- .000e-10

SEQ ID	Database	Description	Results*
NO:	entry ID		7.120e-09 106-120
4050	DD 00500	POLYCYSTIC KIDNEY DISEASE	PR00500B 7.74 7.821e-09 250-
1373	PR00500	PROTEIN SIGNATURE	271
1374	BL00411	Kinesin motor domain proteins.	BL00411H 15.66 7.811e-22 79-
13/4	BEOUTIT	Tamoon motor domain protesting	110 BL00411G 21.39 8.683e-22
			31-73
1374	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380C 13.18 2.385e-16 30-49
			PR00380D 9.93 3.739e-16 80-102
1376	BL00790	Receptor tyrosine kinase class V proteins.	BL00790E 29.58 6.667e-12 767-
			815 PR00010C 11.16 5.636e-10 423-
1376	PR00010	TYPE II EGF-LIKE SIGNATURE	434 PR00010C 11.16 8.071e-09
	ļ		1 148-159
	77.00000	EGF-like domain proteins.	BL00022B 7.54 8.200e-09 427-
1376	BL00022	EGF-like domain proteins.	434
1376	PR00907	THROMBOMODULIN SIGNATURE	PR00907B 11.29 7.312e-10 224-
13/0	PK00907	111KOMBOMODOBA STORA COL	241 PR00907G 11.63 5.297e-09
			62-89 PR00907B 11.29 8.354e-09
			98-115 PR00907B 11.29 9.451e-
			09 334-351
1376	BL01187	Calcium-binding EGF-like domain proteins	BL01187B 12.04 5.235e-15 62-78
	ì	pattern proteins.	BL01187B 12.04 5.765e-15 418-
			434 BL01187B 12.04 3.000e-12 143-159 BL01187B 12.04 7.333e-
1		·	12 297-313 BL01187B 12.04
	•	·	7.000e-11 338-354 BL01187B
j .			12.04 4.857e-10 378-394
İ			BL01187B 12.04 5.886e-10 102-
			118 BL01187A 9.98 6.571e-10
			321-333 BL01187A 9.98 5.125e-
			09 126-138 BL01187A 9.98
			9.625e-09 362-374
1377	BL00048	Protamine P1 proteins.	BL00048 6.39 4.038e-09 396-423
1381	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 8.500e-27 342-
			373 PR00109B 12.27 5.412e-12 342-
1381	PR00109	TYROSINE KINASE CATALYTIC	7R00109B 12.27 5.412e-12 542-
		PROTEIN GLYCOPROTEIN PRECURSOR	PD00306A 10.26 6.143e-09 25-39
1381	PD00306	RE.	F D00300A 10.20 0.1430-03 23-33
1200	DD 00010	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 6.036e-09 48-61
1382	PR00910	SIGNATURE	
1388	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.261e-10 69-83
1300	1100015	EBOOM AGOIT TO THE TENT OF THE	PR00019B 11.36 4.600e-09 66-80
1392	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 6.870e-09 42-55
1396	BL00790	Receptor tyrosine kinase class V proteins.	BL00790B 21.59 1.000e-40 61-
			113 BL00790C 16.65 1.000e-40
			165-219 BL00790K 9.30 1.000e-
			40 657-711 BL00790Q 15.61
			1.000e-40 855-904 BL007900
			7.68 5.929e-39 797-830
	1		BL00790G 22.06 5.114e-36 376- 420 BL00790R 16.20 7.469e-36
			951-995 BL00790E 29.58 7.250e-
			35 273-321 BL00790J 14.21
			8.200e-33 605-645 BL00790N
			13.25 1.214e-31 763-790
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			532 BL00790D 12.41 2.500e-27
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SEQ ID	Database	Description	Results*
NO:	entry ID		
			243-268 BL00790H 13.42
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			8.74 8.683e-25.741-763
			BL00790P 12.33 3.755e-24 830- 855 BL00790F 15.90 5.200e-24
			339-366 BL00790L 11.16 5.909e-
	1		21 721-741 BL00790A 19.74
			1.964e-19 31-53
1396	BL00240	Receptor tyrosine kinase class III proteins.	BL00240F 17.74 9.500e-16 789-
			837 BL00240E 11.56 1.439e-15
			736-774 BL00240G 28.45
1206	DI 00107	Description Amplication	8.793e-15 836-889
1396	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.647e-20 750-
			781 BL00107B 13.31 5.091e-13
1396	PR00109	TYROSINE KINASE CATALYTIC	818-834 PR00109D 17.04 9.100e-22 819-
1370	1100105	DOMAIN SIGNATURE	842 PR00109E 14.41 7.429e-19
		20.2	863-886 PR00109B 12.27 5.125e-
			18 750-769 PR00109A 15.00
			2.895e-13 713-727 PR00109C
			12.85 5.235e-12 800-811
1396	BL00239	Receptor tyrosine kinase class II proteins.	BL00239E 17.14 5.426e-27 790-
			840 BL00239B 25.15 3.000e-23
			684-732 BL00239F 28.15 8.132e- 21 844-889 BL00239D 16.81
			2.143e-10 762-788 BL00239C
			18.75 3.348e-10 737-760
1396	BL50001	Src homology 2 (SH2) domain proteins	BL50001B 17.40 2.714e-11 747-
		profile.	768 BL50001D 11.00 7.300e-10
			818-829 BL50001C 10.17 1.000e-
			09 799-810
1396	PR00014	FIBRONECTIN TYPE III REPEAT	PR00014C 15.44 8.071e-13 490-
		SIGNATURE	509 PR00014B 14.77 3.400e-10 467-478 PR00014D 12.04 6.824e-
		1	10 508-523 PR00014A 8.22
			3.455e-09 342-352
1401	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.000e-11 84-127
1403	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.958e-09 387-
			441
1404	BL01113	C1q domain proteins.	BL01113B 18.26 2.500e-13 841-
440.0			877
1406	BL01206	Amiloride-sensitive sodium channels	BL01206D 30.58 3.025e-28 363-
		proteins.	412 BL01206G 21.72 6.063e-27
			530-576 BL01206F 16.40 7.643e- 15 485-506 BL01206E 20.72
			5.650e-14 427-454 BL01206C
		·	12.30 3.455e-12 333-352
			BL01206B 13.56 1.205e-10 313-
			327
1408	BL01220	Phosphatidylethanolamine-binding protein	BL01220B 16.65 1.000e-40 59-
		family proteins.	100 BL01220C 14.75 5.846e-34
			100-128 BL01220A 22.62
1409	BL00815	Alpha isonepsylmolete and have altered	3.400e-31 21-52
1407	[סדיייסוס	Alpha-isopropylmalate and homocitrate synthases proteins.	BL00815C 21.36 3.118e-09 786- 815
1412	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 4.051e-09 1-16
1412	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.640e-09 3-17
1418	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.200e-09 453-

SEQ ID NO:	Database entry ID	Description	Results*
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1418	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e-14 524- 541 BL00028 16.07 8.269e-11
	1		555-572 BL00028 16.07 2.543e- 09 437-454 BL00028 16.07 4,600e-09 408-425 BL00028
			16.07 6.657e-09 465-482
1418	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.160e-09 521- 535 PR00048A 10.52 4.960e-09
			434-448 PR00048A 10.52 6.760e- 09 552-566 PR00048A 10.52 7.840e-09 462-476
1419	BL00022	EGF-like domain proteins.	BL00022A 7.48 5.000e-09 177-
			184 BL00022A 7.48 5.000e-09 241-248 BL00022A 7.48 8.000e- 09 49-56
1419	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 5.696e-09 182-
1419	PRODUIT	I II E M DOI-BILL SIGIVITORE	201 PR00011D 14.03 6.478e-09
			86-105 PR00011D 14.03 9.087e- 09 118-137
1419	DM01842	1 CELLULOSE-BINDING DOMAIN, BACTERIAL TYPE.	DM01842 11.31 9.922e-09 94-141
1421	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE	PR00371D 14.55 4.536e-11 385- 405
1421	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE	PR00406D 10.02 6.538e-10 385- 405
1421	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 2.484e-09 385- 405
1421	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466E 6.82 6.958e-17 386- 404 PR00466C 10.17 8.244e-09 195-216
1422	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.462e-11 1087- 1104
1422	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.478e-11 1075- 1088
1422	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 4.375e-10 1154- 1188
1422	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 4.522e-10 1084- 1098 PR00048B 6.02 1.474e-09 1072-1082 PR00048A 10.52 6.760e-09 1056-1070
1423	PR00260	BACTERIAL CHEMOTAXIS SENSORY TRANSDUCER SIGNATURE	PR00260C 10.26 9.294e-09 146- 167
1424	BL00845	CAP-Gly domain proteins.	BL00845 16.43 6.442e-21 405- 430 BL00845 16.43 9.820e-19 203-228
1426	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.769e-15 369- 382 PD00066 13.92 4.462e-15 285-298 PD00066 13.92 2.800e- 14 257-270 PD00066 13.92 5.200e-14 313-326 PD00066 13.92 8.962e-10 341-354
1426	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.050e-13 269- 286 BL00028 16.07 5.050e-13 297-314 BL00028 16.07 2.500e- 10 325-342 BL00028 16.07 5.200e-10 353-370 BL00028

SEQ ID NO:	Database entry ID	Description	Results*
			16.07 7.000e-10 241-258 BL00028 16.07 9.700e-10 381- 398
1426	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.500e-17 266- 280 PR00048A 10.52 5.500e-14
		•	294-308 PR00048A 10.52 4.706e-
	İ		12 350-364 PR00048B 6.02
			6.000e-12 310-320 PR00048B 6.02 6.538e-11 394-404
			PR00048A 10.52 2.565e-10 238-
			252 PR00048B 6.02 2.688e-10
			254-264 PR00048B 6.02 4.375e- 10 338-348 PR00048A 10.52
			5.304e-10 378-392 PR00048A
			10.52 9.609e-10 322-336
			PR00048B 6.02 5.263e-09 282-
	-		292 PR00048B 6.02 6.211e-09 366-376
1429	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 5.345e-09 9-29
1431	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.855e-09 215-
1431	BL00226	Intermediate filaments proteins.	236
			BL00226D 19.10 7.400e-09 390- 437
1432	DM01803	1 HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 6.855e-09 251- 272
1432	BL00226	Intermediate filaments proteins.	BL00226D 19.10 7.400e-09 426- 473
1434	PR00545	RETINOIC ACID RECEPTOR SIGNATURE	PR00545A 5.35 9.430e-09 383- 398
1436	BL01238	GDA1/CD39 family of nucleoside phosphatases proteins.	BL01238A 11.72 7.840e-16 76-91
1437	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 2.800e-26 1256-
		ACTIVATION.	1297 PD00930A 25.62 3.864e-13
1437	PF00620	GTPase-activator protein for Rho-like	1152-1178 PF00620B 14.20 7.000e-12 1205-
		GTPases.	1222
1437	PR00683	SPECTRIN PLECKSTRIN HOMOLOGY	PR00683B 16.62 2.603e-10 946-
		DOMAIN SIGNATURE	968 PR00683D 15.87 2.773e-09
1437	PR00543	OESTROGEN RECEPTOR SIGNATURE	PR00543H 10.86 7.573e-09 556-
1427	DDoorod		576
1437	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 7.600e-09 90-101
1437	BL00275	Shiga/ricin ribosomal inactivating toxins proteins signatu.	BL00275A 12.16 7.677e-09 1226-
1441	BL00223	Annexins repeat proteins domain proteins.	BL00223B 28.47 1.000e-40 140-
			190 BL00223C 24.79 1.000e-40
			217-272 BL00223A 15.59 5.500e-32 21-55 BL00223A
			15.59 4.783e-14 230-264
			BL00223C 24.79 2.515e-10 8-63
			BL00223A 15.59 6.250e-10 71-
1441	PR00199	ANNEXIN TYPE III SIGNATURE	PR00199G 9.09 8.364e-21 239-
l			265 PR00199F 16.19 5.636e-16
			158-185 PR00199D 5.65 5.375e-
			14 25-47 PR00199B 6.86 1.574e-
			13 30-53 PR00199D 5.65 7.987e-

SEQ ID NO:	Database entry ID	Description	Results*
			13 234-256 PR00199H 12.62 5.339e-12 282-296 PR00199D 5.65 9.276e-10 75-97
1441	PR00200	ANNEXIN TYPE IV SIGNATURE	PR00200F 13.72 1.118e-35 158- 185 PR00200G 9.43 1.000e-34
			238-265 PR00200B 7.39 1.643e- 29 30-53 PR00200H 13.68 1.766e-18 282-296 PR00200E 10.00 6.160e-16 75-97 PR00200E 10.00 2.111e-14 25-47 PR00200A 4.93 2.125e-14 5-16 PR00200C 8.76 1.500e-12 54-63 PR00200E 10.00 2.859e-11 234-256 PR00200G 9.43 5.294e-11 29-56 PR00200D 10.01 9.722e-10 70-87
1441	PR00197	ANNEXIN TYPE I SIGNATURE	PR00197F 9.03 5.250e-16 238- 259 PR00197D 7.50 1.250e-15 25-47 PR00197E 11.89 8.463e-14 158-185 PR00197D 7.50 1.542e- 12 234-256 PR00197D 7.50 5.451e-10 75-97 PR00197B 7.56 2.206e-09 30-53
1441	PR00198	ANNEXIN TYPE II SIGNATURE	PR00198G 8.09 7.943e-16 238- 259 PR00198D 7.65 2.271e-13 234-256 PR00198D 7.65 9.894e- 13 25-47 PR00198E 14.67 6.381e-11 158-185 PR00198H 12.05 1.462e-10 282-296 PR00198B 8.71 9.357e-10 30-53 PR00198D 7.65 4.845e-09 75-97
1441	PR00201	ANNEXIN TYPE V SIGNATURE	PR00201G 11.02 9.419e-26 238- 265 PR00201A 6.05 4.770e-16 30-53 PR00201E 12.37 4.103e-15 158-185 PR00201H 12.04 4.375e- 14 282-296 PR00201D 10.49 4.150e-10 75-97 PR00201G 11.02 8.402e-10 29-56 PR00201D 10.49 6.179e-09 25-47
1441	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301D 15.51 7.395e-09 38-59
1441	PR00196	ANNEXIN FAMILY SIGNATURE	PR00196D 21.86 3.032e-24 158- 185 PR00196E 9.19 8.333e-23 238-259 PR00196A 11.16 9.100e- 21 30-53 PR00196F 13.89 2.714e-15 266-282 PR00196C 10.36 5.167e-15 25-47 PR00196G 11.72 3.000e-14 282-296 PR00196C 10.36 7.344e-13 234- 256 PR00196C 10.36 1.703e-12 75-97 PR00196G 11.72 9.217e-10 207-221 PR00196F 13.89 4.188e- 09 107-123 PR00196A 11.16 7.840e-09 80-103
1441	PR00202	ANNEXIN TYPE VI SIGNATURE	PR00202G 8.01 4.833e-28 238- 265 PR00202E 13.00 4.643e-16 158-185 PR00202D 5.58 9.604e- 13 75-97 PR00202B 11.44 2.763e-11 29-53 PR00202H 9.20

SEQ ID NO:	Database entry ID	Description	Results*
			4.740e-11 282-296 PR00202D 5.58 1.908e-09 25-47 PR00202G
1444	DM01513	CAMP-DEPENDENT PROTEIN KINASE	8.01 9.237e-09 29-56 DM01513A 13.61 8.568e-14 15-
1445	BL00603	REGULATORY CHAIN.	56
1443	DE00003	Thymidine kinase cellular-type proteins.	BL00603C 30.02 1.000e-40 152- 207 BL00603A 20.71 4.500e-33
		·	63-96 BL00603D 10.53 5.091e-
			18 217-232 BL00603B 11.39 3.455e-15 132-147
1446	PD01922	PROTEIN PHOSPHODIESTERASE HYDROL.	PD01922B 21.83 7.328e-14 162-
1447	BL00061	Short-chain dehydrogenases/reductases	BL00061B 25.79 1.931e-13 99-
1448	BL01160	family proteins. Kinesin light chain repeat proteins.	137
			BL01160B 19.54 5.958e-09 64-
1449 1449	PF00856 PF00628	SET domain proteins.	PF00856A 26.14 8.579e-11 5-42
1452	BL00030	PHD-finger. Eukaryotic RNA-binding region RNP-1	PF00628 15.84 5.500e-10 11-26 BL00030B 7.03 3.400e-10 116-
		proteins.	126
1454	PF00075	RNase H.	PF00075D 10.71 7.000e-11 517-
			528 PF00075C 11.58 9.786e-11 484-496 PF00075B 12.56 4.073e-
			10 449-460 PF00075A 14.44
1454	PR00211	GLUTELIN SIGNATURE	2.143e-09 402-419
			PR00211B 0.86 4.417e-09 138- 159
1456	BL00262	Insulin family proteins.	BL00262B 16.89 8.286c-17 68-88
1456	PR00277	INSULIN B CHAIN SIGNATURE	BL00262A 12.48 4.600e-15 32-50 PR00277A 14.82 2.421e-13 29-43
1456	PR00276	INSULIN A CHAIN SIGNATURE	PR00277B 12.79 2.350e-11 43-56
		· · · ·	PR00276A 11.84 4.750e-13 69-79 PR00276B 8.02 7.828e-10 78-88
1457	PR00213	MYELIN PO PROTEIN SIGNATURE	PR00213E 5.51 9.775e-12 264- 289
1459	BL00856	Guanylate kinase proteins.	BL00856C 29.21 2.658e-26 539-
			587 BL00856B 9.61 2.946e-18 511-532
1459	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 2.750e-09 369-
1459	PD00289	PROTEIN OUR POLICE	385
	FD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.586e-09 298-312
1459	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 8.800e-09 295-306
1461	PR00475	HEXOKINASE FAMILY SIGNATURE	PR00475B 14.92 6.143e-26 186-
			212 PR00475E 16.08 2.742e-22
			327-350 PR00475F 9.68 4.000e- 20 407-430 PR00475A 14.06
			3.118e-19 118-135 PR00475C
	·		11.92 6.684e-19 239-256
			PR00475G 9.08 1.692e-16 479- 496 PR00475D 13.30 2.653e-13
1			262-277 PR00475G 9.08 2.650e-
1461	BL00378	Warshinger matrix	10 32-49
1701	PF002/9	Hexokinases proteins.	BL00378C 16.14 1.000e-40 243- 287 BL00378E 22.92 5.821e-40
}			313-359 BL00378B 14.23 3.647e-

SEQ ID NO:	Database entry ID	Description	Results*
NO:	entry ID		32 98-135 BL00378F 8.27 2.688e-17 481-496 BL00378D 10.94 1.474e-13 291-303 BL00378A 19.01 8.694e-11 59-87 BL00378F 8.27 3.714e-10 34-49
1464	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (SI) SIGNATURE	PR00722A 12.27 8.448e-14 56-72
1464	BL00021	Kringle domain proteins.	BL00021B 13.33 1.763e-13 55-73
1464	PR00839	V8 SERINE PROTEASE FAMILY SIGNATURE	PR00839B 11.20 4.945e-09 55-73
1464	BL01253	Type I fibronectin domain proteins.	BL01253E 16.01 6.381e-09 125- 162
.1464	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 3.813e-15 55-72 BL00134B 15.99 7.200e-10 186- 210 BL00134C 13.45 9.206e-09 219-233
1466	BL00291	Prion protein.	BL00291A 4.49 9.379e-09 105- 140
1467	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 9.581e-12 398- 422
1468	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 2.868e-25 126- 178
1469	PF01105	emp24/gp25L/p24 family.	PF01105B 25.12 2.868e-25 151- 203
1470	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305A 9.33 9.500e-36 37-67 PR00305E 13.01 4.316e-32 177- 204 PR00305D 16.34 3.647e-30 150-177 PR00305F 15.95 1.964e- 26 204-234 PR00305C 8.68 3.182e-26 115-138 PR00305B 9.99 4.857e-24 84-109 PR00305F 15.95 8.975e-15 215-245
1470	BL00796	14-3-3 proteins.	BL00796C 17.44 1.000e-40 99- 149 BL00796D 17.39 1.000e-40 150-196 BL00796B 10.67 7.000e- 39 37-70 BL00796E 14.15 3.045e-33 198-234 BL00796A 10.52 4.656e-26 5-32 BL00796E 14.15 2.742e-11 209-245
1474	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 7.796e-10 676-687 PF00642 11.59 7.055e-09 276-287
1475	PF00588	SpoU rRNA Methylase family.	PF00588B 17.18 8.200e-10 281- 303
1476	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.653e-09 791- 845
1477	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.255e-14 364- 385
1477	BL00306	Caseins alpha/beta proteins.	BL00306B 8.28 1.900e-09 557- 568
1477	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00318E 7.23 5.320e-09 220- 230
1479	BL01305	moaA / nifB / pqqE family proteins.	BL01305D 14.97 7.279e-09 7-22
1480	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE	PR00918A 13.76 5.807e-09 458- 479
1480	PR00674	LIGHT HARVESTING PROTEIN B CHAIN SIGNATURE	PR00674A 20.10 9.870e-09 133- 154
1481	PR00171	SUGAR TRANSPORTER SIGNATURE	PR00171E 14.87 1.000e-08 73-86

SEQ ID NO:	Database entry ID	Description	Results*
1482	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.	DM01418A 20.83 5.650e-23 101- 149 DM01418B 22.51 8.500e-11
		N. C.	166-208 DM01418C 20.48 8.655e-10 236-278
1482	BL00291	Prion protein.	BL00291A 4.49 9.349e-10 23-58
1482	BL01113	C1q domain proteins.	BL01113A 17.99 6.114e-11 38-65
			BL01113A 17.99 2.915e-10 35-62 BL01113A 17.99 6.538e-09 17-44 BL01113A 17.99 6.712e-09 29-56
1483	DM01418	352 FIBRILLAR COLLAGEN	BL01113A 17.99 8.442e-09 32-59 DM01418A 20.83 5.650e-23 117-
		CARBOXYL-TERMINAL.	165 DM01418B 22.51 8.500e-11 182-224 DM01418C 20.48 8.655e-10 252-294
1483	BL00291	Prion protein.	BL00291A 4.49 9.349e-10 23-58
1483	BL01113	C1q domain proteins.	BL01113A 17.99 6.114e-11 38-65 BL01113A 17.99 2.915e-10 35-62 BL01113A 17.99 6.538e-09 17-44 BL01113A 17.99 6.712e-09 29-56 BL01113A 17.99 8.442e-09 32-59
1484	BL01052	Calponin family repeat proteins.	BL01052B 15.31 3.308e-11 30-56
1484	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE	PR00888C 12.27 2.141e-09 30-46
1486	BL00795	Involucrin proteins.	BL00795C 17.06 7.600e-09 239- 284
1486	BL00415	Synapsins proteins.	BL00415N 4.29 9.409e-09 818- 862
1490	BL01046	ATP-dependent serine proteases, lon family, serine active sit.	BL01046D 19.61 4.938e-35 452- 493 BL01046C 17.03 9.581e-31 377-421 BL01046B 19.24 4.977e- 29 331-377
1490	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830D 8.08 2.552e-20 767- 787 PR00830A 8.41 7.545e-18 375-395 PR00830E 13.94 8.500e- 15 790-809 PR00830C 8.47 2.837e-13 737-757 PR00830B 14.73 7.429e-13 654-671
1490	BL01128	Shikimate kinase proteins.	BL01128A 18.84 8.027e-12 371- 405
1490	PR00300	ATP-DEPENDENT CLP PROTEASE ATP- BINDING SUBUNIT SIGNATURE	PR00300A 9.56 1.254e-10 371- 390
1490	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 2.350e-10 370- 386
1490	BL00674	AAA-protein family proteins.	BL00674B 4.46 8.071e-10 368- 390
1490	PR00364	DISEASE RESISTANCE PROTEIN SIGNATURE	PR00364A 8.19 1.818e-09 370- 386
1490	BL00113	Adenylate kinase proteins.	BL00113A 12.74 7.369e-09 372- 389
1491	BL00824	Elongation factor 1 beta/beta/delta chain proteins.	BL00824B 9.21 2.338e-09 150- 170
1495	BL00615	C-type lectin domain proteins.	BL00615A 16.68 3.880e-11 47-65 BL00615B 12.25 2.286e-10 149- 163
1498	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE	PR00119B 13.94 8.714e-12 35-50 PR00119E 8.48 7.716e-11 420- 440

SEQ ID NO:	Database entry ID	Description	Results*
1498	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 7.037e-10 420- 437
1498	BL00154	E1-E2 ATPases phosphorylation site proteins.	BL00154E 20.37 5.275e-19 263- 304 BL00154F 8.23 6.175e-19 417-441 BL00154C 12.38 4.326e- 13 31-50 BL00154D 12.57 5.935e-09 191-202
1499	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 3.455e-33 476- 522 BL00039A 18.44 8.548e-23 145-184 BL00039C 15.63 8.500e- 16 277-301 BL00039B 19.19 1.837e-12 191-217
1499	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 8.990e-12 450- 497
1499	PF00271	Helicases conserved C-terminal domain proteins.	PF00271 7.99 5.500e-10 507-515
1501	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 9.669e-09 116- 165
1502	PF00168	C2 domain proteins.	PF00168B 11.83 8.000e-10 38-49
1502	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 6.806e-10 43-56 PR00360B 13.61 2.227e-09 67-81 PR00360B 13.61 5.909e-09 223- 237
1503	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 4.165e-13 780- 835 PF00791B 28.49 6.767e-10 888-943 PF00791C 20.98 8.059e- 09 794-833
1504	PF00023	Ank repeat proteins.	PF00023A 16.03 5.875e-10 437- 453 PF00023A 16.03 7.000e-10 563-579 PF00023A 16.03 8.500e- 10 248-264 PF00023A 16.03 9.250e-10 95-111 PF00023A 16.03 3.250e-09 596-612 PF00023A 16.03 3.893e-09 716- 732 PF00023A 16.03 6.786e-09 62-78 PF00023A 16.03 9.036e-09 496-512
1504	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 2.957e-09 88- 101 PD00078B 13.14 5.696e-09 556-569 PD00078B 13.14 9.217e- 09 742-755
1504	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 5.024e-15 215- 270 PF00791B 28.49 7.750e-14 62-117 PF00791B 28.49 9.795e- 14 530-585 PF00791B 28.49 9.505e-13 683-738 PF00791B 28.49 7.253e-12 95-150 PF00791B 28.49 2.636e-11 716- 771 PF00791C 20.98 5.696e-11 697-736 PF00791B 28.49 3.359e- 10 404-459 PF00791B 28.49 5.369e-10 248-303 PF00791B 28.49 6.767e-10 563-618 PF00791C 20.98 8.052e-10 544- 583 PF00791C 20.98 3.382e-09 229-268 PF00791B 28.49 7.275e- 09 371-426 PF00791C 20.98 9.912e-09 385-424

SEQ ID	Database	Description	Results*
NO:	entry ID		
1505	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.714e-09 143- 159
1506	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 8.714e-09 167- 183
1507	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 5.286e-10 239- 248
1507	BL01282	BIR repeat proteins.	BL01282B 30.49 1.900e-09 220- 259
1507	BL00264	Neurohypophysial hormones proteins.	BL00264 8.98 4.884e-09 341-368
1510	BL00122	Carboxylesterases type-B serine proteins.	BL00122G 11.67 2.500e-15 15-26
1511	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 1.986e-11 340- 353 PR00910A 2.51 1.986e-11 342-355 PR00910A 2.51 1.986e- 11 344-357 PR00910A 2.51 9.778e-10 346-359 PR00910A 2.51 1.107e-09 338-351 PR00910A 2.51 3.464e-09 336-
1511	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 4.508e-09 324-
1512	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	357 DM01970B 8.60 8.475e-15 175- 188
1514	PR00833	POLLEN ALLERGEN POA PI SIGNATURE	PR00833H 2.30 8.375e-10 149- 164 PR00833H 2.30 2.846e-09 147-162
1514	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 9.630e-11 150- 165 PR00308C 3.83 8.892e-10 104-114 PR00308C 3.83 8.892e- 10 105-115 PR00308C 3.83 8.892e-10 151-161 PR00308C 3.83 8.892e-10 152-162 PR00308C 3.83 8.892e-10 153- 163 PR00308C 3.83 8.892e-10 154-164 PR00308C 3.83 7.545e- 09 103-113 PR00308C 3.83 7.896e-09 150-160 PR00308B 4.28 8.397e-09 150-162 PR00308A 5.90 9.047e-09 101- 116
1514	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.188e-10 144- 159 PR00456E 3.06 1.684e-09 145-160 PR00456E 3.06 7.949e- 09 97-112 PR00456E 3.06 9.430e-09 98-113
1515	PF00992	Troponin.	PF00992A 16.67 3.368e-09 448- 483
1521	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 7.333e-09 322- 336 PR00019B 11.36 9.280e-09 319-333
1522	BL00315	Dehydrins proteins.	BL00315A 9.35 7.197e-10 93-121
1524	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 4.240e-16 235- 276
1524	PR00234	HIV-1 MATRIX PROTEIN SIGNATURE	PR00234E 11.78 7.268e-09 361- 375
1525	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 8.338e-14 44-92
1527	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 6.850e-10 132- 146 PR00019A 11.19 2.667e-09 135-149 PR00019B 11.36 9.640e-

SEQ ID NO:	Database entry ID	Description	Results*
. NO:	end y 1D		09 180-194 PR00019B 11.36 1.000e-08 277-291
1529	BL00625	Regulator of chromosome condensation (RCC1) proteins.	BL00625A 16.21 2.033e-16 567- 596 BL00625B 17.69 4.205e-12 561-595 BL00625B 17.69 9.423e- 11 93-127 BL00625B 17.69 1.444e-10 152-186 BL00625A
i			16.21 1.759e-10 99-128 BL00625A 16.21 2.739e-09 515- 544 BL00625B 17.69 3.172e-09 43-77 BL00625A 16.21 4.170e- 09 158-187
1529	PR00633	CHROMOSOME CONDENSATION REGULATOR RCC1 SIGNATURE	PR00633B 13.02 3.535e-09 561- 575 PR00633A 9.32 6.260e-09 527-544 PR00633F 10.03 7.949e- 09 528-543
1530	BL00414	Profilin proteins.	BL00414A 13.85 6.344e-13 2-16 BL00414E 15.46 6.283e-09 121- 136
1530	PR00392	PROFILIN SIGNATURE	PR00392C 18.98 2.350e-12 41-62 PR00392A 14.10 4.176e-12 4-14 PR00392D 12.00 5.250e-11 63-78 PR00392F 17.40 7.955e-11 122- 140 PR00392E 12.06 6.500e-09 109-123
1531	BL00414	Profilin proteins.	BL00414A 13.85 6.344e-13 2-16 BL00414E 15.46 6.283e-09 105- 120
1531	PR00392	PROFILIN SIGNATURE	PR00392C 18.98 2.350e-12 41-62 PR00392A 14.10 4.176e-12 4-14 PR00392D 12.00 5.250e-11 63-78 PR00392F 17.40 7.955e-11 106- 124 PR00392E 12.06 8.833e-09 93-107
1532	PD00301	PROTEIN REPEAT MUSCLE CALCIUM- BI.	PD00301A 10.24 8.200e-09 131- 142
1533	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930F 14.16 1.310e-27 24-60
1534	BL00411	Kinesin motor domain proteins.	BL00411G 21.39 2.200e-39 77- 119 BL00411H 15.66 8.800e-33 125-156 BL00411F 14.77 6.250e- 18 33-58
1534	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380D 9.93 7.923e-26 126- 148 PR00380C 13.18 1.000e-21 76-95 PR00380B 12.64 1.621e-16 42-60
1534	BL00893	mutT domain proteins.	BL00893 18.99 8.826e-09 176- 201
1536	BL00600	Aminotransferases class-III pyridoxal- phosphate attachment si.	BL00600E 16.43 5.725e-15 164- 193 BL00600G 12.43 7.000e-14 242-261 BL00600F 8.77 7.480e- 11 207-220 BL00600D 8.71 1.750e-10 143-157
1537	BL00838	Interleukins -4 and -13 proteins.	BL00838A 12.35 8.696e-09 136-
1537	PD01847	PHOTOSYSTEM II PROTEIN REACTION CENTRE I TRANSM.	PD01847 9.59 8.946e-09 137-173
1539	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE	PR00121D 16.72 3.012e-12 261- 283

SEQ ID NO:	Database entry ID	Description	Results*
1539	BL00154	E1-E2 ATPases phosphorylation site proteins.	DI COLEAR CO. OF D. ACC. ACC.
		B1-B2 A17 ases phospholylation site proteins.	BL00154E 20.37 8.468e-16 532- 573 BL00154C 12.38 3.520e-12 264-283
1539	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 6.400e-11 660- 685
1539	PR00119	P-TYPE CATION-TRANSPORTING	PR00119B 13.94 3.333e-11 268-
1540		ATPASE SUPERFAMILY SIGNATURE	283 PR00119D 9.56 6.063e-10 548-559
1540	BL00289	Pentaxin family proteins.	BL00289A 30.36 9.031e-09 331- 362
1542	BL01279	Protein-L-isoaspartate(D-aspartate) O- methyltransferase signa.	BL01279A 24.27 1.000e-11 67- 115
1542	BL00422	Granins proteins.	BL00422C 16.18 7.176e-09 303- 331
1545	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.462e-32 244- 287
1545	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 3.143e-12 230- 246
1545	PR00024	HOMEOBOX SIGNATURE	PR00024C 7.49 3.500e-12 276-
	,		286 PR00024A 11.87 7.000e-12
1545	Process		251-263 PR00024B 11.27 1.409e- 10 266-277
1545	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.414e-10 267-
1545	BL00032	'Homeobox' antennapedia-type protein.	284
		antennapedia-type protein.	BL00032B 10.83 1.675e-37 233- 272 BL00032C 11.28 4.429e-21
			272-290 BL00032A 18.38 5.750e-10 193-216
1546	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 6.400e-16 245-
			258 PD00066 13.92 8.615e-15
			329-342 PD00066 13.92 6.000e-
			13 301-314 PD00066 13.92 4.857e-12 217-230 PD00066
			13.92 1.346e-10 273-286
			PD00066 13.92 8.200e-09 357- 370
1546	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.950e-13 313-
,			330 BL00028 16.07 7.261e-12
			229-246 BL00028 16.07 3.077e-
			11 16-33 BL00028 16.07 3.769e-
			11 285-302 BL00028 16.07 9.308e-11 341-358 BL00028
			16.07 3.100e-10 397-414
			BL00028 16.07 5.800e-10 201-
		•	218 BL00028 16.07 6.400e-10
			369-386 BL00028 16.07 7.600e-
			10 257-274 BL00028 16.07 8.800e-10 72-89 BL00028 16.07
			9.229e-09 101-118
1546	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.118e-12 310-
		İ	324 PR00048B 6.02 5.000e-12
			326-336 PR00048A 10.52 6.294e-
			12 13-27 PR00048B 6.02 1.692e- 11 242-252 PR00048A 10.52
ĺ			3.842e-11 338-352 PR00048A
		•	10.52 5.263e-11 366-380
			PR00048A 10.52 8.579e-11 226-
	l		240 PR00048A 10.52 8.579e-11

CEO ID	Database	Description	Results*
SEQ ID NO:	entry ID	Description	
NO:	entry 110		254-268 PR00048A 10.52 3.348e- 10 394-408 PR00048A 10.52 4.913e-10 282-296 PR00048B 6.02 7.188e-10 298-308 PR00048B 6.02 9.053e-09 57-67 PR00048A 10.52 9.640e-09 98- 112
1547	BL00585	Ribosomal protein S5 proteins.	BL00585B 18.78 6.143e-18 303- 340 BL00585A 28.43 4.286e-16 220-272
1548	PR00482	OMPTIN SERINE PROTEASE SIGNATURE	PR00482C 11.02 7.968e-09 816- 842
1549	PR00500	POLYCYSTIC KIDNEY DISEASE PROTEIN SIGNATURE	PR00500B 7.74 7.359e-10 56-77
1551	PR00917	SMALL ROUND STRUCTURED VIRUS (C37) CYSTEINE PROTEASE FAMILY SIGNATURE	PR00917G 10.59 8.990e-09 812- 830
1553	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.486e-09 109- 126
1555	PF00638_	RanBP1 domain proteins.	PF00638 11.91 4.600e-18 67-82
1555	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.	DM01269A 23.35 1.600e-20 68- 96 DM01269B 11.71 3.323e-09 138-148
1556	BL00406	Actins proteins.	BL00406E 8.44 8.541e-28 323- 373 BL00406B 5.47 1.375e-27 82-137 BL00406D 12.58 3.160e- 26 266-321 BL00406C 6.75 6.943e-25 141-196 BL00406A 9.95 2.575e-20 7-42
1556	PR00190	ACTIN SIGNATURE	PR00190F 7.80 3.647e-13 139- 159 PR00190C 11.49 2.029e-12 60-83 PR00190G 12.62 2.050e-09 233-250
1558	BL00048	Protamine P1 proteins.	BL00048 6.39 3.700e-09 153-180
1558	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 9.328e-11 157- 177 DM01206B 10.69 1.247e-10 236-256 DM01206B 10.69 7.781e-10 188-208 DM01206B 10.69 6.582e-09 234-254
1559	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE	PR00315A 11.81 5.688e-10 126- 140
1559	PR00326	GTPI/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.000e-09 127- 148
1559	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.431e-09 125- 147
1559	PR00755	AFLATOXIN BIOSYNTHESIS REGULATORY PROTEIN SIGNATURE	PR00755F 10.99 9.722e-09 30-52
1563	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780B 23.03 9.908e-09 14-57
1567	BL00162	Eukaryotic-type carbonic anhydrases proteins.	BL00162C 17.78 1.000e-40 88- 125 BL00162E 14.93 7.231e-39 171-204 BL00162F 22.68 5.050e- 31 208-242 BL00162A 22.92 8.714e-30 16-47 BL00162D 15.06 7.158e-24 126-151 BL00162B 21.43 1.375e-19 51-74
1568	PR00457	ANIMAL HAEM PEROXIDASE SIGNATURE	PR00457E 20.67 1.621e-24 414- 441 PR00457D 16.81 8.258e-21

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	custy 1D		389-410 PR00457B 13.29 3.455e- 18 223-239 PR00457G 17.45 7.000e-18 595-616 PR00457C 19.25 4.414e-16 371-390 PR00457H 15.90 8.650e-14 666- 681 PR00457A 15.80 5.645e-12 169-181 PR00457F 13.69 8.875e- 11 467-478
1569	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.571e-11 50-64
1569	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 3.769e-10 50-73
1569	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE	PR00757A 6.64 5.552e-10 50-70
1569	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 2.929e-09 50-69
1569	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE	PR00420A 14.78 6.455e-09 50-73
1569	BL00064	L-lactate dehydrogenase proteins.	BL00064A 21.16 7.203e-09 50-88
1569	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370A 3.35 9.772e-09 50-66
1571	BL00019	Actinin-type actin-binding domain proteins.	BL00019D 15.33 3.880e-17 145- 175
1573	BL00893	mutT domain proteins.	BL00893 18.99 5.500e-16 127- 152
1573	PR00502	MUTT DOMAIN SIGNATURE	PR00502B 15.92 4.600e-13 138- 154 PR00502A 15.06 2.636e-09 124-139
1574	PF00632	HECT-domain (ubiquitin-transferase).	PF00632B 18.45 7.000e-16 488- 516 PF00632C 20.66 7.851e-14 533-565
1576	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 9.566e-10 292- 304
1576	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 5.632e-09 243- 292
1576	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.118e-11 296- 329 DM00215 19.43 9.647e-11 327-360 DM00215 19.43 8.232e- 10 322-355 DM00215 19.43 2.068e-09 291-324 DM00215 19.43 2.983e-09 265-298 DM00215 19.43 4.356e-09 292- 325 DM00215 19.43 7.712e-09 275-308 DM00215 19.43 8.017e- 09 266-299 DM00215 19.43 8.475e-09 271-304 DM00215 19.43 8.780e-09 286-319
1582	BL01280	Glucose inhibited division protein A family proteins.	BL01280A 15.97 6.727e-36 69- 110 BL01280B 23.56 8.105e-27 128-180
1582	BL00076	Pyridine nucleotide-disulphide oxidoreductases class-I.	BL00076A 18.83 6.745e-12 68-98
1582	BL00836	Alanine dehydrogenase & pyridine nucleotide transhydrogenase.	BL00836D 22.30 9.576e-12 69- 106
1582	BL00504	Fumarate reductase / succinate dehydrogenase FAD-binding site proteins.	BL00504A 10.76 3.870e-11 69-91
1582	BL00977	FAD-dependent glycerol-3-phosphate dehydrogenase proteins.	BL00977A 20.76 8.583e-11 69- 121

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1582	PR00411	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-I SIGNATURE	PR00411A 15.95 1.000e-10 69-92
1582	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 2.151e-10 71- 103
1582	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE	PR00368A 17.76 8.846e-13 69-92 PR00368C 15.74 5.263e-10 69-95
1582	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE	PR00419A 14.89 3.571e-09 69-92
1582	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE	PR00757A 6.64 6.226e-09 69-89
1582	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE	PR00469A 15.46 1.851e-10 69-92 PR00469F 16.51 8.063e-09 65-90
1582	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 8.586e-09 69-88
1586	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 6.714e-09 70-87
1587	PD01861	PROTEIN NUCLEAR RIBONUCLEOPROTEIN SMALL MRNA RNA.	PD01861A 14.06 6.318e-10 60-84
1588	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.586e-09 46-60
1588	PF00595	PDZ domain proteins (Also known as DHR or GLGF).	PF00595 13.40 9.400e-09 43-54
1591	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 1.250e-29 184- 234
1592	PR00010	TYPE II EGF-LIKE SIGNATURE	PR00010C 11.16 6.667e-11 363- 374
1592	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 6.538e-16 358- 374 BL01187A 9.98 3.250e-09 278-290
1592	BL00022	EGF-like domain proteins.	BL00022B 7.54 8.200e-09 367- 374
1593	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625A 12.84 4.600e-20 14-34 PR00625B 13.48 8.759e-20 46-67
1593	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 4.176e-18 18-35 BL00636B 15.11 1.000e-15 46-67
1594	PD02448	TRANSCRIPTION PROTEIN DNA- BINDIN.	PD02448A 9.37 3.854e-09 351- 390
1598	PD02448	TRANSCRIPTION PROTEIN DNA- BINDIN.	PD02448A 9.37 1.511e-20 50-89 PD02448B 10.17 8.071e-19 89- 137
1602	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 9.816e-11 144- 159 PR00403B 12.19 8.167e-10 103-118
1602	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 23-56
1602	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 5.224e-10 144- 159 BL01159 13.85 6.891e-09 103-118
1602	PR00571	ENDOTHELIN-B RECEPTOR SIGNATURE	PR00571G 5.36 7.750e-09 107- 126
1603	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 9.816e-11 107- 122
1603	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 5.224e-10 107- 122
1603	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.644e-09 23-56
1605	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929B 4.38 4.600e-10 358- 370
1605	DM00303	6 LEA 11-MER REPEAT REPEAT.	DM00303A 13.20 7.708e-10 306-

NO:	entry ID		Results*
			356 DM00303A 13.20 2.912e-09 304-354 DM00303A 13.20 7.212e-09 300-350 DM00303A
1605	BL00354	HMG-I and HMG-Y DNA-binding domain	13.20 7.212e-09 311-361 BL00354B 3.16 7.722e-09 357-
1606	PD02379	proteins (Ahook).	370
1000	ED02313	AMINOTRANSFERASE BIOSYNTHESIS PHOSPHOSERINE SER.	PD02379E 11.43 1.000e-40 194- 236 PD02379F 18.62 6.029e-35 245-284 PD02379H 16.03 5.235e-33 352-385 PD02379B
			12.05 3.613e-31 80-113 PD02379A 15.57 2.800e-25 29-60
1.5			PD02379C 13.34 3.700e-21 119-
			139 PD02379D 11.83 9.419e-16 168-181 PD02379G 10.62 2.537e-14 313-328
1606	PR00800	AROMATIC-L-AMINO-ACID DECARBOXYLASE SIGNATURE	PR00800G 11.29 1.889e-09 97-
1607	PD02379	AMINOTRANSFERASE BIOSYNTHESIS	PD02379E 11.43 1.000e-40 194-
·	·	PHOSPHOSERINE SER.	236 PD02379F 18.62 6.029e-35 245-284 PD02379B 12.05 3.613e- 31 80-113 PD02379A 15.57
			2.800e-25 29-60 PD02379H 16.03 7.864e-23 306-339
		•	PD02379C 13.34 3.700e-21 119- 139 PD02379D 11.83 9.419e-16 168-181
1607	PR00800	AROMATIC-L-AMINO-ACID DECARBOXYLASE SIGNATURE	PR00800G 11.29 1.889e-09 97-
1610	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 6.625e-09 33-48
1614	BL00035	'POU' domain proteins.	BL00035B 14.46 6.236e-09 683- 704
1616	PF00168	C2 domain proteins.	PF00168C 27.49 8.412e-13 634- 660
1616	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.105e-10 651- 665
1617	PF00168	C2 domain proteins.	PF00168C 27.49 8.412e-13 115- 141
1617	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 8.105e-10 132- 146
1619	PR00566	DOPAMINE IB RECEPTOR SIGNATURE	PR00566E 13.44 5.255e-18 466- 483 PR00566A 9.32 3.000e-17 200-214 PR00566D 9.35 1.600e- 12 446-455 PR00566C 11.44 2.184e-12 401-412 PR00566B 8.20 3.053e-11 341-351
1619	PR00242	DOPAMINE RECEPTOR SIGNATURE	PR00242E 13.29 1.000e-12 424- 439 PR00242B 11.77 8.650e-11 257-267
1619		G-protein coupled receptors proteins.	BL00237C 13.19 6.786e-20 364- 391 BL00237A 27.68 9.710e-15 266-306 BL00237B 5.28 5.263e- 10 309-321
1619		RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237F 13.57 5.800e-19 369- 394 PR00237B 13.50 6.250e-19 236-258 PR00237E 13.03 9.500e- 15 301-325 PR00237C 15.69

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110.	<u> </u>		3.925e-09 280-303 PR00237A 11.48 7.387e-09 202-227
1620	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 7.851e-11 46-66
1621	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 7.529e-11 183- 216
1621	PF00685	Sulfotransferase proteins.	PF00685C 26.03 5.100e-09 118- 164
1621	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.322e-09 198- 213
1622	BL00951	ER lumen protein retaining receptor proteins.	BL00951B 14.23 1.670e-09 43-74
1623	BL00292	Cyclins proteins.	BL00292B 20.31 3.925e-11 120- 151
1624	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 3.160e-09 111- 125
1624	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.739e-12 114- 131 BL00028 16.07 3.571e-09 145-162
1625	BL01226	Hydroxymethylglutaryl-coenzyme A synthase proteins.	BL01226I 25.06 8.560e-09 256- 304
1629	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.563e-12 72-91 BL00030A 14.39 2.125e-12 156- 175
1637	BL00740	MAM domain proteins.	BL00740B 19.76 3.813e-09 637- 658
1637	PR00597	GELSOLIN FAMILY SIGNATURE	PR00597G 8.55 6.586e-27 637- 660 PR00597A 12.96 5.846e-26 326-348 PR00597E 13.46 2.000e- 22 523-544 PR00597F 16.29
			9.526e-22 582-602 PR00597D 12.77 1.000e-20 469-490 PR00597B 9.78 2.500e-20 415- 432 PR00597C 14.19 6.192e-20 436-455 PR00597H 15.32 7.577e- 19 666-686 PR00597D 12.77
			3.392e-10 94-115 PR00597B 9.78 9.455e-10 36-53 PR00597C 14.19 7.875e-09 61-80 PR00597A 12.96 8.027e-09 689-711 BL00027 26.43 7.000e-11 93-136
1641	BL00027	'Homeobox' domain proteins. STRUCTURE-SPECIFIC RECOGNITION	PR00887D 15.12 8.909e-09 337-
1641	PR00887	PROTEIN SIGNATURE TRANSMEMBRANE FOUR FAMILY	351 PR00259A 9.27 3.308e-18 19-43
1646	PR00259	SIGNATURE	PR00259C 16.40 9.800e-18 88- 117 PR00259D 13.50 2.756e-15 238-265
1646	BL00421	Transmembrane 4 family proteins.	BL00421A 11.79 5.263e-14 15-34 BL00421E 20.97 4.632e-13 235- 265
1651	PR00669	INHIBIN ALPHA CHAIN SIGNATURE	PR00669F 5.57 9.899e-09 223- 241
1652	DM01292	ESICULAR LUMEN DOMAIN.	DM01292L 12.54 9.505e-09 240- 265
1653	PR00128	COLIPASE SIGNATURE	PR00128D 9.77 6.250e-25 47-66 PR00128C 9.28 5.299e-20 24-47
1653	BL00121	Colipase proteins.	BL00121B 9.96 3.160e-33 15-64 BL00121A 14.56 2.107e-09 16-56
1656	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.929e-10 384-

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		<u> </u>	399
1658	BL01118	Translation initiation factor SUI1 proteins.	BL01118B 26.75 8.579e-26 94-
			132 BL01118A 12.46 4.000e-13
			77-92
1659	BL00811	Oleosins proteins.	BL00811A 8.26 3.310e-09 120-
1660			158
1660	BL00674	AAA-protein family proteins.	BL00674B 4.46 9.182e-11 184-
1660	PR00830	EMPONENTED A CELLA (LONG CENTRE	206
1000	FR00030	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 8.544e-10 191-
1660	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-	211 PR00300A 9.56 9.416e-09 187-
1	1100500	BINDING SUBUNIT SIGNATURE	206
1660	PR00051	BACTERIAL CHROMOSOMAL	PR00051A 10.68 9.899e-09 184-
		REPLICATION INITIATOR (DNAA)	205
		SIGNATURE	
1661	DM01871	kw SSR LIGASE CYCLO	DM01871C 20.79 9.836e-10 270-
1665		FORMYLTETRAHYDROFOLATE.	296
1663	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.712e-09 95-110
1665 1666	BL01181 PR00259	Ribosomal protein S21 proteins.	BL01181 15.43 2.500e-10 13-49
1000	PK00259	TRANSMEMBRANE FOUR FAMILY	PR00259C 16.40 6.824e-16 88-
		SIGNATURE	117 PR00259A 9.27 3.423e-14
		·	24-48 PR00259D 13.50 1.574e-13 238-265 PR00259B 14.81 8.714e-
			13 61-88
1666	BL00421	Transmembrane 4 family proteins.	BL00421B 17.62 4.600e-19 67-
			106 BL00421E 20.97 6.211e-13
			235-265 BL00421A 11.79
			5.600e-12 20-39
1668	PR00496	NAPIN SIGNATURE	PR00496A 6.68 6.276e-09 21-43
1671	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY	PR00237G 19.63 2.543e-11 670-
		SIGNATURE	697 PR00237A 11.48 3.000e-10
1671	PR00373	GLYCOPROTEIN HORMONE RECEPTOR	PR00373D 11.16 2.403e-09 503-
	11100575	SIGNATURE	518
1671	BL00237	G-protein coupled receptors proteins.	BL00237A 27.68 6.600e-10 496-
		, , , , , , , , , , , , , , , , , , ,	536 BL00237D 11.23 4.545e-09
			680-697
1671	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 7.429e-09 400-
1.001		SIGNATURE	413
1671	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 6.000e-11 94-
	•		108 PR00019A 11.19 7.300e-11
			215-229 PR00019B 11.36 6.850e-
			10 46-60 PR00019A 11.19 8.043e-10 285-299 PR00019B
			11.36 5.320e-09 212-226
			PR00019B 11.36 9.640e-09 70-84
1672	BL00972	Ubiquitin carboxyl-terminal hydrolases	BL00972A 11.93 7.500e-20 36-54
		family 2 proteins.	BL00972D 22.55 6.806e-16 296-
		<u>,</u>	321 BL00972B 9.45 1.000e-13
			116-126 BL00972E 20.72 8.773e-
1673	DEOCAC	Planta	12 321-343
10/3	PF00646	F-box domain proteins.	PF00646A 14.37 6.906e-09 92-
1675	BL00933	FGGY family of carbohydrate kinases	106
1012	PP00222	proteins.	BL00933D 24.01 7.545e-15 212- 249 BL00933B 15.94 2.200e-09
Ì		p. otomo.	54-65 BL00933E 13.80 3.543e-09
ł			439-455 BL00933A 17.50
1			439-455 BL00933A 17.50

SEQ ID	EQ ID Database Description NO: entry ID		Results*
NO:	entry ID		4.857e-09 20-44
1676	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 1.887e-10 137-
1676	BL00026	Chitin recognition or binding domain proteins.	BL00026 12.95 2.776e-09 55-76
1676	BL01208	VWFC domain proteins.	BL01208B 15.83 2.946e-09 172- 187
1676	BL01282	BIR repeat proteins.	BL01282B 30.49 4.471e-09 130- 169
1676	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875B 5.24 4.649e-09 137- 145
1676	BL00956	Fungal hydrophobins proteins.	BL00956B 8.29 4.682e-09 153- 165
1676	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLOMER.	PD00866L 3.73 6.564e-10 1-11 PD00866L 3.73 1.443e-09 33-43 PD00866L 3.73 2.918e-09 12-22 PD00866L 3.73 2.918e-09 19-29 PD00866L 3.73 4.836e-09 149- 159
1676	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 6.288e-09 141-
1676	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 7.465e-10 17-37 DM01724 8.14 4.434e-09 19-39 DM01724 8.14 6.684e-09 10-30
1676	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 5.883e-09 155- 174 PR00858B 5.93 8.085e-09 136-155
1676	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 9.739e-10 125- 140 PR00874C 4.37 9.000e-09 135-150
1676	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.779e-10 38-8I BL00243I 31.77 4.309e-10 68-111 BL00243I 31.77 5.235e-10 58-101 BL00243I 31.77 7.353e-10 98-141 BL00243I 31.77 1.000e-09 78-121 BL00243I 31.77 1.000e-09 88-131 BL00243I 31.77 1.380e-09 121- 164 BL00243I 31.77 2.648e-09 119-162 BL00243I 31.77 3.662e- 09 61-104 BL00243I 31.77 4.296e-09 131-174 BL00243I 31.77 4.676e-09 48-91 BL00243I 31.77 6.704e-09 109-152 BL00243I 31.77 7.845e-09 25-68 BL00243I 31.77 9.366e-09 134-
1676	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 3.885e-16 128- 174 BL00203 13.94 8.607e-13 123-169 BL00203 13.94 2.780e- 11 153-199 BL00203 13.94 3.571e-11 148-194 BL00203 13.94 4.363e-11 113-159 BL00203 13.94 5.451e-11 139- 185 BL00203 13.94 6.934e-11 144-190 BL00203 13.94 9.209e- 11 131-177 BL00203 13.94 2.436e-10 35-81 BL00203 13.94 4.255e-10 133-179 BL00203

SEQ ID NO:	Database entry ID	Description	Results*
			13.94 6.745e-10 32-78 BL00203
	· ·		13.94 7.032e-10 154-200
			BL00203 13.94 2.929e-09 34-80
Ì			·BL00203 13.94 3.388e-09 149-
	1		195 BL00203 13.94 3.571e-09
	1,		136-182 BL00203 13.94 5.224e-
1	.i	建设施工程 医电影 医	09 127-173 BL00203 13.94
	1		5.776e-09 43-89 BL00203 13.94
,			6.878e-09 140-186 BL00203 13.94 7.796e-09 45-91 BL00203
:			13.94 9.541e-09 42-88
1679	PD01976	KINASE DEHYDROGENASE	PD01976A 8.95 1.493e-09 83-96
		TRANSFERASE.	12017/01 0.95 1.4950-09 03-90
1680	BL00623	GMC oxidoreductases proteins.	BL00623A 12.60 9.859e-10 12-31
1680	PR00419	ADRENODOXIN REDUCTASE FAMILY	PR00419A 14.89 4.729e-09 12-35
		SIGNATURE	12-55
1680	PR00368	FAD-DEPENDENT PYRIDINE	PR00368A 17.76 9.357e-09 12-35
1600	-	NUCLEOTIDE REDUCTASE SIGNATURE	
1683	BL01172	Ribosomal protein L44e proteins.	BL01172B 14.10 8.909e-38 15-57
	·		BL01172C 16.78 7.188e-31 63-
1685	DM01724	I AVIDAGE POR CONTRACTOR OF CO	102
1003	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.	DM01724 8.14 5.909e-11 11-31
		.	DM01724 8.14 6.591e-11 41-61
			DM01724 8.14 6.831e-10 39-59
1686	PR00320	G-PROTEIN BETA WD-40 REPEAT	DM01724 8.14 8.697e-09 55-75
		SIGNATURE	PR00320A 16.74 8.463e-09 73-88
1690	PD02269	CYTIDINE DEAMINASE HYDROLASE	PD02269C 16.36 7.882e-17 79-92
		ZINC AMINOHY.	PD02269A 10.06 1.000e-15 29-41
	,		PD02269D 11.98 5.000e-14 110-
1601	DY 00500		125
1691	BL00790	Receptor tyrosine kinase class V proteins.	BL00790D 12.41 8.297e-09 429-
1692	BL00750	Chamaranian TCD 1	454
1092	BL00730	Chaperonins TCP-1 proteins.	BL00750B 16.17 2.000e-39 69-
			119 BL00750A 20.07 8.286e-36
		4	25-68 BL00750C 25.65 8.579e-23 152-184
1692	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1	PR00304C 8.69 1.250e-18 86-106
		(CHAPERONE) SIGNATURE	PR00304B 11.60 2.059e-17 56-75
		1	PR00304A 9,20 3.605e-15 34-51
1692	PR00298	60 KD CHAPERONIN SIGNATURE	PR00298B 13.59 7.353e-11 88-
			116
1692	BL00296	Chaperonins cpn60 proteins.	BL00296B 15.98 4.115e-13 76-
			130 BL00296A 17.20 5.648e-10
1604	77.00.44.5		12-66
1694	BL00415	Synapsins proteins.	BL00415N 4.29 4.710e-10 225-
1694	PD01224	PROMEDIANICI ELE PROME	269
1054	PD01234	PROTEIN NUCLEAR BROMODOMAIN	PD01234B 15.53 5.875e-10 243-
1694	BL00795	TRANS. Involucrin proteins.	261
	DECC193	involucini proteins.	BL00795C 17.06 7.698e-10 213-
1694	PR00208	GLIADIN AND LMW GLUTENIN	DD000004 10 50 0 204 00 0 45
	- 400200	SUPERFAMILY SIGNATURE	PR00208A 12.59 9.384e-09 247- 265
1694	DM00406	GLIADIN.	
1696	BL00028	Zinc finger, C2H2 type, domain proteins.	DM00406 7.73 9.800e-09 245-258 BL00028 16.07 1.000e-09 212-
			229 BL00028 16.07 1.000e-09 212-
			365-382

SEQ ID NO:	Database entry ID	Description	Results*	
1700	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.143e-13 332- 351	
1700	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 6.943e-09 442- 485	
1701	PF00023	Ank repeat proteins.	PF00023A 16.03 8.500e-10 283- 299 PF00023A 16.03 9.625e-10	
			347-363 PF00023A 16.03 1.321e- 09 184-200 PF00023A 16.03	
1501	DI 00006	Uroporphyrinogen decarboxylase proteins.	1.643e-09 150-166 BL00906D 24.33 7.750e-09 212-	
1701	BL00906		256 PF00791B 28.49 8.159e-14 117-	
1701	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	172 PF00791B 28.49 8.319e-13 217-272 PF00791B 28.49 3.179e-	
			12 184-239 PF00791B 28.49 5.168e-12 347-402 PF00791B	
			28.49 5.727e-11 250-305 PF00791B 28.49 2.817e-09 17-72	
			PF00791B 28.49 8.514e-09 84- 139 PF00791C 20.98 1.000e-08 98-137	
1702	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.643e-10 202- 218	
1702	PF00992	Troponin.	PF00992A 16.67 9.526e-09 749- 784	
1708	PR00671	INHIBIN BETA B CHAIN SIGNATURE	PR00671C 4.18 8.966e-09 212- 232	
1709	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 7.805e-12 292- 315	
1710	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412C 11.30 2.421e-12 169- 183 PR00412A 13.23 7.947e-12 104-123 PR00412B 12.59 7.429e- 10 123-139	
1711	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 7.247e-10 293- 309	
1712	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 9.122e-09 277- 292 PR00320A 16.74 9.780e-09 233-248 PR00320C 13.01 1.000e- 08 233-248	
1713	BL01230	RNA methyltransferase trmA family proteins.	BL01230E 15.79 2.918e-11 487- 503	
1719	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 2.957e-09 434- 480	
1719	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 7.830e-09 408- 455	
1721	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE	PR00453A 12.79 2.957e-10 33-51	
1721	PR00527	GASTRIN RECEPTOR SIGNATURE	PR00527I 5.36 6.559e-09 419-439	
1721	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 6.870e-09 381- 400	
1721	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE		
1725	PR00493	BREAST CANCER TYPE I SUSCEPTIBILITY PROTEIN SIGNATURE	PR00493G 7.57 3.711e-14 693- 714	
1726	BL00443	Glutamine amidotransferases class-II proteins.	BL00443F 16.68 8.714e-09 85- 101	
1728	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.288e-10 167-	

SEQ ID NO:	Database entry ID	h Description	Results*
		PROTEIN.	187
1728	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.411e-10 331-
			364 DM00215 19.43 7.107e-10
			336-369 DM00215 19.43 9.679e
			10 335-368 DM00215 19.43
A			3.136e-09 342-375 DM00215
•			19.43 5.119e-09 315-348
			DM00215 19.43 8.322e-09 326-
			359
1728	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.627e-09 335-
1000			350
1728	BL00048	Protamine P1 proteins.	BL00048 6.39 5.026e-10 152-179
			BL00048 6.39 6.329e-10 173-200
			BL00048 6.39 8.224e-10 161-188
			BL00048 6.39 3.363e-09 155-182
	l	· ·	BL00048 6.39 3.475e-09 163-190
			BL00048 6.39 3.925e-09 167-194
	į		BL00048 6.39 4.150e-09 151-178
			BL00048 6.39 4.150e-09 159-186
			BL00048 6.39 4.825e-09 171-198
			BL00048 6.39 5.838e-09 176-203
			BL00048 6.39 8.200e-09 177-204
			BL00048 6.39 8.200e-09 177-204 BL00048 6.39 9.550e-09 153-180
1728	PR00211	GLUTELIN SIGNATURE	PR00211B 0.86 1.827e-11 345-
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	266 PRO0011P 0 06 2 551
:	·	÷	366 PR00211B 0.86 3.571e-11
	·		339-360 PR00211B 0.86 6.917e-
	ļ		09 325-346 PR00211B 0.86
1731	BL01221	PMP-22 / EMP / MP20 family proteins.	1.000e-08 351-372
		Tivil 227 Elvii 7 Wil 20 family proteins.	BL01221C 26.20 1.281e-34 59-
		i i	104 BL01221D 13.99 5.966e-27
		·	136-163 BL01221A 17.26
			2.385e-26 1-29 BL01221B 13.29
1733	BL00027	'Homeobox' domain proteins.	1.000e-14 38-52
		Tromedox domain proteins.	BL00027 26.43 4.000e-10 297-
1733	PR00024	HOMEOBOX SIGNATURE	340
		HOWIDODOX SIGIVATORE	PR00024A 11.87 4.150e-09 289-
1734	BL00027	'Homeobox' domain proteins.	301
.	DD00027	Tiomeobox domain proteins.	BL00027 26.43 4.000e-10 297-
1734	PR00024	HOMEOBOX SIGNATURE	340
1734	1 X00024	HOMEOBOX SIGNATURE	PR00024A 11.87 4.150e-09 289-
738	BL00303	G 100 KG PP	301
1730	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 5.075e-13 73-
1738	DI 00010		110
1/38	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.400e-12 85-98
			BL00018 7.41 8.043e-09 49-62
738	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.582e-09 44-66
			PR00450C 12.22 9.772e-09 80-
			102
740	PD01941	TRANSMEMBRANE COTRANSPORTER	PD01941C 19.96 4.960e-16 84-
1		SYMP.	139 PD01941B 15.02 2.093e-11
			4-51
742	BL00672	Serine proteases, V8 family, histidine	BL00672B 9.84 3.554e-09 214-
		proteins.	231
742	PR00839	V8 SERINE PROTEASE FAMILY	
		SIGNATURE	PR00839E 12.04 8.062e-09 213- 230
745	BL00674	AAA-protein family proteins.	
		protein taintry proteins.	BL00674B 4.46 7.814e-10 360-
745	DM01022	LRR REPEAT.	382
· <u>·</u>		MAKE KELENI,	DM01022A 7.35 1.900e-09 954-

SEQ ID NO:	Database entry ID	Description	Results*
			961
1745	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.186e-09 267- 282
1746	BL00674	AAA-protein family proteins.	BL00674B 4.46 7.814e-10 360- 382
1746	DM01022	LRR REPEAT.	DM01022A 7.35 1.900e-09 954- 961
1746	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 6.186e-09 267- 282
1747	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.591e-18 206- 231 BL00215A 15.82 4.000e-15 104-129 BL00215A 15.82 9.400e-15 7-32 BL00215B 10.44 1.000e-10 154-167
1747	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927G 11.07 9.036e-11 158- 174 PR00927B 14.66 4.652e-10 239-261
1747	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 2.826e-09 9-32 PR00926F 17.75 3.217e-09 208- 231
1749	BL01013	Oxysterol-binding protein family proteins.	BL01013A 25.14 5.500e-21 537- 573 BL01013D 26.81 2.161e-18 807-851 BL01013C 9.97 4.231e- 13 625-635 BL01013B 11.33 3.017e-11 603-614
1751	BL00711	Lipoxygenases iron-binding region proteins.	BL007111 18.56 8.630e-28 577- 615 BL00711E 19.66 3.550e-22 414-451 BL00711G 21.83
			9.100e-22 503-535 BL00711C 20.75 5.959e-19 268-297 BL00711D 17.56 1.923e-16 347- 373 BL00711H 23.34 1.771e-12 535-574 BL00711F 19.79 2.086e 10 484-501
1751	PR00087	LIPOXYGENASE SIGNATURE	PR00087C 15.00 1.184e-17 423- 444 PR00087A 18.37 7.061e-12 385-403 PR00087B 15.25 5.091e 10 403-421
1751	PR00467	MAMMALIAN LIPOXYGENASE SIGNATURE	PR00467E 9.00 3.400e-14 344- 364 PR00467D 16.69 4.082e-09 243-265
1753	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE	PR00492C 9.68 1.900e-23 122- 139 PR00492B 9.77 8.579e-23 76-95 PR00492D 14.82 8.200e-2 139-155 PR00492A 11.92 1.6436 18 60-76
1756	BL00378	Hexokinases proteins.	BL00378A 19.01 8.500e-09 403- 431
1757	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.615e-33 35-78
1757	BL00032	'Homeobox' antennapedia-type protein.	BL00032B 10.83 4.259e-27 24-6: BL00032C 11.28 5.909e-20 63-8
1757	PR00025	HOMEOTIC ANTENNAPEDIA PROTEIN SIGNATURE	PR00025B 11.94 4.000e-11 21-3
1757	PR00031	LAMBDA AND OTHER REPRESSOR HELIX-TURN-HELIX SIGNATURE	PR00031B 16.29 4.960e-11 58-7
1757	PR00024	HOMEOBOX SIGNATURE	PR00024C 7.49 9.357e-13 67-77 PR00024B 11.27 3.500e-11 57-68 PR00024A 11.87 9.400e-11 42-5

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SEQ		abase ry ID	Description	ממ	Results*	
1758			CALIN SIGNATURE		PR00179B 9.56 1.000e-12 102-	
					115 PR00179C 19.02 1.000e-10	
		V 12.	an' and a second second second second second second second second second second second second second second se		130-146 PR00179A 13.78 5.680e-	
					10 37-50	
1758	BL002	213 Lipo	calin proteins.		BL00213B 8.78 8.000e-10 102-	
		.			113 BL00213A 12.95 9.526e-10	
					37-51	
1759	BL002		inoglobulins and major		BL00290A 20.89 1.818e-11 164-	
1762	BL002	nistor	compatibility complex	proteins.	. 187	
1702	BL002	ios Mam	malian defensins prote	ins.	BL00269C 16.52 7.158e-09 171-	
1762	PD022	83 PRO	TEIN SPORULATION	DEDEAT	200	
	1 2022	PREC	TELIN SEOROLATION	KEPEAI	PD02283C 17.54 5.855e-10 57-85	
		11100			PD02283C 17.54 5.855e-10 87-	
	į	ļ		•	115 PD02283C 17.54 6.566e-10	
1		1	•	•	117-145 PD02283C 17.54 1.450e-	
1			¥		09 47-75 PD02283C 17.54	
1					1.450e-09 77-105 PD02283C 17.54 1.450e-09 107-135	
	ŀ				PD02283C 17.54 5.613e-09 67-95	
	1.0	'			PD02283C 17.54 5.613e-09 67-95	
	- 1	.			125 PD02283C 17.54 6.175e-09	
	. ['			137-165 PD02283C 17.54 7.525e-	
	l				09 37-65 PD02283C 17.54	
					8.875e-09 147-175	
1762	BL002	03 Verte	orate metallothioneins	proteins.	BL00203 13.94 3.379e-12 95-141	
			•		BL00203 13.94 3.690e-12 65-111	
					BL00203 13.94 2.978e-11 35-81	
{		. •			BL00203 13.94 5.549e-11 39-85	
}	İ	1			BL00203 13.94 6.538e-11 55-101	
ľ	1	.			BL00203 13.94 6.538e-11 85-131	
	1				BL00203 13.94 7.231e-11 34-80	
		İ			BL00203 13.94 7.429e-11 125-	
1		j			171 BL00203 13.94 7.527e-11	
	ŀ	l			69-115 BL00203 13.94 8.220e-11	
Ì	l	!			99-145 BL00203 13.94 1.670e-10	
}	ļ				64-110 BL00203 13.94 2.053e-10	
		1			94-140 BL00203 13.94 2.149e-10	
		ļ	<i>*</i>		124-170 BL00203 13.94 2.819e-	
	1				10 159-205 BL00203 13.94	
		}			5.213e-10 54-100 BL00203 13.94	
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		1			5.691e-10 89-135 BL00203 13.94	
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	1				13.94 7.511e-10 115-161	
	1	ļ			BL00203 13.94 7.702e-10 49-95 BL00203 13.94 7.702e-10 79-125	
					BL00203 13.94 1.551e-09 44-90	
		Ì			BL00203 13.94 1.551e-09 74-120	
			•	į	BL00203 13.94 1.331e-09 74-120 BL00203 13.94 3.112e-09 29-75	
	1				BL00203 13.94 4.031e-09 30-76	
		l		. 1	BL00203 13.94 4.214e-09 90-136	
				j	BL00203 13.94 4.306e-09 60-106	
		l			BL00203 13.94 5.133e-09 145-	
		1			191 BL00203 13.94 6.235e-09	
					119-165 BL00203 13.94 6.327e-	
				1	09 50-96 BL00203 13.94 6.327e-	
				1	09 80-126 BL00203 13.94	

SEQ ID Database NO: entry ID		Description	Results*		
.10.	VILLY AD		6.694e-09 45-91 BL00203 13.94		
- •			6.694e-09 75-121 BL00203 13.94		
•			8.898e-09(104-150		
1763	BL00216	Sugar transport proteins.	BL00216B 27.64 5.846e-09 141-		
1703	DLUUZIU	Ough thisport protons.	191		
1266	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 2.080e-30 83-		
1766	BL00430	Souldin.solute Sympolici Tunni protonist	138 BL00456C 24.55 3.721e-29		
			221-276 BL00456B 18.94 1.000e-		
*:- ·		A service of the serv	22,159+189		
1555	DD 00175	SODIUM/ALANIÑE SYMPORTER	PR00175B 10.80 9.878e-09 226-		
1766	PR00175	SIGNATURE	245		
	57.00140	Neutral zinc metallopeptidases, zinc-binding	BL00142 8.38 1.857e-09 494-505		
1767	BL00142		BE00142 0.35 1.0570 07 19 100		
		region proteins.	BL00509B 10.28 1.643e-12 610-		
1768	BL00509	Ras GTPase-activating proteins.	621		
·		THE STATE OF THE S	PR00048A 10.52 6.143e-13 252-		
1772	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	266 PR00048A 10.52 7.429e-13		
			476-490 PR00048A 10.52 3.118e-		
			12 336-350 PR00048A 10.52		
			3.118e-12 364-378 PR00048A		
			10.52 4.706e-12 504-518		
			PR00048A 10.52 8.412e-12 224-		
	i .		238 PR00048A 10.52 3.842e-11		
			392-406 PR00048A 10.52 6.211e-		
	ŀ		11 308-322 PR00048A 10.52		
			6.211e-11 448-462 PR00048B		
	1		6.02 7.231e-11 492-502		
			PR00048B 6.02 3.250e-10 240-		
·	ŀ		250 PR00048A 10.52 6.870e-10		
			420-434 PR00048B 6.02 2.421e-		
}			09 380-390		
	<u> </u>	THE CONTROL OF THE PROPERTY OF	PD00066 13.92 8.800e-14 327-		
1772	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	340 PD00066 13.92 1.500e-13		
1	·		411-424 PD00066 13.92 5.500e-		
1			13 383-396 PD00066 13.92		
			5.500e-13 439-452 PD00066		
i			13.92 7.500e-13 495-508		
1			PD00066 13.92 9.000e-13 467-		
			480 PD00066 13.92 3.571e-12		
1.			355-368 PD00066 13.92 7.000e-		
	1		12 271-284 PD00066 13.92		
	1		7.923e-10 299-312 PD00066		
			12.00.2.50000.242.256		
	<u> </u>		13.92 2.500e-09 243-256		
1772	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 3.250e-13 395-		
1	1		412 BL00028 16.07 5.950e-13		
		1	367-384 BL00028 16.07 6.478e-		
1.			12 451-468 BL00028 16.07		
}			8.435e-12 339-356 BL00028		
1			16.07 1.692e-11 255-272		
	1		BL00028 16.07 3.769e-11 227-		
			244 BL00028 16.07 5.154e-11		
			507-524 BL00028 16.07 2.200e-		
			10 479-496 BL00028 16.07		
			9.400e-10 199-216 BL00028		
			16.07 2.029e-09 423-440		
			BL00028 16.07 3.571e-09 311-		
	ļ		328		
	_1	VACUOLAR ATP SYNTHASE 16 KD	PR00122D 9.97 7.214e-11 103-		

NO: 1773 1774	BL00605 BL00518	SUBUNIT SIGNATURE	127 PR00122C 8.20 9.526e-10
1774		<u></u>	76-103
1774		ATP synthase c subunit proteins.	BL00605 27.67 4.977e-09 70-124
	22003.0	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39
1776	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.610e-09 33-87
	7.3	pw.	BL01160B 19.54 9.619e-09 65-
1783	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 6.786e-15 3967- 4001
1783	PF00856	SET domain proteins.	PF00856B 16.42 6.595e-19 3949-
_		•	3971 PF00856A 26.14 4.125e-12 3896-3933
1783	PF00628	PHD-finger.	PF00628 15.84 3.455e-12 86-101
		,	PF00628 15.84 7.750e-10 38-53 PF00628 15.84 5.645e-09 164-179
1783	BL00115	Eukaryotic RNA polymerase II heptapeptide	BL00115Z 3.12 4.971e-09 2575-
		repeat proteins.	2624 BL00115Z 3.12 7.750e-09 2582-2631
1784	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 9.423e-10 111- 124
1785	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e-10 177- 191
1790	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 7.724e-09 276- 310
1792	PD02059	CORE POLYPROTEIN PROTEIN GAG CONTAINS: P.	PD02059A 28.10 5.950e-10 34-75
1794	BL00326	Tropomyosins proteins.	BL00326D 8.76 8.065e-09 165- " 206
1795	BL00326	Tropomyosins proteins.	BL00326D 8.76 8.065e-09 173- 214
1797	PR00563	BETA-3 ADRENERGIC RECEPTOR SIGNATURE	PR00563B 3.98 8.141e-09 8-28
1799	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.570e-09 285- 307
1801	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.800e-14 290- 303 PD00066 13.92 4.000e-13 234-247 PD00066 13.92 4.429e- 12 262-275 PD00066 13.92
			9.217e-11 206-219 PD00066 13.92 3.769e-10 505-518 PD00066 13.92 4.115e-10 449-
			462 PD00066 13.92 4.462e-10 533-546 PD00066 13.92 6.538e- 10 477-490
1801	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.091e-15 243- 257 PR00048A 10.52 7.750e-14
	·		542-556 PR00048A 10.52 3.647e- 12 215-229 PR00048A 10.52 4.176e-12 486-500 PR00048B
			6.02 6.000e-12 231-241 PR00048B 6.02 6.000e-12 287-
			297 PR00048A 10.52 7.353e-12 187-201 PR00048A 10.52 6.684e-
			11 271-285 PR00048A 10.52 4.130e-10 299-313 PR00048A
			10.52 3.520e-09 430-444 PR00048A 10.52 3.880e-09 514-

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NO.	entry 10		528 PR00048A 10.52 6.400e-09 458-472 PR00048A 10.52 8.560e- 09 159-173
1801	BL00028	Zinc finger, C2H2 type, domain proteins.	/BL0002816.071.563e-15 545- 562 BL0002816.071.450e-13
			218-235 BL00028 16.07 3.348e- 12 489-506 BL00028 16.07 7.652e-12 274-291 BL00028
			16.07 2.385e-11 433-450
			BL00028 16.07 4.115e-11 517- 534 BL00028 16.07 5.154e-11 246-263 BL00028 16.07 1.000e- 10 302-319 BL00028 16.07 5.200e-10 461-478 BL00028
			16.07 6.700e-10 190-207 BL00028 16.07 1.257e-09 357- 374 BL00028 16.07 9.486e-09 162-179
1802	BL00615	C-type lectin domain proteins.	BL00615A 16.68 8.920e-11 137- 155
1802	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE	PR00770F 13.79 1.774e-09 198- 218
1802	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.521e-09 137- 155
1803	BL00615	C-type lectin domain proteins.	BL00615A 16.68 8.920e-11 176- 194
1803	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE	PR00770F 13.79 1.774e-09 237- 257
1803	PR00356	TYPE II ANTIFREEZE PROTEIN SIGNATURE	PR00356B 14.85 2.521e-09 176- 194
1804	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 9.000e-14 65-78
1806	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.000e-09 219- 233
1808	PD02474	SYNTHASE SMALL SUBUNIT ACETOLACT.	PD02474B 21.08 8.568e-09 199- 238
1809	PF00922	Vesiculovirus phosphoprotein.	PF00922A 19.17 1.000e-08 249- 283
1812	PR00289	DISINTEGRIN SIGNATURE	PR00289B 11.79 1.947e-09 522- 535
1814	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242F 12.18 8.522c-09 197- 219
1815	PR00780	LEUSERPIN 2 SIGNATURE	PR00780B 4.89 4.491e-09 262- 285
1816	BL00226	Intermediate filaments proteins.	BL00226D 19.10 8.027e-13 208- 255
1817	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.	PD01876C 21.73 3.326e-15 481- 534 PD01876C 21.73 3.045e-10 735-788
1818	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747C 12.06 8.767e-09 337- 356
1820	DM01782	HYDROGENASE (FE) LARGE CHAIN.	DM01782C 13.88 4.400e-19 349- 368 DM01782F 9.01 4.375e-18 499-515 DM01782B 17.29 3.412e-10 294-327
1821	BL00226	Intermediate filaments proteins.	BL00226D 19.10 7.375e-38 321- 368 BL00226B 23.86 7.107e-32 155-203 BL00226C 13.23 3.100e-

SEQ ID NO:	Database entry ID	Description	Results*
			19 220-251 BL00226A 12.77 7.000e-15 55-70 BL00226D 19.10 7.800e-09 254-301
1822	DM01415	6 SALIVARY GLUE PROTEIN.	DM01415B 13.78 9.518e-10 4-52
1822	BL00026	Chitin recognition or binding domain proteins.	BL00026 12.95 3.013e-09 43-64
1822	PD02283	PROTEIN SPORULATION REPEAT PRECU.	PD02283C 17.54 3.588e-09 110- 138 PD02283C 17.54 3.588e-09 120-148
1822	PD00866	GLYCOPROTEIN PROTEIN SPIKE E2 PRECURSOR PEPLOMER.	PD00866L 3.73 1.443e-09 21-31 PD00866L 3.73 2.770e-09 97-107 PD00866L 3.73 2.770e-09 146- 156 PD00866L 3.73 2.918e-09 7- 17 PD00866L 3.73 2.918e-09 14- 24 PD00866L 3.73 4.541e-09 4- 14
1822	PR00858	CRUSTACEAN METALLOTHIONEIN SIGNATURE	PR00858B 5.93 2.819e-09 84-103 PR00858B 5.93 5.021e-09 114- 133 PR00858B 5.93 5.021e-09 124-143
1822	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875B 5.24 6.595e-09 85-93
1822	PR00874	FUNGI-IV METALLOTHIONEIN SIGNATURE	PR00874C 4.37 9.739e-10 73-88 PR00874C 4.37 7.250e-09 83-98
1822	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243I 31.77 3.143e-11 13-56 BL00243I 31.77 3.647e-10 26-69 BL00243I 31.77 6.426e-10 106- 149 BL00243I 31.77 7.088e-10 96-139 BL00243I 31.77 9.338e- 10 36-79 BL00243I 31.77 1.254e-
			09 46-89 BL00243I 31.77 6.451e- 09 3-46 BL00243I 31.77 6.704e- 09 77-120 BL00243I 31.77 7.211e-09 67-110 BL00243I 31.77 7.592e-09 116-159 BL00243I 31.77 8.606e-09 92-135
1822	BL00198	4Fe-4S ferredoxins, iron-sulfur binding region proteins.	BL00198 10.43 9.700e-09 6-18
1822	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 8.024e-14 102- 148 BL00203 13.94 7.750e-13 127-173 BL00203 13.94 1.103e- 12 97-143 BL00203 13.94 3.172e-12 103-149 BL00203 13.94 3.379e-12 92-138 BL00203 13.94 4.207e-12 98-144 BL00203 13.94 4.207e-12 116-162 BL00203 13.94 5.345e-12 71-117 BL00203 13.94 5.345e-12 107- 153 BL00203 13.94 9.897e-12 106-152 BL00203 13.94 1.791e- 11 118-164 BL00203 13.94 2.879e-11 126-172 BL00203 13.94 3.176e-11 87-133 BL00203 13.94 4.758e-11 61-107 BL00203 13.94 5.846e-11 113-159 BL00203 13.94 6.044e-11 112- 158 BL00203 13.94 7.231e-11

			Results*
SEQ ID	Database	Description	
NO:	entry ID		128-174 BL00203 13.94 2.245e-
	<u>.</u>	la de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	10 76-122 BL00203 13.94
• •	A 1	Programme Programme Control	3.202e-10 23-69 BL00203 13.94
•		1 ♥ * * * * • • • • • • • • • • • • • • •	4.926e-10 78-124 BL00203 13.94
			6.362e-10 81-127 BL00203 13.94
			6.553e-10 82-128 BL00203 13.94
	,		6.553e-10 82-128 BL00203 15.94
	-		6.840e-10 111-157 BL00203
	1	<u> </u>	13.94 8.851e-10 43-89 BL00203
	·		13.94 8.851e-10 96-142 BL00203
			13.94 2.837e-09 8-54 BL00203
		· .	13.94 3.296e-09 72-118 BL00203
	1		13.94 3.847e-09 117-163
			BL00203 13.94 3.939e-09 86-132
			BL00203 13.94 5.592e-09 123-
· ·	1	1	169 BL00203 13.94 5.776e-09
			108-154 BL00203 13.94 6.143e-
			108-154 BL00203 13.94 0.1436-
	}.		09 30-76 BL00203 13.94 6.143e-
			09 79-125 BL00203 13.94
			6.969e-09 121-167 BL00203
			13.94 7.612e-09 16-62 BL00203
	•		13.94 7.796e-09 101-147
		N	BL00203 13.94 8.163e-09 33-79
1.			BL00203 13.94 9.633e-09 77-123
			BL00203 13.94 1.000e-08 66-112
		TOTAL CONTINUE N	PR00860B 7.04 2.929e-20 74-88
1824	PR00860	VERTEBRATE METALLOTHIONEIN	PR00860A 5.46 5.655e-13 52-65
		SIGNATURE	PR00860C 9.61 2.400e-12 88-98
1824	PR00858	CRUSTACEAN METALLOTHIONEIN	PR00858B 5.93 1.419e-11 70-89
1		SIGNATURE	PR00858B 5.93 7.070e-11 65-84
1824	PR00874	FUNGI-IV METALLOTHIONEIN	PR00874C 4.37 3.478e-10 64-79
102-7	111000	SIGNATURE	
1824	BL00243	Integrins beta chain cysteine-rich domain	BL00243H 17.53 7.875e-10 59-85
1824	BL00243	proteins.	BL00243I 31.77 4.803e-09 65-108
	77,00076	NEMATODE METALLOTHIONEIN	PR00876D 5.77 2.191e-10 62-75
1824	PR00876		PR00876A 6.60 5.886e-09 61-74
		SIGNATURE	BL00203 13.94 1.000e-40 62-108
1824	BL00203	Vertebrate metallothioneins proteins.	BL00203 13.94 7.429e-09 54-100
	į		BL00203 13.94 7.4296-09 54-100 BL00203 13.94 8.071e-09 52-98
			BL00203 13.94 8.0716-09 52-98
			BL00203 13.94 8.806e-09 55-101
1824	PR00875	MOLLUSC METALLOTHIONEIN	PR00875D 5.00 9.471e-09 59-70
1024		SIGNATURE	
1825	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.136e-09 572-
1823	FR00300	CZ DOMINI (DIGINI I I I I	586
	77.00000	SYNAPTOTAGMIN SIGNATURE	PR00399A 9.52 8.875e-09 360-
1825	PR00399	SYNAPIOTAGMIN SIGNATORE	376
İ	<u> </u>		DM01206B 10.69 8.767e-10 567-
1829	DM01206	CORONAVIRUS NUCLEOCAPSID	
		PROTEIN.	587 DM01206B 10.69 1.000e-09
1			563-583
1829	PD01351	PROTEIN REPEAT NEUROFILAMENT	PD01351B 13.72 6.786e-10 196-
1029	1 201351	TRIPL.	222 PD01351B 13.72 2.597e-09
[ŀ	11416.	198-224
ļ	Dr. cocce	MOL! domain proteins	BL00035B 14.46 3.127e-09 634-
1829	BL00035	'POU' domain proteins.	655
L			BL00229A 23.57 3.182e-09 178-
1829	BL00229	Tau and MAP proteins tubulin-binding	
	1	domain proteins.	217
1829	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 3.647e-11 204-
1023	1100045		219 PR00049D 0.00 9.471e-11
		,	209-224 PR00049D 0.00 8.500e-
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SEQ ID	Database	,Description	Results*
NO:	entry ID		Results
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1			8.500e-10 207-222 PR00049D
1000			0.00 3.746e-09 182-197
1829	BL00319	Amyloidogenic glycoprotein extracellular	BL00319C 17.12 3.132e-09 265-
		domain proteins.	299 BL00319C 17.12 4.553e-09
.1			1013-1047 BL00319C 17.12
1 .			5.618e-09 1019-1053 BL00319C
:	***		17.12 7.395e-09 267-301
1			BL00319C 17.12 7.632e-09 1017- 1051
1829	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.089e-10 185-
			218 DM00215 19.43 8.393e-10
			190-223 DM00215 19.43 2.373e-
			09 186-219 DM00215 19.43
			7.102e-09 183-216 DM00215
1829	BL00422	C	19.43 8.169e-09 188-221
1029	DL00422	Granins proteins.	BL00422C 16.18 8.588e-09 263-
1829	BL00412	Neuromodulin (GAP-43) proteins.	291 BL00412D 16.54 9.182e-11 1005-
		Treat of the visy proteins.	1056 BL00412D 16.54 9.120e-10
	1		1004-1055 BL00412D 16.54
			4.857e-09 1003-1054 BL00412D
			16.54 8.347e-09 1008-1059
			BL00412D 16.54 9.449e-09 1001-7
1829	PR00832	DAVILL DI GEOLUME	1052
1029	PR00832	PAXILLIN SIGNATURE	PR00832B 9.87 9.526e-09 377-
1829	PD02059	CORE POLYPROTEIN PROTEIN GAG	401
	1202055	CONTAINS: P.	PD02059B 24.48 9.620e-09 196- 231
1829	PF00992	Troponin.	PF00992A 16.67 9.882e-09 1005-
			1040
1829	BL00048	Protamine P1 proteins.	BL00048 6.39 6.949e-15 569-596
			BL00048 6.39 1.885e-14 568-595
			BL00048 6.39 3.361e-14 570-597
			BL00048 6.39 8.377e-14 577-604
			BL00048 6.39 8.377e-14 578-605
		•	BL00048 6.39 3.631e-13 571-598 BL00048 6.39 4.738e-13 576-603
			BL00048 6.39 7.369e-13 582-609
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		•	BL00048 6.39 3.515e-12 567-594
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			BL00048 6.39 5.632e-12 583-610
İ			BL00048 6.39 7.221e-12 557-584
			BL00048 6.39 2.250e-11 572-599 BL00048 6.39 2.875e-11 585-612
			BL00048 6.39 4.875e-11 586-613
	ŀ		BL00048 6.39 5.375e-11 591-618
	1	•	BL00048 6.39 7.375e-11 589-616
Ī	1		BL00048 6.39 7.500e-11 580-607
			BL00048 6.39 8.625e-11 588-615
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	1		BL00048 6.39 5.382e-10 574-601
	l		BL00048 6.39 5.500e-10 566-593
	ł		BL00048 6.39 5.618e-10 584-611 BL00048 6.39 9.171e-10 561-588
		•	BL00048 6.39 9.882e-10 592-619
			1 10 10 0.07 7.0020-10 372-019

NO:	SEQ ID	Database	Description	Results*
BL00048 6.39 1.450e-09 590-617			Description	
BL.00048 6.39 3.292-69 560-587	110.	entry 1D		BL00048 6.39 1.450e-09 590-617
BL00048 6.39 4.38-09 562-589 BL00048 6.39 4.398-09 579-606 BL00048 6.39 5.275-09 564-591 BL00048 6.39 5.275-09 564-591 BL00048 6.39 5.275-09 564-591 BL00048 6.39 5.275-09 564-591 BL00048 6.39 5.275-09 587-614 BL00048 6.39 5.275-09 587-614 BL00048 6.39 5.275-09 587-614 BL00048 6.39 6.625-09 555-582 BL00048 6.39 7.075-09 555-582 BL00048 6.39 9.488-09 555-582 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 600-627 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00048 6.39 9.488-09 613-415 BL00022B 7.54 4.600-09 138-145 BL000022B 7.54 4.600-09 104-120 BL001187B 12.04 4.600-09 104-120 BL011				
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1833 PR00011 TYPE III EGF-LIKE SIGNATURE PR00011A 14.06 4.822e-09 208-227 PR00011D 14.03 8.957e-09 67-86 1833 BL00243 Integrins beta chain cysteine-rich domain proteins. BL00243I 31.77 1.000e-08 34-77 1835 BL01279 Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa. H67 1835 BL01131 Ribosomal RNA adenine dimethylases proteins. BL01131A 26.62 4.600e-09 421-467 1835 BL01230 RNA methyltransferase trmA family proteins. BL01230E 15.79 6.607e-11 571-587 BL01230A 17.88 8.962e-10 409-428 BL01230B 11.62 8.475e-09 436-449 1835 PR00049 WILM'S TUMOUR PROTEIN SIGNATURE PR00049D 0.00 8.780e-09 598-613 1837 PD01719 PRECURSOR GLYCOPROTEIN SIGNAL RE. PD01719A 12.89 2.603e-11 259-287 PD01719A 12.89 8.105e-10 199-227 1838 BL01162 Quinone oxidoreductase / zeta-crystallin proteins. BL01162C 22.80 1.269e-18 151-195 BL01162A 15.38 1.265e-11 64-87 1838 BL00279 Membrane attack complex components / perforin proteins. BL00279C 31.64 3.156e-09 134-188 1838 BL00059 Zinc-containing alcohol dehydrogenases proteins. BL00059B 16.08 7.273e-09 93-121 1841 PD01066 PROTEIN ZINC FINGER ZINC-FINGER PD01066 19.43 5.415e-26 46-85	-			• •
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METAL-BINDING NU.	1841	PD01066		PD01000 19.43 3.4156-26 46-85
	L	<u></u>	METAL-BINDING NU.	<u> </u>

SEQ ID		Description	Results*
NO:	entry ID		Acourts
1841	PR00048	G2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.737e-11 140-
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1841	DI 00020	T' C COYYO	224-238
1041	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 4.130e-12 227-
			244 BL00028 16.07 7.577e-11
			352-369 BL00028 16.07 3.400e-
			10 380-397 BL00028 16.07
	٠,		6.400e-10 199-216 BL00028 16.07 1.257e-09 143-160
1			BL00028 16.07 2.029e-09 171-
			188 BL00028 16.07 5.886e-09
1041			408-425
1841	PR00967	ACUTE MYELOID LEUKEMIA 1	PR00967I 12.41 8.130e-09 466-
1841	PD00066	PROTEIN SIGNATURE	481
1041	PD00000	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.038e-10 187-
			200 PD00066 13.92 1.600e-09
			396-409 PD00066 13.92 9.400e- 09 215-228
1841	BL00479	Phorbol esters / diacylglycerol binding	BL00479A 19.86 6.553e-09 214-
		domain proteins.	237 BL00479A 19.86 9.809e-09
			367-390
1842	PD02910	TRANSCRIPTION PROTEIN FACTOR	PD02910A 15.43 9.839e-09 62-97
1040	77777	REGULATION A.	
1843	PD02199	SUBUNIT HYDROGEN ION TRANSPORT	PD02199A 20.58 1.000e-40 10-61
		T.	PD02199D 13.18 1.000e-40 364-
			405 PD02199F 15.02 1.000e-40
	ļ ·		440-482 PD02199J 11.42 1.000e-
			40 723-762 PD02199K 15.22 1.000e-40 792-831 PD02199G
	1		9.43 4.447e-24 531-555
			PD02199B 27.90 1.474e-22 263-
			306 PD02199H 13.62 2.636e-21
			576-599 PD02199E 7.56 8.642e-
			19 405-424 PD02199C 17.60
			8.085e-14 313-329 PD02199I
1844	BL00218	Amino acid permeases proteins.	8.90 4.780e-09 616-624
	1 - 2 - 3 - 2 - 3	ramio dold permeases proteins.	BL00218E 23.30 5.920e-10 343- 383
1845	BL00048	Protamine P1 proteins.	BL00048 6.39 9.526e-10 160-187
1845	BL00422	Granins proteins.	BL00422C 16.18 4.000e-09 590-
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1845	PR00833	POLLEN ALLERGEN POA PI	PR00833H 2.30 8.385e-09 943-
1845	Process	SIGNATURE	958
1043	PF00992	Troponin.	PF00992A 16.67 7.900e-13 568-
			603 PF00992A 16.67 4.090e-11
]			566-601 PF00992A 16.67 5.817e-
			10 570-605 PF00992A 16.67
			8.479e-10 579-614 PF00992A 16.67 2.066e-09 564-599
		· ·	PF00992A 16.67 4.789e-09 575-
			610 PF00992A 16.67 4.908e-09
	1		532-567 PF00992A 16.67 6.803e-
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	l		7.632e-09 562-597 PF00992A
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			618 PF00992A 16.67 9.289e-09
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SEQ ID	Database	Description	Results*
NO:	entry ID PF01140	Matrix protein (MA), p15.	PF01140D 15.54 8.500e-12 505-
1845	PF01140	Matrix protein (MA), p13.	540 PF01140D 15.54 7.120e-11
	1 .		584-619 PF01140D 15.54 9.760e-
	1	A second	11 586-621 PF01140D 15.54
]		3.813e-10 588-623 PF01140D
			15.54 4.938e-10 563-598
			PF01140D 15.54 6.738e-10 519-
1			554 PF01140D 15.54 8.313e-10
	,		503-538 PF01140D 15.54 9.325e-
j			10 549-584 PF01140D 15.54 9.663e-10 567-602 PF01140D
			15.54 9.775e-10 565-600
İ			PF01140D 15.54 1.000e-09 582-
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			15.54 4.140e-09 533-568
			PF01140D 15.54 4.872e-09 578-
			613 PF01140D 15.54 6.860e-09
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1			7.384e-09 576-611 PF01140D 15.54 7.593e-09 572-607
			PF01140D 15.54 8.640e-09 570-
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			507-542 PF01140D 15.54 8.744e-
		·	09 596-631 PF01140D 15.54
			9.163e-09 577-612 PF01140D
			15.54 9.267e-09 579-614
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İ			609 PF01140D 15.54 1.000e-08
			531-566
1848	BL00811	Oleosins proteins.	BL00811B 10.57 9.791e-09 307-
			336 BL00415N 4.29 4.153c-09 301-
1852	BL00415	Synapsins proteins.	345
10.50	D) 100((0	ZEDI	DM00668B 22.01 8.018e-09 291-
1852	DM00668	ZEIN.	343
1853	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-17 133-
1653	DL00107	Floteth killases All -billang region proteins.	164
1853	PR00109	TYROSINE KINASE CATALYTIC	PR00109E 14.41 3.045e-11 254-
1633	1 Koolos	DOMAIN SIGNATURE	277
1853	PF00791	Domain present in ZO-1 and Unc5-like netrin	PF00791B 28.49 2.317e-16 689-
1000		receptors.	744 PF00791B 28.49 3.753e-15
		-	523-578 PF00791B 28.49 4.316e-
			12 656-711 PF00791B 28.49
			1.727e-11 589-644 PF00791B
1			28.49 3.636e-11 556-611
			PF00791C 20.98 4.913e-11 570-
			609 PF00791B 28.49 6.330e-10
			722-777 PF00791C 20.98 5.853e-
			09 703-742 PF00023A 16.03 5.200e-13 722-
1853	PF00023	Ank repeat proteins.	738 PF00023B 14.20 1.000e-12
			652-662 PF00023A 16.03 2.000e-
			12 755-771 PF00023A 16.03
			7.857e-11 656-672 PF00023A
L			

SEQ ID NO:	Database entry ID	Description	Results*
ř			16.03 8.286e-11 622-638 PF00023B 14.20 4.682e-09 519- 529 PF00023A 16.03 6.143e-09 589-605 PF00023A 16.03 6.786e- 09 689-705
1853	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 9.000e-11 582- 595 PD00078B 13.14 8.435e-09 649-662
1854	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 4.971e-14 4-26
1856	BL00317	WAP-type 'four-disulfide core' domain proteins.	BL00317B 14.58 3.550e-13 48-70
1856	PR00003	4-DISULPHIDE CORE SIGNATURE	PR00003C 7.69 6.357e-09 54-64
1857	BL01019	ADP-ribosylation factors family proteins.	BL01019B 19.49 7.517e-21 95-
1857	BL01020	SAR1 family proteins.	BL01020C 15.35 2.301e-18 79- 130
1857	PR00328	GTP-BINDING SARI PROTEIN SIGNATURE	PR00328C 13.16 2.841e-10 78- 104
1858	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.385e-15 128- 141 PD00066 13.92 5.714e-12 100-113
1858	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048B 6.02 7.188e-10 97-107 PR00048B 6.02 3.842e-09 125- 135 PR00048A 10.52 6.040e-09 137-151
1859	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 1.000e-11 174- 188 PR00048B 6.02 1.692e-11
1859	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	162-172 PD00066 13.92 3.739e-11 165- 178
1859	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 2.385e-11 177- 194 BL00028 16.07 3.769e-11 121-138 BL00028 16.07 8.269e-
1860	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	11 149-166 PF00651 15.00 2.895e-11 45-58
1860	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 2.038e-10 419- 432 PD00066 13.92 7.231e-10 391-404
1860	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 5.696e-10 400- 414 PR00048A 10.52 8.435e-10
1860	BL00028	Zinc finger, C2H2 type, domain proteins.	428-442 BL00028 16.07 8.269e-11 403- 420 BL00028 16.07 3.400e-10 375-392 BL00028 16.07 3.057e- 09 431-448
1861	DM00547	I kw CHROMO BROMODOMAIN SHADOW GLOBAL.	DM00547F 23.43 7.643e-34 606- 653 DM00547B 11.28 7.907e-16 155-169 DM00547C 17.30 8.650e-14 209-231 DM00547D 11.60 6.500e-13 277-291 DM00547E 13.94 1.000e-11 307- 330
	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 6.379e-10 590-
1862	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.330e-11 18-62

SEQ ID NO:	Database entry ID	Description	Results*
1862	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 1.809e-09 52-92
1862	PR00449	TRANSFORMING PROTEIN P21 RAS	PR00449C 17.27 3.647e-19 59-82
		SIGNATURE	PR00449A 13.20-7.000e-15 18-40
			PR00449D 10.79 8.875e-14 121-
			135 PR00449E 13.50 8.920e-14
		•	157-180 PR00449B 14.34 8.500e-
			09 41-58
1867	BL01283	T-box domain proteins.	BL01283D 11.70 7.868e-31 59-92
1007	220.200		BL01283C 13.05 2.537e-14 25-39
1867	PR00937	T-BOX DOMAIN SIGNATURE	PR00937D 13.41 5.378e-15 24-39
1007	1100/5/	. 501. 501.1111	PR00937F 12.53 1.450e-12 83-92
			PR00937E 11.86 5.592e-12 62-76
-	, , , , , , , , , , , , , , , , , , ,		PR00937C 10.51 5.219e-10 5-15
1870	DM01803	I HERPESVIRUS GLYCOPROTEIN H.	DM01803A 10.51 8.699e-09 100-
1870	UMU1903	I HERFESVIROS GET COT ROTEIN II.	121
	DY 00450	Isocitrate and isopropylmalate	BL00470A 16.25 5.179e-14 10-31
1872	BL00470		BL00470C 15.43 4.103e-10 223-
		dehydrogenases proteins.	238 BL00470E 16.52 1.900e-09
			287-297
_,			PF00023A 16.03 3.893e-09 44-60
1873	PF00023	Ank repeat proteins.	PF00023A 16.03 3.893E-09 44-00 PF00023B 14.20 9.182E-09 40-50
1874	PF00023	Ank repeat proteins.	PF00023A 16.03 3.893e-09 72-88
			PF00023B 14.20 9.182e-09.68-78
1877	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.019e-26 51-90
1877	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 6.786e-16 427-
10//	2200020	, , , , ,	444 BL00028 16.07 1.900e-13
			287-304 BL00028 16.07 3.700e-
			13 481-498 BL00028 16.07
		·	1.000e-12 315-332 BL00028
	İ		16.07 1.000e-12 399-416
	}		BL00028 16.07 3.348e-12 453-
	ł		470 BL00028 16.07 4.522e-12
	· ·		371-388 BL00028 16.07 6.885e-
			11 343-360 BL00028 16.07
	i		4.600e-10 509-526
1000	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.500e-17 424-
1877	PK00048	C2H2-1 IFE ZINC FINGER SIGNATORE	438 PR00048A 10.52 7.000e-14
			312-326 PR00048A 10.52 1.643e-
			13 396-410 PR00048A 10.52
	1	· ·	3.571e-13 478-492 PR00048B
	1		6.02 9.000e-12 300-310
			PR00048A 10.52 1.000e-11 506-
	1.		520 PR00048A 10.52 5.737e-11
			340-354 PR00048A 10.52 1.391e-
			10 284-298 PR00048B 6.02
			6.063e-10 412-422 PR00048B
			6.02 1.474e-09 494-504
		,	PR00048B 6.02 2.895e-09 356-
			366
1877	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.600e-14 415-
13,,			428 PD00066 13.92 7.000e-14
			469-482 PD00066 13.92 5.500e-
			13 303-316 PD00066 13.92
			4.429e-12 331-344 PD00066
	.		13.92 9.217e-11 497-510
1			PD00066 13.92 2.038e-10 387-
l	i i	1	PIJUUU00 13.94 4.030c=10.307=

SEQ ID NO:	Database entry ID	Description	Results*
			359-372
1878	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	PR00830A 8.41 4.927e-13 222- 242
1878	PR00300	ATP-DEPENDENT CLP PROTEASE ATP- BINDING SUBUNIT SIGNATURE	PR00300A 9.56 1.545e-11 218- 237
1878	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE	PR00051A 10,68 3.647e-10 215- 236
1878	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 9.213e-10 217- 233
1878	BL00674	AAA-protein family proteins.	BL00674B 4.46 9.000e-24 215-
			237 BL00674C 22.60 8.448e-20 248-291 BL00674D 23.41 5.140e-18 308-355 BL00674E 15.24 9.217e-16 390-410 BL00674A 16.91 5.304e-09 181-202
1878	BL00113	Adenylate kinase proteins.	BL00113A 12.74 8.615e-09 219- 236
1879	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 1.957e-32 35-90 BL00456B 18.94 9.780e-17 111-
1880	BL00456	Sodium:solute symporter family proteins.	BL00456A 22.59 1.957e-32 35-90 BL00456C 24.55 1.225e-31 173- 228 BL00456B 18.94 9.780e-17
1884	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 1.818e-11 159-
1885	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE	182 PR00830A 8.41 5.897e-10 352- 372
1885	BL00847	MCM family proteins.	BL00847D 15.16 8.568e-25 343- 384 BL00847B 24.76 8.971e-25 194-237 BL00847C 18.79 9.270e- 10 301-335
1885	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.931e-09 346- 368
1885	BL00674	AAA-protein family proteins.	BL00674B 4.46 5.378e-09 345- 367
1886	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 7.000e-10 50-63
1886	PR00501	KELCH REPEAT SIGNATURE	PR00501A 8.25 5.295e-09 507- 521
1886	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 6.625e-09 479- 489
887	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544- 558
887	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544- 560
888	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544- 558
888	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544- 560
889	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 6.625e-13 544-
889	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.	PD01364B 13.94 5.500e-09 544-
890	PF00938	Lipoprotein.	560 PF00938E 19.50 6.096e-09 272-

SEQ ID NO:	Database entry ID	Description	Results*
2.01			307
1891	PF00925	GTP cyclohydrolase II.	PF00925F 13.23 9.850e-09 356- 367
1893	BL00226	Intermediate filaments proteins.	BL00226A 12:77 5:355e-13 139- 154
1895	PF00035	Double-stranded RNA binding motif.	PF00035B 12.08 7.750e-09 273- 287
1896	PF00622	Domain in SPla and the RYanodine Receptor.	PF00622B 21.00 9.250e-11 170- 192

TABLE 4

SEQ ID	Model	Description	E-value	Score	Repeats	Position
950	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	6.6e-26	99.5	1	825-886
950	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	2.5e-15	64.4	1	266-297
952	efhand	EF hand	0.0034	24.0	1	322-350
952	Adeno_E	Early E1A protein	8.9	-168.3	1	298-448
953	SH2	SH2 domain	1.5e-16	68.4	1	320-396
954	SH2	SH2 domain	1.5e-16	68.4	1	347-423
955	RCC1	Regulator of chromosome condensation (RCC1)	1.3e-13	58.6	4	148- 197:200- 249:318- 367:370- 418
050	BRCT	BRCA1 C Terminus (BRCT) domain	7.2	1.2	1	45-130
958 962	UQ con	Ubiquitin-conjugating enzyme	5.4e-39	143.0	i	2-117
963	UQ_con	Ubiquitin-conjugating enzyme	1.6e-57	204.5	1	2-132
971	kinesin	Kinesin motor domain	2.2e- 154	526.3	1	47-372
971	WD40	WD domain, G-beta repeat	1e-53	191.9	7	1327- 1361:1367- 1402:1432- 1466:1472- 1511:1523- 1557:1564- 1600:1606- 1640
971	filament	Intermediate filament protein	2.6	-195.6	1	423-805
971	HDV ag	Hepatitis delta virus delta antigen	6.2	-47.5	1	703-880
971	PFEMP	Plasmodium falciparum erythrocyte membrane p	8.9	-86.8	1	475-585
971	G6PD	Glucose-6-phosphate dehydrogenase, NAD bindi	9.6	-123.8	1	912-1049
971	DUF232	Putative transcriptional regulator	9.7	-30.1	1	616-750
975	Kelch	Kelch motif	5.7e-62	219.3	4	267- 312:314- 359:361- 406:408- 453
975	BTB	BTB/POZ domain	3.1e-38	140.4	1	23-130
977	kinesin	Kinesin motor domain	9.7e-	520.8	ī	53-353

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	 		153	<u> </u>	<u> </u>	
977	FHA	FHA domain	0.078	16.9	1	470-534
977	KMP11	Kinetoplastid membrane protein 11	3.5	-3.2	1	355-438
977	SART-1	SART-1 family	7.1	-360.1	1	325-881
977	Transposa se_22	L1 transposable element	8.7	-180.7	1	322-622
979	Ribosoma i_Liû	Ribosomal protein L10	6	-33.3 	1	70-173
980	Aa_trans	Transmembrane amino acid transporter	1.6e-75	264.3	ì	69-479
980	oxidored_ q1	NADH-Ubiquinone/plastoquinone	7.6	-169.3	1 ·	63-326
980	xan_ur_pe rmease	Permease family	8.4	-201.3	1	137-471
980	Trp_Tyr_ perm	Tryptophan/tyrosine permease family	9.6	-297.9	1	70-474
982	HYR	HYR domain	2e-35	131.1	2	106- 187:188- 267
982	EGF	EGF-like domain	3.9e-24	93.6	3	742-
						773:780- 811:818- 849
982	sushi	Sushi domain (SCR repeat)	0.28	12.5	3	1-38:43-
		(Correspond)	0.20	12.3		104:272-
982	TNFR_c6	TNFR/NGFR cysteine-rich region	0.74	9.6	1	563-601
982	laminin_E GF	Laminin EGF-like (Domains III and V)	6.6	-12.8	1	746-791
982	metalthio	Metallothionein	7.6	-11.6	1	744-804
982	HMG_Co A_synt	Hydroxymethylglutaryl-coenzyme A synthas	8.7	-342.7	1	336-625
986	MHC_II_ alpha	Class II histocompatibility antigen, alp	8.8c-13	55.9	1	37-106
986	ig	Immunoglobulin domain	8e-05	29.5	1	122-186
987	LRR	Leucine Rich Repeat	2.6e-12	54.3	4	68-91:92- 114:115- 137:138- 159
987	UVR	UvrB/uvrC motif	5.3	-1.5	1	453-486
990	UVR	UvrB/uvrC motif	3.8	-0.3	1	552-588
991	CK_II_be ta	Casein kinase II regulatory subunit	4.5e-69	242.9	1	5-124
994	RNA_pol _B	RNA polymerase beta subunit	0	1199.4	1	26-1010
994	PHD	PHD-finger	5.9	-17.0	1	1013-1048
995	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.9e-05	30.2	1.	10-59
995	zf-B_box	B-box zinc finger	0.0022	24.7	1	92-134
996	HLH	Helix-loop-helix DNA-binding domain	2e-07	38.1	1	276-327
997	ras	Ras family	3.3e-12	2.0	1	23-145
998 1000	pkinase ig	Protein kinase domain Immunoglobulin domain	3.1e-08 2.7e-06	-16.4 34.4	2	1-139 42-95:225-
1001	Y_phosph	Protein-tyrosine phosphatase	4.2	-86.2	1	281 180-409
1002	atase PX	PX domain	5 00 10	76.4		00 100
1002	Peptidase S21	Assemblin (Peptidase family S21)	5.8e-19 8.9	76.4 -173.6	1	76-352
1003	Y_phosph	Protein-tyrosine phosphatase	1.1	-79.3	1	08 227
.000	Thirophii	1 10:011 171001110 bitospitatase	1.1	-17.3	1	98-327

		N	E-value	Score	Repeats	Position
SEQ ID	Model	Description	E-value	Score	Керень	A OSICION
	atase		10	96.2	1	180-409
1004	Y_phosph	Protein-tyrosine phosphatase	4.2	-86.2	1	160-403
	atase			1660		(4 211
1008	oxidored_	NADH-Ubiquinone/plastoquinone	5.2	-165.9	1	64-311
	ql	(complex I)				
1010	filament	Intermediate filament protein	1.7	-190.5	1	331-647
1010	Tektin	Tektin family	1.8	-228.5	1	192-507
1010	bZIP	bZIP transcription factor	4.4	-3.7	1	253-317
1010	spectrin	Spectrin repeat	5.6	-18.0	1	320-429
1010	SART-1	SART-1 family	8	-362.0	1	54-675
1010	Myosin t	Myosin tail	9.8	-555.1	1	6-734
1010	ail	ivijosiii taii		Table 4	l · · ·	
1013	Defensin	Defensin propeptide	1.2e-26	102.0	1	45-97
1013	. –	Detensiti propeptide	1.20 20	102.0	[-	
1010	propep	Mammalian defensin	7.3e-14	59.5	1	110-138
1013	defensins		0.69	-180.5	1	314-579
1014	filament	Intermediate filament protein		-64.5	1	348-463
1014	PolyA_po	Poly A polymerase family	2.5	-04.3	1	340-403
	1		0.5	202.2	 	226-487
1014	ERM	Ezrin/radixin/moesin family	8.7	-223.3	1	
1014	Transposa	Transposase	9.4	-152.0	1	155-465
	se_12		· .			100
1015	zf-C2H2	Zinc finger, C2H2 type	1.2e-55	198.2	13	129-
				,		152:349-
	· .					371:379-
						401:407-
					l	429:446-
					1	468:474-
			ľ			496:505-
				1		527:533-
						556:562-
]			585:903-
1						925:931-
İ	1					953:959-
	,					981:987-
Ì		·				1010
1015	60s ribos	60s Acidic ribosomal protein	0.23	-21.0	1	61-194
1015	omal					
1015	TFIIS	Transcription factor S-II (TFIIS)	0.82	2.1	1	446-484
1015	rubredoxi	Rubredoxin	2.8	-8.3	1	900-943
1013	n	Rabication			İ	
1015	zf-BED	BED zinc finger	9	-7.0	i ·	972-1011
		Sodium:solute symporter family	1.7e-05	-65.8	1	5-184
1021	SSF		4.3e-30	113.4	5	100-
1028	zf-C2H2	Zinc finger, C2H2 type	4.56-30	113.4	"	122:132-
1				1		154:160-
				[182:188-
			· ·		1	
						210:216-
			 	1000	 	238
1028	KRAB	KRAB box	7.1e-24	92.8	1	4-44
1028	zf-BED	BED zinc finger	0.63	3.4	1	78-123
1029	fn3	Fibronectin type III domain	1.8e-13	58.2	1	146-231
1029	ig	Immunoglobulin domain	0.0013	25.5	1	275-335
1031	polypreny	Polyprenyl synthetase	0.013	-82.6	1	119-332
	1_synt			<u> </u>		
1032	Defensin	Defensin propeptide	1.2e-26	102.0	1	68-120
1032	propep					
1022	defensins	Mammalian defensin	7.3e-14	59.5	1	133-161
1032		MAGE family	3.8e-34	126.8	1	1-208
1033	MAGE	IVIAGE IMINIY	1 3.00-34	1.20.0		

SEQ ID	Model	D. C.			· .	
1034	LRR	Description Leucine Rich Repeat	E-value		Repeats	
1034	LKK	Leucine Rich Repeat	2.3e-17	71.1	6	62-84:87-
						110:111-
						134:135-
				1		158:159-
		→新聞號的第三人称形式				181:186-
1034	LRRCT	Leucine rich repeat C-terminal domain	74.05	100		209
1034	ig	immunoglobulin domain	7.4e-05	29.6	1	221-271
1034	LRRNT	Leucine rich repeat N-terminal domain	0.061	19.9	1	283-343
1035	CoaE	Dephospho-CoA kinase	0.19	18.3	1	33-60
1035	Cytidylylt	Cytidylyltransferase	3e-93	323.2	1	359-537
1033	ransf	Cyndyfyffransferase	8.3e-06	31.4	1	191-315
1035	SKI	Shikimate kinase	1064	(7.0	<u> </u>	<u> </u>
1035	ArgK	ArgK protein	0.64	-65.2	1	356-510
1038	lipase		7.5	-212.4	1	341-541
1044	homeobox	Lipase Homeobox domain	1.1e-12	49.8	1	1-198
1048	SKI	Shikimate kinase	2.6e-30	114.1	1	155-211
1049	fn3		0.49	-63.6	1	6-185
1049	1113	Fibronectin type III domain	4.7e-78	272.7	5	159-
						245:257-
					ĺ	343:360-
	ļ ·					459:480-
						565:577-
1049	ig	Immunoglobulin domain	2 2 2 2			665
1050	ig	Immunoglobulin domain	2.5e-05	31.1	1	79-137
1050	15	minimoground domain	0.019	21.5	2	1-58:93-
1051	MHC I	Class I Histocompatibility antigen,	-			142
1		domains	2.1	-83.5	1	24-116
1053	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.88	0.0		
1057	p450	Cytochrome P450		0.8	1	198-232
1060	Ribosoma	Ribosomal protein S21	5.7e-08	-1.4	1	66-377
7.00	1 S21	Ribosomai protein 521	0.5	-7.2	1	753-810
1060	Tropomyo	Tropomyosin	9	100.0		
	sin	Tropomyoum	9	-120.2	1 .	208-412
1064	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.88	0.0.		
1065	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.88	0.8	1	141-175
1066	aa_perme	Amino acid permease	3.2e-06	-173.3	1	191-225
	ases		3.26-00	-1/3.3	1	46-455
1066	Aa trans	Transmembrane amino acid transporter	0.4	172.1	1	40.40
1066	Trp_Tyr_	Tryptophan/tyrosine permease family	2.6	-172.1 -282.5	1	48-434
	perm	27F 3100mo pormease family	2.0	-202.3	1	48-392
1066	oxidored	NADH-Ubiquinone/plastoquinone	4.6	-164.9	1	170 404
	q1		7.0	-104.9	1	170-421
1066	xan_ur_pe	Permease family	9.7	-202.9		60.005
·	rmease		"	-202.9	1	60-397
1068	zf-C2H2	Zinc finger, C2H2 type	6.8e-	428.3	22	101
			125	420.3	22	101-
	-		123	ł		128:169-
						191:197-
-			ļ		:	219:225-
]		İ	ļ			247:253-
			1		. }	275:281-
				1	[303:309-
	İ			- !	j	324:330-
			1	1	1	352:358-
ľ			ľ			380:386-
						408:414-
]	Ì	.		436:442-
						464:470-

070 70			70		Damagés	Donistan
SEQ ID	Model	Description	E-value	Score	Repeats	Position 492:524-
					· ·	546:552-
						565:571-
	1					593:599-
			1 11			621:627-
			1 :			649:655-
						677:683-
				1.50		705:711-
	1					733:739- 761
1000	EDAD	KD AD I	4.1e-25	96.9	1	4-44
1068	KRAB	KRAB box	2.6	-7.8	1	279-325
1068	GATA	GATA zinc finger	4.3	-17.1	- 	
1068	LIM	LIM domain				311-368
1068	zf-BED	BED zinc finger	4.7	-4.4	1	315-353
1068	zf-TRAF	TRAF-type zinc finger	4.9	-6.5	1	163-212
1068	FYVE	FYVE zinc finger	6.7	-24.5	1	245-320
1068	TFIIS	Transcription factor S-II (TFIIS)	7.3	-6.0	1	281-319
1070	C2	C2 domain	1.1e-38	142.0	2	178-
].		263:319-
	1		 	<u> </u>	L	406
1071	ig	Immunoglobulin domain	1.9	12.9	1	19-66
1075	WD40	WD domain, G-beta repeat	1.7e-27	104.8	6	12-53:59-
	1.					96:160-
						194:200-
•						236:245-
	1.	,				281:287-
						322
1078	WD40	WD domain, G-beta repeat	2.2e-25	97.8	5	16-52:60-
		·				96:106-
			1 .		*	142:191-
		· .		i		227:234- 270
1000	TOTAL	DATE : C	0- 20	87.9	1	279-353
1078	FYVE	FYVE zinc finger	2e-22 3.1	-45.6	1	304-360
1078	DnaJ_CX	DnaJ central domain (4 repeats)	3.1	-45.0	1	304-300
	XCXGX	•				
1079	G PH	PH domain	1.5e-25	98.3	2	120-
1079	PH	PH domain	1.56-25	98.3	2	215:298-
				·	,	391
1001	TOAD	VDAD1	6- 01	83.0		45-81
1081	KRAB	KRAB box	6e-21		1	
1082	Ribosoma	Ribosomal protein L11	le-64	228.4	1	117-248
1004	1_L11	7: - C COND	(1)	627.7	25	100
1084	zf-C2H2	Zinc finger, C2H2 type	6.4e-	02/./	25	109-
		· .	185			131:137-
					,	159:165-
			ĺ			187:221-
	ļ ·					243:249-
	· ·	·				271:277-
	1					299:305- 327:333-
				}		
				1		355:361-
						383:389-
		•		12		411:445-
						467:473-
				1		495:501-
				}		523:529-
				[551:557-
						579:585-
	1	l	L	<u> </u>		607:641-

SEQ	ID Model	Description	E-value	Score	Di-t-	T 70
		Description	L-value	Score	Repeats	Position 663:669-
						691:697-
1			1.		1 .	719:753-
						775:781-
						803:809-
						831:837-
!				1		859:865-
						887:893-
1084	CDV 1	Power Land Co. 11 12 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	4			915
1084	CBM_1	Fungal cellulose binding domain LIM domain	2.6	4.4	1	38-66
1084	zf-BED	BED zinc finger	3	-15.7	1	783-847
100,	ZI-DED	BED zinc linger	5.9	-5.3	2	205-
		, i				244:737-
1085	Band 7	SPFH domain / Band 7 family	8.1e-42	152.3	1	776
1087	TPR	TPR Domain	4.5e-16	66.8	2	39-214 58-91:92-
			1.50-10	00.0	2	125
1090	WH1	WH1 domain	0.0017	11.6	1	11-119
1091	zf-DHHC	DHHC zinc finger domain	0.033	-11.5	1	120-158
1094	Calx-beta	Calx-beta domain	0.19	-11.6	1	23-117
1095	zf-C2H2	Zinc finger, C2H2 type	5.4e-82	285.8	12	288-
-						311:337-
.] -						359:365-
	-					387:393-
	·					415:421-
						443:449-
	- 1 :		1			471:477-
1			·			499:505-
						527:533-
						555:561- 583:589-
						611:617-
						639
1095	SCAN	SCAN domain	1.5e-54	194.6	1	46-141
1095	zf-BED	BED zinc finger	3.3	-3.0	2	434-
1		·				472:574-
1007						612
1097	7tm_2	7 transmembrane receptor (Secretin	6.8e-21	82.8	1	325-580
1097	CDC	family)				
1097	GPS Srg	Latrophilin/CL-1-like GPS domain	9.5e-13	55.8	1	273-323
1007	Sig	C.elegans Srg family integral membrane prote	4.5	-217.5	1	309-565
1099	lectin c	Lectin C-type domain	0.0011	70		
1100	PDZ	PDZ domain (Also known as DHR or	0.0011	7.2 25.3	1	6-100
		GLGF)	0.0014	23.3	1	12-91
1100	Tymo_45	Tymovirus 45/70Kd protein	1.8	-283.9	1	1 200
	kd_70kd	protein	1.0	-203.9	1	1-398
1101	cadherin	Cadherin domain	8.9e-95	328.3	5	64-
]			0.70,0	520.5		156:170-
ļ						265:279-
		•]			381:394-
ļ				ľ		485:498-
1101						595
1101	Cadherin_	Cadherin cytoplasmic region	4.7e-80	279.4		643-794
1102	C_term	0.1				
1103	COesteras	Carboxylesterase	0.98	-265.9	1	31-265
1104	e DCPo	Duel georificity about		112.5		
1104	DSPc	Dual specificity phosphatase, catalytic	9.7e-30	112.2	1	133-315

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1105		doma	3.1e-21	84.0	3	124-
1105	efhand	EF hand	3.10-21	04.0	3	152:160-
•						188:208-
						236
1100	-6 (2017)	Zinc finger, C2H2 type	3.5e-68	239.9	10	189-
1108	zf-C2H2	Zinc linger, CZHZ type	3.30-00	227.7	10	212:240-
		•				262:268-
***	. 1					290:296-
						319:325-
					·	347:353-
						375:382-
						404:909-
						931:937-
						960:966-
					<u> </u>	988
1108	SET	SET domain	0.0012	-18.9	1	37-175
1108	zf-BED	BED zinc finger	0.1	10.4	2	276-
1100	21-000	<i></i>			ľ	320:922-
	· ·				l	961
1108	FYVE	FYVE zinc finger	6.8	-24.6	1	262-364
1109	Nucleosid	Na+ dependent nucleoside transporter	2.5e-	635.7	1	198-613
1107	e tra2		187		i	
1109	TLC	TLC ATP/ADP transporter	5.6	-382.0	1	95-407
1109	ATP-	ATP synthase A chain	6.5	-79.5	1	365-503
1107	synt_A					
1110	PHD	PHD-finger	5.2	-16.5	1	77-120
1113	Peptidase	Ulp1 protease family, C-terminal cataly	6.5e-34	126.1	1	254-415
1115	C48	Capa province among the same and the same an	}			
1114	ras	Ras family	5.5e-31	116.4	1	54-222
1114	arf	ADP-ribosylation factor family	0.0054	-80.3	1	37-213
1115	SPRY	SPRY domain	7.3e-10	46.2	1	281-419
1115	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00076	26.2	1	88-134
1116	LRR	Leucine Rich Repeat	2.1e-05	31.4	6	37-64:65-
		•			ł	92:93-
						120:121-
				•		142:175-
					i .	198:255-
	1				<u></u>	278
1117	RasGAP	GTPase-activator protein for Ras-like	6.4e-28	106.2	1	268-440
,		GTPase	<u> </u>		<u></u>	
1117	PH	PH domain	0.28	15.7	1	7-78
1117	C2	C2 domain	1.9	-9.5	1	91-171
1117	bZIP	bZIP transcription factor	9	-6.7	1	997-1054
1118	COX3	Cytochrome c oxidase subunit III	1.7	-228.9	1	77-195
1118	sugar_tr	Sugar (and other) transporter	2.2	-179.3	1	32-413
1120	LMWPc	Low molecular weight phosphotyrosine	9.7e-56	198.6	1	7-138
	1	protein				1
1122	M	M protein repeat	6.6	13.1	2	148-
	1				İ	168:216-
}				<u> </u>		236
1123	lectin_c	Lectin C-type domain	4.3e-11	50.3	1	579-646
1123	Tropomyo	Tropomyosin	0.17	-90.1	1	304-500
II	sin				1:	
	- U144		0.17	-164.6	1	287-537
1123	filament	Intermediate filament protein	1 0.17	1 -104.0	1 4	
1123	filament	Intermediate filament protein	0.17	-18.2	1	422-523
1123 1123 1127	filament spectrin vwa	Intermediate filament protein Spectrin repeat von Willebrand factor type A domain	5.8 4.1e-63			

SEQ ID	Model	Description	E-value	Score	Damasta	T 70 144
1127	sushi	Sushi domain (SCR repeat)	2.4e-24	94.3	Repeats	Position 37-85:86-
,		(Contropolar)	2.10-21	74.5	, ,	140:147-
			1			200
1128	Neur_cha	Neurotransmitter-gated ion-channel tra	1e-88	308.2	1	84-334
	n_memb				-	04-334
1128	oxidored_	NADH-Ubiquinone oxidoreductase	7.	-14.7	i	123-183
	ql_N				j -	105
1129	C4	C-terminal tandem repeated domain in	1.4e-	507.0	2	477-
	,	type 4	148		1.	584:585-
1120	 					699
1129	Collagen	Collagen triple helix repeat (20 copies)	1.9e-60	214.3	7	20-78:84-
				1 .		142:143-
j	1					202:205-
						265:266-
						325:329-
		<u>'</u>				388:405-
1132	filament	Intermediate filament protein	2.1	102.0	 	464
1132	Tropomyo	Tropomyosin	7.7	-193.2	1	90-330
	sin	110pointy 05in	1.7	-119.0	1	151-353
1135	zf-C2H2	Zinc finger, C2H2 type	8.3e-26	99.2	5	270
		and anger, carre type	0.36-20	33.2	3	278-
		1.	1.			303:312- 339:345-
						369:375-
	,					399:405-
	<u> </u>	<u> </u>				429
1136	Ribosoma	Ribosomal protein S2	1.7e-78	274.2	1	34-198
	1_S2				1	31.130
1137	ATP-	ATP synthase alpha/beta family, beta-	5.2e-26	99.8	1	63-129
	synt_ab_	ba				
1120	N					
1139	ATP-	ATP synthase alpha/beta family,	3.1e-06	-33.1	1	71-183
1139	Synt_ab ATP-	nucleot				
1139		ATP synthase alpha/beta family, beta-	0.015	14.4	1	10-68
	synt_ab_ N	ba				
1140	ATP-	ATP synthase alpha/beta family, beta-				
1140	Synt ab	ba	5.2e-26	99.8	1	63-129
	N N	:	İ			
1140	ATP-	ATP synthase alpha/beta family,	2.6e-06	-31.8	1	100 061
	synt_ab	nucleot	2.00-00	-21.0	ı	132-261
1141	ank	Ankyrin repeat	6.7e-34	126.0	3	462
			0.70 34	120.0	,	463- 495:496-
			[.			528:529-
		<u> </u>	.			561
1141	BRCT	BRCA1 C Terminus (BRCT) domain	1.5e-15	65.1	2	578-
						689:705-
						812
1141	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.083	9.7	T	86-122
1143	GTP_EFT	Elongation factor Tu GTP binding	0.031	-59.5	ī	68-140
1145	U	domain			_	
1145	RF-1	Peptidyl-tRNA hydrolase domain	3.3e-05	10.5	1	46-159
1146	RF-1	Peptidyl-tRNA hydrolase domain	6.4	-51.5	1	46-114
1148	WD40	WD domain, G-beta repeat	6.9e-07	36.3	1	44-80
1149	Band_41	FERM domain (Band 4.1 family)	1.1e-77		1	45-235
1150	Metallothi	Plant PEC family metallothionein	5	-38.3	1	90-139
1153	o_PEC	Drottin Islanda de				
1133	pkinase	Protein kinase domain	1.7e-90	314.1	1	43-299

1155 SCP SCP-like extracellular protein 6.2e-14 56.1 1156 ras Ras family 1.5e-15 40.0 1159 6PF2K 6-phosphofructo-2-kinase 5.2e-158.4 152 152 1159 PGAM Phosphoglycerate mutase family 6e-100 345.5 1160 zf-C2H2 Zinc finger, C2H2 type 1.3e-104 361.0	1 1 1 13	28-200 5-98 26-249 250-435 223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501- 523:529-
1159 6PF2K 6-phosphofructo-2-kinase 5.2e- 152 1159 PGAM Phosphoglycerate mutase family 6e-100 345.5 1160 zf-C2H2 Zinc finger, C2H2 type 1.3e- 361.0	1 13	26-249 250-435 223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
152 152 159 PGAM Phosphoglycerate mutase family 6e-100 345.5 1160 zf-C2H2 Zinc finger, C2H2 type 1.3e- 361.0	1 13	250-435 223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
1159 PGAM Phosphoglycerate mutase family 6e-100 345.5 1160 zf-C2H2 Zinc finger, C2H2 type 1.3e- 361.0	13	223- 245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
1160 zf-C2H2 Zinc finger, C2H2 type 1.3e- 361.0		245:251- 273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
1100 21 02112 1 21110 1111601 0 0 1 1 1 1		273:279- 301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
	1	301:307- 329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
	1	329:335- 357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
	1	357:363- 385:391- 413:419- 441:447- 469:475- 497:501-
	1	385:391- 413:419- 441:447- 469:475- 497:501-
	1	413:419- 441:447- 469:475- 497:501-
	1	441:447- 469:475- 497:501-
		469:475- 497:501-
	1	497:501-
		523:529-
	1	
	 	551:557-
	1	579
1160 PHD PHD-finger 0.55 -7.5		448-509
1160 zf-BED BED zinc finger 1.4 0.3	2	264-
		302:542-
		580
1160 DnaJ CX DnaJ central domain (4 repeats) 2.9 -45.3	1	509-572
XCXGX Bind contain contain (100)	- 1	
G L		
1160 LIM LIM domain 7.7 -19.2	1	477-539
1160 TFIIS Transcription factor S-II (TFIIS) 7.9 -6.3	1	450-485
1162 Patatin Patatin-like phospholipase 0.00033 -0.6	1	1-171
1163 pkinase Protein kinase domain 2.3e-94 326.9	1	53-303
1163 RIO1 RIO1/ZK632.3/MJ0444 family 0.37 -100.2	1	47-245
1164 Oxysterol Oxysterol-binding protein 3.8e-47 170.0	1	173-571
BP Oxysteror Oxysteror-ounding protein	1	.1
1166 OATP C Organic Anion Transporter Polypeptide 9.9e- 660.3	1	68-443
(OATP) 195		
1166 OATP_N Organic Anion Transporter Polypeptide 1e-67 238.4	-1	520-680
(OATP)		
1166 7tm 5 7TM chemoreceptor 6.1 -167.4	1	184-503
1166 sugar tr Sugar (and other) transporter 7.8 -195.1		48-570
1167 pentaxin Pentaxin family 2.3e-07 -7.3	1	25-98
1107	 	537-574
1168 zf-C3HC4 Zinc finger, C3HC4 type (RING finger) 1.7e-05 31.7 1169 Peptidase Peptidase family M1 4e-156 532.1	1	69-458
M1	<u> </u>	
1170 ig Immunoglobulin domain 0.0016 25.1	1	30-109
11/0 25 20 20 20		104-214
11/2 D.D D.D. D.D.	 i	16-64
1175	 	301-334
1177 11.00	$\frac{1}{1}$	527-648
11/5	1	327-040
FeII Oxy	1	301-334
11/3	- - 	557-678
11/0	'	337-078
FeII Oxy	1	236-381
1177 Na_Ca_E Sodium/calcium exchanger protein 1.1e-23 92.1	1	230-381
X		12 010
1179 lactamase Metallo-beta-lactamase superfamily 0.059 -4.5	1	13-212
B 10.00 101.0	 	207 416
1180 fibrinogen Fibrinogen beta and gamma chains, C- 1.6e-32 121.5	1 7	
C term	1	207-416

SEQ ID		Description	E-value	Score	Repeats	Position
1181	MIF	Macrophage migration inhibitory factor (MIF)	7.6e-67	235.5	1	2-115
1182	SSF	Sodium:solute symporter family	1.7e- 234	792.4	1	69-503
1182	xan_ur_pe rmease	Permease family	4.3	-193.8	1	143-514
1182	PNTB	NAD(P) transhydrogenase beta subunit	5	-389.7	1	72 205
1182	60KD_IM	60Kd inner membrane protein	6.2	-129.6	1	33-325
1100	P		0.2	-129.0	1	113-241
1182	oxidored_ q1	NADH-Ubiquinone/plastoquinone	7.4	-169.1	1	87-298
1183	Cation_ef flux	Cation efflux family	2.3e-58	207.3	1	73-311
1185	AAA	ATPase family associated with various	4e-89	309.5	2	236-
		cel	10-05	309.5	4	421:500-
1185	HypB_Ur	Hump/HacCountry 1.1. 1. 1.	-			620
	eG	HypB/UreG nucleotide-binding domain	3.2	-65.8	1	234-337
1185	ArsA_AT Pase	Anion-transporting ATPase	8.5	-195.7	1 ,	234-482
1186	HCO3_co transp	HCO3- transporter family	0	1389.6	1	141-1023
1186	xan_ur_pe rmease	Permease family	0.33	-164.5	1	518-985
1187	homeobox	Homeobox domain	2.4e-16	67.7	1	51 100
1188	efhand	EF hand	6.7	9.0	1	51-107
1191	GST_C	Glutathione S-transferase, C-terminal domain	0.93	0.3	1	13-41 134-326
1194	PPR	PPR repeat	0.0019	24.9	1	ļ. <u></u>
1195	thiored	Thioredoxin	0.0019	-13.7	1	14-48
1197	ENV_pol yprotein	ENV polyprotein (coat polyprotein)	1.2e-08	-24.1	1	390-497 86-529
1200	UQ_con	Ubiquitin-conjugating enzyme	1.2- 02	01.0		
1202	7tm_1	7 transmembrane receptor (rhodopsin	1.3e-23	91.9	1	60-190
		family)	2.1e-23	91.2	1	59-306
1202	7tm_5	7TM chemoreceptor	4.3	-164.7	1	37-314
1203	7tm_1	7 transmembrane receptor (rhodopsin family)	5.9e-37	136.2	1	59-341
1203	7tm_5	7TM chemoreceptor	2.2	-159.4	1	37-338
1204	SH3	SH3 domain	2.5e-05	31.1	i	257-317
1204	UBA	UBA/TS-N domain	0.00013	28.8	1	36-76
1204	PGAM	Phosphoglycerate mutase family	0.00044	-75.5	<u>i</u>	438-625
1205	heme 1	Heme/Steroid binding domain	0.00053	19.5	1	37-112
1207	transmem	Tetraspanin family	0.29	-69.8	1	11-110
1200	brane4					
1208	OATP_C	Organic Anion Transporter Polypeptide	1.3e- 135	464.0	1	148-524
1208	kazal	Kazal-type serine protease inhibitor d	0.11	4.9	1	555-601
1208	sugar_tr	Sugar (and other) transporter	0.15		1	128-626
1208	lig_chan	Ligand-gated ion channel	3.3		ì	193-524
1208	7tm_1	7 transmembrane receptor	4.2		1	177-473
1208	Cytidylylt rans	Phosphatidate cytidylyltransferase	4.6		1	177-268
1215	thyroglob ulin_1	Thyroglobulin type-1 repeat	3.2e-35	130.4	2	90- 153:216- 281
1215	kazal	Kazal-type serine protease inhibitor	7.5e-09	42.8	1	40-84
1215	efhand				2	40-84 351-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						379:388-
				0155		416
1216	annexin	Annexin	7e-61	215.7	2	72-
						139:144-
			00.00	200.4	3	211 44-
1217	annexin	Annexin	2.2e-86	300.4]	111:116-
					ļ	183:199-
						267
			7e-61	215.7	2	44-
1218	annexin	Annexin	/6-01	213.7	 ~ .	111:116-
	\		;			183
1010	Armadillo	Armadillo/beta-catenin-like repeat	5.3e-30	113.1	5	351-
1219	ſ	Armaumo/oeta-catemii-nke repeat	3.30-30	****	-	393:405-
	_seg				1	447:448-
	1	·			i	498:499-
				İ		541:543-
				\		585
1219	GA	GA module	8.3	-5.7	1	180-224
1221	p450	Cytochrome P450	1e-122	421.1	i	30-483
1222	p450	Cytochrome P450	1.7e-06	-35.8	1	30-328
1223	A2M_N	Alpha-2-macroglobulin family N-	4.3e-12	-71.6	1	1-468
1443	YEM IN	terminal regi			l ⁻	
1225	Thymosin	Thymosin beta-4 family	2.3e-16	67.8	1	2-41
1227	WD40	WD domain, G-beta repeat	1.6e-37	138.1	7	115-
1241	11240	W domain, o dome report				151:165-
						201:207-
						244:250-
	! .				·	286:293-
						328:334-
						370:391-
		<u> </u>				431
1236	F-box	F-box domain	5e-07	36.8	1	210-258
1236	UvrD-	UvrD/REP helicase	0.00011	-157.2	1	441-920
	helicase					<u> </u>
1237	LRR	Leucine Rich Repeat	2.3e-25	97.7	8	42-65:66-
				İ	İ	88:89-
						111:112-
						134:135-
						157:158-
	1	•				180:181-
						203:204-
· .						227
1238	TPR	TPR Domain	9.6e-54	192.0	10	22-55:56-
				1		86:87-
				1]	120:121-
				1		154:155-
			Ì			188:189-
						222:223-
			} .	}	1	255:290-
			1	1		323:328-
						361:362-
				<u> </u>	<u> </u>	395
1241	cadherin	Cadherin domain	0.00011	29.0	2	48-
						151:165-
				<u> </u>	<u> </u>	254
1243	TTL	Tubulin-tyrosine ligase family	3.6e-31	117.0	1	1-225
1245	UCH-1	Ubiquitin carboxyl-terminal hydrolases	4.2e-08	40.4	1	190-221
		famil	1	1	ī	1

331

SEQ ID		Description	E-value	Score	Repeats	Position
1245	zf-UBP	Zn-finger in ubiquitin-hydrolases and	1.2e-05	32.2	1	62-148
	1 1	other			•	02-140
1246	ank	Ankyrin repeat	3.8e-92	319.5	11	12-44:45-
, ,					1	77:79-
			1,		1	111:112-
					1	144:145-
						177:179-
	i		i	i	İ	211:212-
• "					1.	244:245-
	1	• .				277:278-
	1	•	1		1	310:312-
	1					344:345-
1250	101-					374
1250	Clq	C1q domain	0.00033	-3.8	1	827-946
	filament	Intermediate filament protein	1.3	-187.6	1	360-645
1250	spectrin	Spectrin repeat	1.9	-12.5	1	492-591
1250	TNF	TNF(Tumor Necrosis Factor) family	4.1	-20.5	1	835-946
1250	Apolipopr	Apolipoprotein A1/A4/E family	5.7	-113.3	1	200-469
1050	otein			1]	
1250	sigma70	Sigma-70 factor	9	-116.2	1	462-650
1252	laminin_	Laminin N-terminal (Domain VI)	3.2e-52	186.9	1	1-223
1050	Nterm			İ		
1252	laminin_E	Laminin EGF-like (Domains III and V)	2e-38	141.0	3	225-
	GF			,		292:295-
			1			355:358-
1252	1					409
1252 1252	NTR	NTR/C345C module	7.2e-30	112.6	1	479-591
1232	Keratin_B	Keratin, high sulfur B2 protein	6.7	-81.2	1	318-451
1253	2					
1256	enolase	Enol-ase	0.038	-162.0	1	11-136
1257	HIT	HIT family	1.5e-55	198.0	1	51-162
1237	ank	Ankyrin repeat	5.9e-24	93.0	4	39-67:68-
]					100:101-
						133:134-
1258	lectin c	Testi Ot				164
1258		Lectin C-type domain	1.3e-21	85.2	1	51-181
1262	lectin_c	Lectin C-type domain	1.3e-21	85.2	1	51-181
1202	mito_carr	Mitochondrial carrier protein	8.7e-67	235.3	3	7-100:102-
				ļ	ĺ	221:224-
263		0 1 / 1				319
روس	serpin	Serpin (serine protease inhibitor)	8.7e-	374.8	1	87-463
264	MHC_I	Class I III	109			
204	MHC_1	Class I Histocompatibility antigen,	1.3e-	483.9	1	25-203
.265	MICI	domains	141			
.203	MHC_I	Class I Histocompatibility antigen,	2.3e-	446.5	1	25-203
266	MHC I	domains	130			
200	MPIC_I	Class I Histocompatibility antigen,	2.7e-	403.1	1	22-187
267	MITO	domains	117			
207	MHC_I	Class I Histocompatibility antigen,	1.le-	397.7	1	25-196
268	MICI	domains	115			
200	MHC_I	Class I Histocompatibility antigen,	2.9e-	406.3	1	25-196
268		domains	118			-
268	ig	Immunoglobulin domain	9.5e-08	39.2	1	221-286
269	MHC_I	Class I Histocompatibility antigen,	4.2e-	452.3		25-204
	\ (Y \ C \ -	domains	132			
271	MHC_I	Class I Histocompatibility antigen,	1e-144	494.2	1	25-203
272	1000	domains			}	
<i>) []</i>	MHC I	Class I Histocompatibility antigen,	2.8e-95	329.9	i	25-204

SEQ ID	Model	Description	E-value	Score	Repeats	Position
		domains				
1273	MHC_I	Class I Histocompatibility antigen, domains	3.3e- 140	479.2	1	25-203
1274	Kelch	Kelch motif	1.4e-91	317.7	6	271-
12/4	Kolon	Rolon moni				316:318-
•		•				366:368-
		•				413:415-
						460:462-
					l	507:509-
	[·				554
1274	BTB	BTB/POZ domain	3.1e-38	140.4	1	23-130
1275	IQ	IQ calmodulin-binding motif	0.0037	23.9	1	394-414
1276	Glycos_tr	Glycosyl transferase	2.2e-22	87.8	1	126-308
	ansf 2					
1276	Ricin B I	QXW lectin repeat	0.0045	23.7	2	478-
	ectin				1	518:520-
						557
1280	ig	Immunoglobulin domain	3.4e-05	30.7	2	62-
	"				l	145:174-
					<u> </u>	240
1281	UCH-1	Ubiquitin carboxyl-terminal hydrolases famil	1.5e-12	55.1	1	100-131
1285	UBX	UBX domain	2.9e-22	87.4	1	205-284
1286	UBX	UBX domain	2.9e-22	87.4	1	251-330
1287	DnaJ	DnaJ domain	9e-38	138.9	1	8-70
1288	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.9e-09	42.8	1	9-57
1288	zf-B box	B-box zinc finger	1.8e-06	34.9	1	177-217
1288	SPRY	SPRY domain	0.0016	14.8	1	479-605
1288	zf-UBR1	Putative zinc finger in N-recognin	2.2	-18.4	1	180-237
1289	PKD	PKD domain	0	1026.8	16	293-
1407	,					372:397-
						483:485-
		·				568:572-
						677:679-
] .					763:765-
	1		į			846:849-
			l			931:933-
						1017:1019-
	1					1099:1101-
					1	1183:1185-
	1					1269:1271-
				٠	1	1353:1355-
						1438:1440-
	1		1		i	1522:1524-
			-			1612:1614-
		<u></u>		·		1696
1289	REJ	REJ domain	2.3e-	978.0	1	1723-2248
			290			
1289	PLAT	PLAT/LH2 domain	2.6e-25	97.5	1	2673-2789
1289	GPS	Latrophilin/CL-1-like GPS domain	1.1e-15	65.5	1	2566-2615
1289	lectin_c	Lectin C-type domain	0.59	-23.7	1	2-87
1289	DUF26	Domain of unknown function DUF26	7.8	-16.5	1	2220-2262
1290	CNH	CNH domain	2.7e-24	94.2	1	69-375
1292	RhoGAP	RhoGAP domain	1.8e-59	211.0	1	125-279
1293	Peptidase	Matrixin	8.2e-	378.2	1	48-211
	_M10		110			
1293	fn2	Fibronectin type II domain	3.5e-84	293.1	3	230-
1	I	· .	<u> </u>	1	<u> </u>	271:288-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	1.					329:347-
1293	hemopexi	Hemopexin	1.00	1.00.0		388
	n	Tientopexiti	1e-33	125.5	3	486-
	1			1.		530:608-
				}		654:656-
1294	Peptidase	Matrixin	8.2e-	378.2	1	699 48-211
	M10		110	376.2	1	46-211
1294	fn2	Fibronectin type II domain	3.5e-84	293.1	3	230-
				1	Ī	271:288-
	'			1		329:347-
1007	110					388
1297	UQ_con	Ubiquitin-conjugating enzyme	3.3e-20	80.6	1	400-557
1297	TT_ORF2	<u></u>	3.6	-92.9	1	546-667
1297	UQ con	Ubiquitin-conjugating enzyme	3.3e-20	80.6	1	400-557
1297	TT_ORF2	TT viral ORF2	3.6	-92.9	1	546-667
1298	ig	Immunoglobulin domain	2.9e-	798.3	21	25-84:119-
		·	236	}		177:245-
						303:339-
			}			397:432-
:	•			1		490:524-
						583:618-
			1		•	676:709-
			İ	į į		768:801-
						859:894-
						954:990-
		·				1048:1121-
						1179:1217-
						1275:1382-
						1440:1477-
						1535:1569-
						1627:1664- 1722:1756-
]			1816:1851-
				1		1911:1947-
						2005:2040-
						2098
298	Adeno_E	Adenovirus E3 region protein CR1	0.062	-3.7	1	1212-1288
299	3_CR1 cNMP bi	Coding to the second				
233	nding	Cyclic nucleotide-binding domain	6.2e-28	106.2	1	363-459
299	ion_trans	Ion transport protein	8.9e-21	92.5	, 	60.065
299	ATP-	ATP synthase, Delta/Epsilon chain,	6.8	82.5	1	69-265
	synt_DE	long	0.8	6.0	1	478-525
301	RGS	Regulator of G protein signaling	1.6e-49	177.9	, 	56 150
i		domain	1.06-49	177.9	1	56-172
302	THF DH	Tetrahydrofolate	1e-99	344.7	1	60 225
	G_CYH_	dehydrogenase/cyclohyd	10-99	344.7	1	60-235
	c	,				
303	gln-synt	Glutamine synthetase	1.3e-	610.1	1	1-321
			179	010.1	•	1-321
	gln-synt	Glutamine synthetase		-214.4	1	1-95
	SCAN	SCAN domain				42-137
	Methyltra	MraW methylase family				70-205
	nsf_5	· · · · · · · · · · · · · · · · · · ·			-	, 0-203
	ion_trans	Ion transport protein	8.3e-18	72.6	1	438-672
307	ank	Ankyrin repeat				77-
ŀ	ļ				1	108:163-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						195
307	Srg	C.elegans Srg family integral membrane prot	8.1	-222.4	1	418-669
1310	Ammoniu m_transp	Ammonium Transporter Family	1.9e-56	200.9	1	25-429
310	FecCD	FecCD transport family	0.89	-200.6	1	97-331
311	Kelch	Kelch motif	2.6e-60	213.8	6	311-
	12010.1					359:361-
						411:413-
			•].		458:460-
		·			Ì	505:507-
	·			·	j	556:559-
			1 (00	100.1	 	23-181
1311	BTB	BTB/POZ domain	1.6e-28	108.1	2	92-
1313	zf-B_box	B-box zinc finger	9.6e-30	112.2	2	133:418-
						459
1012	-E C211C4	Zinc finger, C3HC4 type (RING finger)	1.3e-23	91.8	2	15-59:341-
1313	zf-C3HC4	Zine iniger, C3AC4 type (Kir40 iniger)	1.50-25	1	-	385
1313	SPRY	SPRY domain	3.2e-23	90.6	1	672-813
1313	PHD	PHD-finger	0.97	-9.8	1	14-62
1313	NB-ARC	NB-ARC domain	9.5	-151.3	1	48-311
1313	zf-UBR1	Putative zinc finger in N-recognin	9.8	-24.7	1	421-470
1314	SRCR	Scavenger receptor cysteine-rich	1.7e-25	98.1	1	37-133
	<u> </u>	domain		1	<u> </u>	00.000
1315	adh_short	short chain dehydrogenase	5.8e-33	122.9	1	38-293
1317	ANP	Atrial natriuretic peptide	1.2e-51	185.0	6	43-150
1318	EGF	EGF-like domain	3.6e-26	100.4	0	512- 547:553-
			1	1		591:597-
						634:640-
						675:747-
]			781:787-
	1			1		827
1318	ig	Immunoglobulin domain	2.1e-06	34.7	1	170-227
1318	TIL	Trypsin Inhibitor like cysteine rich dom	1.9	-6.8	1	741-787
1318	Idl_recept a	Low-density lipoprotein receptor domain	6.6	-8.8	1	551-593
1318	TILa	TILa domain	6.9	-8.5	1	733-792
1321	FKBP	FKBP-type peptidyl-prolyl cis-trans isomeras	5.7e-45	162.8	l	234-336
1322	PX	PX domain	1.1e-25	98.8	1	273-382
1322	SH3	SH3 domain	6.5e-12	53.0	1	3-59_
1323	ras	Ras family	5.2e-16	45.4	1	35-218
1323	GTP_EFT U	domain	0.53	-76.1	1	31-223
1323	MobB	Molybdopterin guanine dinucleotide synthesis	4.8	-45.8	1	36-150
1323	GTP_CD	Cell division protein	5.7	-217.6	1	36-247
1324	pkinase	Protein kinase domain	4.6e-51	183.1	1	199-527
1325	pkinase	Protein kinase domain	4.6e-51	183.1	1	199-527
1327	Peptidase	Papain family cysteine protease	7.3e-	378.4	1	73-349
	_C1		110			
1328	Peptidase C1	Papain family cysteine protease	7.3e- 110	378.4	1	114-390
1330	ig	Immunoglobulin domain	4.6e-07	36.9	2	52-
	7					108:145-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	<u> </u>					201
1332	Sec7	Sec7 domain	1.3e-71	251.3	1	345-536
1332	PH	PH domain	0.25	16.2	1	567-676
1332	IQ	IQ calmodulin-binding motif	0.35	17.4	1	13-33
1333	cadherin	Cadherin domain	1.6e-94	327.4	5	68-
		· ·	1		1	159:173-
		·		1	1	268:282-
i	i ·	j .	İ	İ	İ	386:399-
					1	490:503-
1222	10			ļ	· .	600
1333	Cadherin_	Cadherin cytoplasmic region	1.6e-76	267.6	1	648-819
1225	C_term		ļ			
1335	lipocalin	Lipocalin / cytosolic fatty-acid binding	7.5e-35	129.2	1	5-133
1226	GTTO	pr	ļ <u> </u>			
1336 1336	SH3	SH3 domain	2.4e-10	47.8	1	495-549
1330	PID	Phosphotyrosine interaction domain	0.29	-13.3	1	52-181
1226	0434 837	(PTB/PID)	<u> </u>			
1336	SAM_PN	Sterile alpha motif (SAM)/Pointed	6	-25.0	1	608-687
1336	T	domain				
1338	SH2	SH2 domain	8.6	-25.5	1	268-347
1338	UCH-2	Ubiquitin carboxyl-terminal hydrolase	1.5e-20	81.7	1	350-411
1338	UCH-1	Ubiquitin carboxyl-terminal hydrolases	1.1e-12	55.5	1	111-142
	TFIIA	Transcription factor IIA, alpha/beta s	1.7	-151.4	1	386-698
1338	Tymo_45	Tymovirus 45/70Kd protein	3.3	-291.1	1	310-647
1338	kd_70kd MARCKS	MARCKOC				
1340		MARCKS family	6.8	-95.6	1	573-865
1340	RCC1	Regulator of chromosome condensation	5.6e-10	46.6	6	77-
		(RCC1)				136:140-
						192:195-
						245:248-
						298:301-
•	•					356:359-
1342	Peptidase	Peptidase family M1	4.6	-194.5	1	406
10.2	M1	1 opticuse family (VI)	4.0	-194.5	1	159-470
1342	ubiquitin	Ubiquitin family	5.4	-4.4	1	520 616
1345	crystall	Beta/Gamma crystallin	3.3e-38	140.4	2	538-616
		· · · · · · · · · · · · · · · · · · ·	3.56-56	140.4	2	1-53:61- 144
1345	WD40	WD domain, G-beta repeat	6.7e-09	43.0	1	269-305
1348	AAA	ATPase family associated with various	0.97	-33.9	1	
		cellul	0.51	-33.9	1	131-307
1349	AAA	ATPase family associated with various	0.97	-33.9	1	121 207
		cellul	0.77	33.9	'	131-307
1351	PHD	PHD-finger	6.3e-15	63.0	1	100 227
1351	PHD	PHD-finger	6.3e-15	63.0	1	190-237
1353	CUB	CUB domain	3.3e-13	57.3		190-237
1353	sushi	Sushi domain (SCR repeat)	1.5e-05	31.9	1	416-524
1355	SPRY	SPRY domain			1	357-412
1355	fn3	Fibronectin type III domain	3.4e-19	77.2	1	396-519
1355	zf-B box	B-box zinc finger	1e-08		1	259-345
1356	Patatin	Patatin-like phospholipase	8.9e-07	35.9	1	44-86
1358	ELM2	ELM2 domain	0.59	-42.1	1	10-118
1358	myb DN	Myb-like DNA-binding domain	3.2e-21		1	195-256
.,,,,	A-binding	wyo-nke Diva-binding domain	1.1e-09	45.6	1	299-345
1359		Penrolygin (M12P) for the control				
1373	Reprolysi	Reprolysin (M12B) family zinc metallo	1.4e-12	55.3	1	239-457
1359	n Pep M12	Daniel Smile and the second				
1333		Reprolysin family propeptide	3.6e-12	53.9	1	90-216
1	B propep					

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1359	tsp_1	Thrombospondin type 1 domain	3.4e-07	37.4	5	551-
	WF					601:829-
			į			884:888-
						944:946-
			ļ			1002:1007-
			•			1057
1359	EB	EB module	8.4	-11.7	1	452-531
1363	ank	Ankyrin repeat	6.2e-26	99.6	5	72-
	1			1		104:105-
	i		1			137:138-
]		1	l		170:180-
	1				Ì	212:222-
	1					255
1366	C2	C2 domain	le-75	264.9	2	161-
	1	•	1		1	247:293-
						381
1367	C2	C2 domain	1e-75	264.9	2	161-
		•				247:293-
					ļ <u> </u>	381
1368	p450	Cytochrome P450	5e-110	378.9	1	47-502
1370	aa_perme	Amino acid permease	1.3e-08	-108.1	1	49-452
	ases			<u> </u>	<u> </u>	220 505
1370	Neur_cha	Neurotransmitter-gated ion-channel tr	0.37	-96.5	1	330-585
	n_memb			<u> </u>		200 615
1370	ion_trans	Ion transport protein	1.4	-2.3	1	288-615
1370	Transp_cy	Permease for cytosine/purines, uracil	1.5	-178.6	1	47-442
	t_pur			<u> </u>	<u> </u>	CT 400
1370	Aa_trans	Transmembrane amino acid transporter	1.9	-190.3	1	67-409
1370	DUF140	Domain of unknown function DUF140	2.6	-156.6	1	109-312
1370	Nucleosid	Nucleoside transporter	3.2	-154.9	1	357-658
	e_tran		1 -	102.2	1	56-429
1370	xan_ur_pe	Permease family	4.1	-193.2	1 '	30-429
1000	rmease	7 A DITE	7.1	-22.4	1	536-671
1370	DUF6	Integral membrane protein DUF6	7.3	-213.9	1	212-616
1370	NADHdh	NADH dehydrogenase Sodium:neurotransmitter symporter	9.2	-458.6	 	117-450
1370	SNF		9.2	-436.0	1 1	117-450
1050	1.	fam Kinesin motor domain	2.1e-	463.2	 	53-341
1372	kinesin	Kinesin motor domain	135	703.2	1.	33 5
1000	Translin	Translin family	10	-82.4	†i	315-462
1372	Translin LRR	Leucine Rich Repeat	1.9e-27	104.6	7	60-83:84-
1373	LKK	Leucine Rich Repeat	1.50 27		1	107:108-
				Ì		131:132-
						155:157-
						i '
	1			1	i	180:181-
	1					204:205- 225
		5 11 11 1	1.0- 05	32.1	1	310-368
1373	ig	Immunoglobulin domain	1.2e-05	30.2	1	249-294
1373	LRRCT	Leucine rich repeat C-terminal domain	4.7e-05	29.6	1 1	425-505
1373	fn3	Fibronectin type III domain	7.1e-05	13.7	1 .	27-58
1373	LRRNT	Leucine rich repeat N-terminal domain	0.83	13.7	1	1-131
1374	kinesin	Kinesin motor domain	9.5e-14		1	101-165
1375	zf-DHHC	DHHC zinc finger domain	9.1e-34	125.6		
1376	EGF	EGF-like domain	3.2e-45	163.6	9	49-84:90-
	-[126:132-
	1					167:177-
					1	213:217-
			1	1		252:286-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						321:327-
		·	·			362:368-
			ŀ	ł		401:407-
44-4	 					442
1376	CUB	CUB domain	9.6e-18	72.4	1	809-918
1376	TIL	Trypsin Inhibitor like cysteine rich	0.73	-2.0	1	84-132
1376	77	domai	<u>. </u>			
12/0	Keratin_B	Keratin, high sulfur B2 protein	0.9	-67.6	1	111-242
1376	granulin	Granulin	 		ļ	
1376	metalthio	Metallothionein	1.1	-12.1	1	285-323
1376	DUF141	Domain of unknown function DUF141	5.9	-10.3	1	363-431
1380	ion_trans	Ion transport protein	6.7	-15.1	1	799-922
1380	ABC2_m	ABC-2 type transporter	0.066	16.8	1	153-318
	embrane	ADO-2 type transporter	6.1	-130.1	1	145-334
1380	oxidored	NADH-Ubiquinone/plastoquinone	6.2	-167.5	1	46.017
	q1	o o o o o o o o o o o o o o o o o o o	0.2	107.3	1	46-317
1380	OATP_C	Organic Anion Transporter Polypeptide	9.5	-236.4	1	75-316
1381	pkinase	Protein kinase domain	9.7e-80	278.3	1	205-486
1384	ig	Immunoglobulin domain	0.00034	27.4	1	65-142
1388	LRR	Leucine Rich Repeat	4.9e-16	66.7	4	20-43:44-
		·	1.55	00.7	"	67:68-
					ł	91:92-115
1388	LRRCT	Leucine rich repeat C-terminal domain	7.4e-09	42.9	1	125-175
1388	GPS	Latrophilin/CL-1-like GPS domain	0.0041	20.8	1	641-693
1388	HRM	Hormone receptor domain	0.0076	16.3	1	285-354
1388	7tm_2	7 transmembrane receptor (Secretin	0.01	-96.0	1	704-981
		family)		20.0	•	704-301
1388	ig	Immunoglobulin domain	3.3	10.9	1	196-265
1389	MACPF	MAC/Perforin domain	0.016	-71.3	1	30-313
1391	HD .	HD domain	8.3e-07	36.1	1	32-127
1392	efhand	EF hand	1.5e-05	31.8	2	1-25:33-61
1394	MORN	MORN repeat	1.1e-32	122.1	7	39-61:62-
		·	1			85:86-
1						108:109-
						131:132-
						154:155-
						177:178-
1205	1/0717					200
1395	MORN	MORN repeat	3.1e-31	117.2	6	39-61:62-
ı		·	}	ļ	}	85:86-
						108:143-
			1 [}	165:166-
		•	1 1	Ì	İ	188:189-
		· .	!!	1	1	211
1396	EPH_lbd	Ephrin receptor ligand binding domain	4.6e-	462.1	ī	31-204
1306	nleina	D	135			•
396 396	pkinase	Protein kinase domain	8e-74	258.7	1	635-892
טענ	fn3	Fibronectin type III domain	2.5e-31	117.5	2	329-
				1		425:437-
396	SAM	CAM domain (St. 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				524
	PHD	SAM domain (Sterile alpha motif)	2.5e-21		1	928-992
	Exo_endo	PHD-finger				259-296
371	_phos	Endonuclease/Exonuclease/phosphatase fa	0.34	-11.2	1	357-643
397	sugar tr		-	10.0		
	Exo_endo	Sugar (and other) transporter Endonuclease/Exonuclease/phosphatase				7-343
	TWO 211(1()	CHUUHUUUUUKKK EYONUCIASSA/nhoonhoteen	0.24	-11.2	1 T	357-643

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1397	sugar_tr	Sugar (and other) transporter	8.8	-196.7	1	7-343
1401	homeobox	Homeobox domain	0.097	-3.3	1	78-126
1403	Tropomyo sin	Tropomyosin	2.4	-110.1	1	341-547
1403	filament	Intermediate filament protein	2.6	-195.5	1	412-760
1403	UvrD- helicase	UvrD/REP helicase	8	-249.4	1	153-720
1403	Myosin_t ail	Myosin tail	8.9	-551.2	1	20-777
1404	Clq	C1q domain	0.00033	-3.8	1	827-946
1404	filament	Intermediate filament protein	1.3	-187.6	1	360-645
1404	spectrin	Spectrin repeat	1.9	-12.5	1	492-591
1404	TNF	TNF(Tumor Necrosis Factor) family	4.1	-20.5	1	835-946
1404	Apolipopr	Apolipoprotein A1/A4/E family	5.7	-113.3	1	200-469
1404	sigma70	Sigma-70 factor	9	-116.2	1	462-650
1405	Cache	Cache domain	6.5e-12	53.0	2	402- 481:721- 813
1406	ASC	Amiloride-sensitive sodium channel	2e-125	430.1	i	159-579
1407	pkinase	Protein kinase domain	0.22	-115.5	1	5-217
1408	PBP	Phosphatidylethanolamine-binding protein	1.8e-71	250.9	1	1-167
1410	abhydrola se	alpha/beta hydrolase fold	1.4	-12.1	1	75-318
1412	rrm	RNA recognition motif.	2.7e-12	54.3	3	259- 329:360- 433:477- 550
1414	DEP	Domain found in Dishevelled, Egl-10, and Ple	3.5e-32	120.3	2	173- 247:275- 349
1414	PH	PH domain	1e-09	45.7	1	29-144
1414	PDZ	PDZ domain (Also known as DHR or GLGF)	0.013	18.7	2	375- 456:460- 531
1418	SCAN	SCAN domain	2.6e-51	183.9	†1	36-131
1418	zf-C2H2	Zinc finger, C2H2 type	4.6e-25	96.7	5	406-
1410	21-02112	Zine iniget, GZNZ type				428:435- 457:463- 485:522- 545:553- 575
1418	KRAB	KRAB box	0.023	14.2	1	220-260
1418	zf-BED	BED zinc finger	10	-7.4	1	438-486
1419	EGF	EGF-like domain	5.1e-28	106.5	9	13-40:45- 72:77- 104:109- 136:141- 168:173- 200:205- 232:237- 264:269-
1419	Keratin_B	Keratin, high sulfur B2 protein	1.2	-69.3	1	296 100-251
1419	Gamma- thionin	Gamma-thionins family	4.8	-8.7	1	124-163

SEQ ID	Model	Description	E-value	Score	Repeats	Doctor
1421	Ferric_red	Ferric reductase like transmembrane	2.8e-64	227.0	Repeats	Position 63-564
	uct	com		227.0	1.	03-304
1421	NAD_bin ding	Oxidoreductase NAD-binding domain	4	-34.1	1	381-551
1421	FAD_bin ding 6	Oxidoreductase FAD-binding domain	5	-28.7	1	245-335
1421	rubredoxi n	Rubredoxin	6.9	-11.0	1	409-436
1422	zf-C2H2	Zinc finger, C2H2 type	5e-12	53.4	2	1057- 1079:1085- 1109
1422	zf-TRAF	TRAF-type zinc finger	5	-6.6	1	1056-1101
1422	Tymo_45 kd_70kd	Tymovirus 45/70Kd protein	6	-298.2	1	343-700
1422	zf-BED	BED zinc finger	7.1	-6.0	1	1070-1110
1423	7tm_5	7TM chemoreceptor	3.3	-162.5	i	181-451
1423	Cytidylylt rans	Phosphatidate cytidylyltransferase	5	-87.9	1	21-135
1424	CAP_GL Y	CAP-Gly domain	7.2e-46	165.8	2	196- 238:398- 440
1424	ank	Ankyrin repeat	9.2e-09	42.5	3	1-40:42- 76:79-111
1425	PAP2	PAP2 superfamily	1.5e-08	41.8	1	166-313
1426	SCAN	SCAN domain	6.2e-70	245.7	1	33-128
1426	zf-C2H2	Zinc finger, C2H2 type	1.5e-44	161.4	6	239- 261:267- 289:295- 317:323- 345:351- 373:379- 401
1426	zf-BED	BED zinc finger	0.67	3.1	1	280-318
1426	DC1	DC1 domain	5.1	3.6	1	295-338
1426	zf-C4	Zinc finger, C4 type (two domains)	9.7	-55.1	1	323-364
1427	xan_ur_pe rmease	Permease family	7.1	-199.5	1	104-453
1428	LRR	Leucine Rich Repeat	2.3e-16	67.8	4	80- 103:104- 127:128- 151:152- 175
1428	LRRCT	Leucine rich repeat C-terminal domain	0.00079	26.2	1	185-234
1431	PH	PH domain	7.6e-15	62.8	1	19-117
1432 1434	PH	PH domain	6.4e-21	82.9	1	55-153
1434	filament	Intermediate filament protein	2.9	-196.8	1	128-488
1434	K-box OspD	K-box region	4.1		1	277-357
1434	Apolipopr otein	Borrelia outer surface protein D Apolipoprotein A1/A4/E family	5.3		1	151-409 56-318
1437	RhoGAP	RhoGAP domain	5.7e-57	202.7		11.50 :5:
1437		PH domain	3.5e-18		1	1152-1305
1437	PDZ	PDZ domain (Also known as DHR or GLGF)			1	922-1030 28-128
1441		Annexin	4.1e- 109	375.9		18-79:80- 135:151- 219:227- 294

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1443	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0075	18.7	1	1256-1307
1443	PHD	PHD-finger	0.18	-2.9	1	1255-1310
1443	WD40	WD domain, G-beta repeat	2.9	13.4	1	189-225
1443	K_tetra	K+ channel tetramerisation domain	3.5	-39.5	1	830-916
1443	Clathrin	Region in Clathrin and VPS	8.9	-25.2	1	976-1129
1444	RIIa	Regulatory subunit of type II PKA R-s	0.31	10.8	1	17-54
1444	Alpha_ad aptin_C	Alpha adaptin AP2, C-terminal domain	7	-63.6	1	91-155
1445	TK	Thymidine kinase	3.4e-98	339.6	1	61-231
1446	GDPD	Glycerophosphoryl diester phosphodies	5.4e-08	40.0	1	154-403
1446	Glycos_tr ansf 4	Glycosyl transferase	4.9	-87.4	1	22-145
1447	adh short	short chain dehydrogenase	0.98	-91.8	1	2-196
1448	K-box	K-box region	0.64	-28.5	1	61-126
1449	PHD	PHD-finger	0.01	8.4	1	1-42
1452	rrm	RNA recognition motif.	4.5e-19	76.8	1	77-148
1454	rvt	Reverse transcriptase	3.6e-34	126.9	1	385-570
1454	Gag MA	Matrix protein (MA), p15	0.0018	-21.0	1	10-131
1454	Gag_p30	Gag P30 core shell protein	0.54	-80.3	1	211-390
1458	COX5A	Cytochrome c oxidase subunit Va	1.2e-55	198.3	1	42-131
1459	Guanylate kin	Guanylate kinase	6.2e-38	139.4	1	515-624
1459	PDZ	PDZ domain (Also known as DHR or GLGF)	6.8e-11	49.6	1	256-335
1459	SH3	SH3 domain	0.027	5.9	1	348-415
1459	L27	L27 domain	0.049	20.1	1	186-238
1459	Caulimo_ mov	Caulimovirus movement protein	7.1	-185.3	1	420-673
1459	A_deamin ase	Adenosine/AMP deaminase	7.8	-138.5	1	64-421
1461	hexokinas e	Hexokinase	4.3e- 284	957.2	1	53-499
1463	Occludin	Occludin/ELL family	6.3	-249.1	1	33-394
1464	trypsin	Trypsin	4.7e-72	252.8	1	30-232
1466	DDHD	DDHD domain	8.6e- 117	401.4	1	613-860
1466	DUF203	Domain of unknown function	8.7	-69.8	1	254-460
1467	Glycos_tr ansf 1	Glycosyl transferases group 1	1.8e-27	104.7	1	286-470
1468	EMP24_ GP25L	emp24/gp25L/p24 family	3.5e-70	246.6	1	5-183
1469	EMP24_ GP25L	emp24/gp25L/p24 family	3.5e-81	283.1	1	5-208
1470	14-3-3	14-3-3 protein	2.2e- 142	486.5	1	5-249
1471	filament	Intermediate filament protein	0.53	-177.6	1	2-249
1471	spectrin	Spectrin repeat	7.1	-19.1	1	34-130
1472	MtN3 slv	MtN3/saliva family	5.4	-31.6	1	35-139
1472	ATP- synt_A	ATP synthase A chain	7.4	-80.2	1	91-214
1474	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	4.3e-07	37.0	2	531- 557:663- 688
1474	zf-C2H2	Zinc finger, C2H2 type	6.3	11.3	2	205- 229:618- 642
1475	SpoU_me thylase	SpoU rRNA Methylase family	2.1e-27	104.5	1	145-301

SEQ ID		Description	E-value	Score	Repeats	Position
1476	filament	Intermediate filament protein	2.4	-194.5	1	427-720
1476	Tropomyo sin	Tropomyosin	3	-111.7	1	539-761
1476	spectrin	Spectrin repeat	3.3	-15.3	1	427-526
1476	K-box	K-box region	7.1	-41.3	1	248-335
1476	Borrelia_	Borrelia ORF-A	9.8	-102.9	 	440-736
	orfA		"	102.5	*	1440-736
1477	MMR_HS R1	GTPase of unknown function	1.5e-90	314.2	1	178-521
1477	DUF258	Protein of unknown function, DUF258	9.6	-84.6	1	343-465
1479	RNase_P	3' exoribonuclease family	1.2e-96	334.5	2	48-
	H				-	251:358-
	ļ			1		581
1479	S1	SI RNA binding domain	0.057	19.9	1	675-750
1479	KH-	KH domain	0.35	9.3	 î 	609-651
	domain	·		"	1 *	005-051
1482	COLFI	Fibrillar collagen C-terminal domain	5.8e-29	109.6	1	97-277
1482	Collagen	Collagen triple helix repeat (20 copies)	8.5e-05	29.4	1	2-61
1483	COLFI	Fibrillar collagen C-terminal domain	1.6e-35	131.4	ī	110-293
1483	Collagen	Collagen triple helix repeat (20 copies)	8.5e-05	29.4	1	2-61
1484	CH	Calponin homology (CH) domain	5.6e-14	59.9	1	4-104
1485	MoaE	MoaE protein	7	-55.7	1	21-96
1486	zf-C2H2	Zinc finger, C2H2 type	6.8	10.9	2	871-
						896:904- 929
1487	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	2.6	-3.3	1	336-377
1489	FH2	Formin Homology 2 Domain	0.00017	-49.7	1	3-329
1490	AAA	ATPase family associated with various	4e-45	163.3	1	370-565
1490	SKI	Shikimate kinase	0.068	-52.5	1	369-506
1490	Viral_heli case1	Viral (Superfamily 1) RNA helicase	1.8	-67.0	1	371-563
1490	LON	ATP-dependent protease La (LON) domai	3.6	-69.4	1	12-220
1491	Tropomod ulin	Tropomodulin	4.1e-78	272.9	1	34-402
1491	WH2	WH2 motif	0.83	16.1		
1491	pkinase	Protein kinase domain	5.9	-136.0	1	534-553
1494	xan_ur_pe	Permease family	2.9	-189.3	1	334-538
	rmease	·	2.9	-109.5	1	72-377
1494	Na_sulph _symp	Sodium:sulfate symporter transmembran	5.3	-356.1	1	212-541
1494	Glycos_tr	Glycosyl transferase	7.0			
	ansf_4	Cipcosyi transierase	7.3	-90.3	1	374-528
1494	STE3	Pheromone A receptor	7.5	202.0		
1494		Domain of unknown function DUF221			1	314-603
1494		7TM chemoreceptor		-234.2	1	196-576
1494		NADH-Ubiquinone/plastoquinone		-171.0	1	122-365
	q1	- 12 12 O orquinono plastoquinone	9.7	-171.5	1	42-264
1495		Lectin C-type domain	17- 24	1000		
1496		Cytochrome b561			1	53-164
	me B561	Cylodinome (501	2.1e- 113	390.2	1	1-240
1498		haloacid dehalogenase-like hydrolase		160	1	
1498		Cation transporting ATPase, C-terminu				31-443
	TPase_C	ampoining All ase, O-iciminu	0.26	-25.8	1	535-706
1498		NADH-ubiquinone/plastoquinone	4.4	-34.0		621 707
		oxidore	7,14	ا ۵.4۰	1	631-705
1499		DEAD/DEAH box helicase	3e-64	226.9	1	139-356
1499		Helicase conserved C-terminal domain	JUTUT 1	WW 0.7		174-176

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	С		10.61	104.0	2	28-
1502	C2	C2 domain	1.3e-51	184.9	2	109:184-
					ļ.	264
			1 6 01	1100		743-
1503	ank	Ankyrin repeat	1.6e-31	118.2	6	L .
						775:776-
				 		807:808-
						840:842- 874:875-
	1				·	915:916-
	1	· *		İ		948
			1.4e-	570.1	16	57-89:90-
1504	ank	Ankyrin repeat	1.4e-	370.1	10	122:123-
	1		107			155:210-
		·	,			242:243-
						275:276-
					İ	308:363-
					l	398:399-
						431:432-
					İ	464:525-
		·				557:558-
	· ·				ĺ	590:591-
		·			Į.	623:644-
					į	675:678-
	1 ·				[710:711-
	1]		743:744-
	ļ					776
1504	SAM	SAM domain (Sterile alpha motif)	1.3c-09	45.4	1	872-934
1504	PARP	Poly(ADP-ribose) polymerase catalytic	0.022	-59.4	1	954-1161
1501		domai				
1504	3Beta_HS	3-beta hydroxysteroid	1.3	-204.0	1	208-536
	D	dehydrogenase/isomera		<u> </u>		<u> </u>
1505	PHD	PHD-finger	0.26	-4.5	1	132-191
1505	DC1	DC1 domain	2.8	5.8	1 1	131-159
1506	PHD	PHD-finger	0.26	-4.5	1	156-215
1506	DC1	DC1 domain	2.8	5.8	1	155-183
1507	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.6e-08	40.6	1	224-261
1507	LON	ATP-dependent protease La (LON)	0.007 .	-21.6	1	305-510
	1	domain				
1507	TPR	TPR Domain	1.6	13.6	2	41-74:75-
						108
1508	ig	Immunoglobulin domain	1e-76	268.3	12	78-
			İ		ľ	131:171-
					-	245:276-
			1			330:364-
					ł	432:463-
			1		İ	516:552-
						623:654-
	1					705:740-
		·				797:828-
						880:914-
	1		1			981:1012-
						1067:1101-
	1			<u></u>		1169
1512	FYVE	FYVE zinc finger	3.2e-14	60.7	1	152-261
1512	НурА	Hydrogenase expression/synthesis	0.81	-51.2	1	97-194
		hypA		1	 	1.00.000
	RNA PO	RNA polymerases M/15 Kd subunit	2.1	-1.7	1	160-212
1512	L_M_15K		I.	L .	ł	

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	D				1	ZOSILION
1516	Gelsolin	Gelsolin repeat	0.76	5.9	1	1011-1052
1518	VIR	Vomeronasal organ pheromone receptor family	2.3e-11	41.1	Ī	73-338
1518	7tm_1	7 transmembrane receptor (rhodopsin family)	0.044	-69.7	1	62-325
1520	SPRY	SPRY domain	5.2e-24	93.2	1	95-230
1521	Tropomod ulin		0.065	-128.4	1	214-495
1521	LRR	Leucine Rich Repeat	1.8	15.0	4	348- 371:376- 403:404- 427:432- 456
1522	zf-CCHC	Zinc knuckle	0.051	15.9	1	13-30
1523	Skp1	Skpl family	6.3e-10	46.4	1	17-80
1524	RhoGAP	RhoGAP domain	4.2e-31	116.8	1	125-285
1525	UQ_con	Ubiquitin-conjugating enzyme	1.4e-39	144.9	1	1-126
1527	LRR	Leucine Rich Repeat	1.6e-35	131.4	9	86- 109:110- 133:134- 157:158- 181:182- 205:206- 229:230- 251:254- 277:279-
1527	LRRNT	Leucine rich repeat N-terminal domain	-		<u> </u>	302
1527	LRRCT	Leucine rich repeat C-terminal domain	6.6e-06	33.1	1	33-60
1528	K_tetra	K+ channel tetramerisation domain	0.048	17.9 -5.0	1	312-362
1529	MORN	MORN repeat	1.8e-24	94.7	7	117-220 1049- 1071:1072- 1094:1100- 1122:1123- 1143:1151- 1171:1198- 1220:1221-
1529	VPS9	Vacuolar sorting protein 9 (VPS9) domain	8.3e-06	32.7	1	1244 1551-1656
1529	RCC1	Regulator of chromosome condensation (RCC1)	8.5e-06	32.7	3	168- 216:527- 574:579- 625
1529	RhoGEF	RhoGEF domain	0.097	-40.8	1	694-884
1529	PH	PH domain	0.23	16.5	1	901-1005
1530	profilin	Profilin	1.4e-63	224.6	1	3-135
1531	profilin	Profilin	7.4e-48	172.4	1	3-119
1532	60s_ribos omal	60s Acidic ribosomal protein	3.3	-34.2	ī	39-153
1533	jmjC	jmjC domain	0.01	-0.1	1	1-50
1533	PHD	PHD-finger	0.042	2.9	2	508- 549:609- 655
1534	kinesin	Kinesin motor domain	3.5e-64	226.7	1	1-177
1536	aminotran	Aminotransferase class-III	7.8e-42	152.4	$\frac{1}{1}$	
	_3		7.00-72			1-373

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1536	LEA	Late embryogenesis abundant protein	5.6	-4.7	1	109-177
1539	Hydrolase	haloacid dehalogenase-like hydrolase	0.0064	15.3	1	264-685
1539	Cation_A TPase_C	Cation transporting ATPase, C-terminu	4.6	-46.1	1	784-916
1541	TPR	TPR Domain	0.00036	27.3	2	135- 168:204- 237
1542	PCMT	Protein-L-isoaspartate(D-aspartate) O-methyl	1.2e-11	21.8	1	9-224
1543	Peptidase C54	Peptidase family C54	3.1e-58	206.9	1	76-364
1545	homeobox	Homeobox domain	4.8e-26	100.0	1	233-286
1546	zf-C2H2	Zinc finger, C2H2 type	3.1e-85	296.6	14	14-36:42- 64:70- 92:99- 122:128- 150:163- 185:199- 221:227- 249:255- 277:283- 305:311- 333:339- 361:367- 389:395- 417
1546	TFIIS	Transcription factor S-II (TFIIS)	1.9	-1.0	1	202-237
1546	zf-BED	BED zinc finger	2.3	-1.7	1	324-362
1546	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.6	-5.4	1	341-372
1547	Ribosoma 1 S5	Ribosomal protein S5	3.4e-09	44.0	i	222-352
1548	ĪQ	IQ calmodulin-binding motif	1e-24	95.5	5	748- 768:771- 791:794- 814:935- 955:958- 978
1552	DUF6	Integral membrane protein DUF6	0.14	6.6	1	150-279
1552	SBF	Sodium Bile acid symporter family	9.2	-75.2	1	143-321
1553	zf-C2H2	Zinc finger, C2H2 type	2.1e-05	31.4	3	80- 105:107- 130:144- 169
1554	F-box	F-box domain	7.7e-05	29.5	1	4-52
1555	Ran_BP1	RanBP1 domain	1.1e-88	308.0	1	37-161
1555	WH1	WH1 domain	6.8	-26.8	1	45-159
1556	actin	Actin	8.4e- 151	514.4	1	1-372
1557	GTP_EFT U	Elongation factor Tu GTP binding doma	9.7	-93.3	1	91-355
1557	Defensin_ propep	Defensin propeptide	9.8	-11.4	1	1-50
1559	GTP_EFT U	Elongation factor Tu GTP binding domain	1.5e-11	51.8	1	125-348
1559	GTP_EFT U D3	Elongation factor Tu C-terminal domain	8.1e-07	33.1	1	451-541
1559	GTP_EFT U D2	Elongation factor Tu domain 2	1e-06	35.8	1	363-446

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1559	ATP-bind	Conserved hypothetical ATP binding protei	8.5	-132.9	1	126-312
1559	dynamin	Dynamin family	8.7	-85.0	1	110-278
1567	carb_anhy drase	Eukaryotic-type carbonic anhydrase	4.6e- 170	578.4	1	5-241
1568	An_perox idase	Animal haem peroxidase	8.1e- 164	557.6	1	144-683
1568	DUF37	Domain of unknown function DUF37	6.5	-36.0	1	462-518
1569	DAO	FAD dependent oxidoreductase	0.055	-90.8	1	49-381
1571	CH	Calponin homology (CH) domain	1.4e-25	98.4	1	126-233
1573	NUDIX	MutT-like domain	5.5e-12	53.3	1	96-221
1574	HECT	HECT-domain (ubiquitin-transferase)	4.3e-16	66.9	1	281-573
1575	ig	Immunoglobulin domain	2.8	11.5	1	122-187
1577	7tm_1	7 transmembrane receptor	3.4	-113.2	1	42-246
1577	Bac_rhod opsin	Bacteriorhodopsin	9.6	-139.9	1	111-313
1578	fn3	Fibronectin type III domain	0.21	11.2	1	121-211
1579	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1 - <i>Q</i>	548-624
1580	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1	653-729
1580	Acetyltran sf	Acetyltransferase (GNAT) family	2.4e-14	61.1	1	653-729
1582	GIDA	Glucose inhibited division protein A	0.0017	-414.5	1	68-196
1583	efhand	EF hand	1.2	14.9	1	23-51
1585	Dynein_h eavy	Dynein heavy chain	3.6e-18	-92.1	1	1-363
1587	Sm	Sm protein	2e-07	38.1	1	43-124
1588	PDZ	PDZ domain (Also known as DHR or GLGF)	3.1e-15	64.1	1	3-83
1590	MAP1_L C3	Microtubule associated protein 1A/1B, light	0.04	-35.1	1	99-187
1591	Syntaxin	Syntaxin	2.3e-09	38.1	1	1-266
1591	synaptobr evin	Synaptobrevin	5.8	-14.5	1	184-272
1591	DUF148	Domain of unknown function DUF148	7.7	-38.1	1 .	17-129
1592	laminin_E GF	Laminin EGF-like (Domains III and V)	1.2	-4.2	1	153-196
1592	EGF	EGF-like domain	2.4	10.9	3	140- 177:284- 313:351- 380
1592	metalthio	Metallothionein	4.8	-9.3	1	288-348
1593	DnaJ	DnaJ domain	3.4e-40	146.9	1	3-69
1594	HMG_bo x	HMG (high mobility group) box	2.6e-27	104.1	1	346-414
1598	HMG_bo x	HMG (high mobility group) box	3.4e-30	113.8	- 1	45-113
1600	CUB	CUB domain	6.9	-43.0	1	224-313
1601	DUF6	Integral membrane protein DUF6	1.1e-12	55.6	2	113- 238:266- 390
1601	sugar_tr	Sugar (and other) transporter	5.7	-191.4	1	55-405
1601	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex I)	6	-167.3	1	131-389
1602	FF	FF domain	2.3e-33	124.3	5	272- 321:339- 388:406-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						461:486-
				. `		541:622-
	·			2-2	<u> </u>	673
1602	ww	WW domain	4.3e-20	80.2	2	88-
						117:129-
		<u></u>				158
1603	FF	FF domain	2.3e-33	124.3	5	235-
					"	284:302-
		•				351:369-
						424:449- 504:585-
						636
			110.00	15.6	<u> </u>	92-121
1603	WW	WW domain	1.1e-09	45.6	1	360-372
1605	AT_hook	AT hook motif	1.9	11.9	1	
1606	aminotran	Aminotransferase class-V	1.3e-	437.3	1	37-377
 	_5		127	206.2	1	37-331
1607	aminotran	Aminotransferase class-V	3.5e-94	326.3	1	3/-331
1	5	0 : (1	66	1050	1	125-609
1611	Granin	Granin (chromogranin or secretogranin)	6.6	-185.2 -7.8	1	551-610
1612	PHD	PHD-finger	0.59			46-313
1613	Branch	Core-2/I-Branching enzyme	1e-77	271.6 349.7	4	78-
1614	mbt	mbt repeat	3.2e-	349.7	4	153:192-
			101			265:304-
	1					381:412-
				1		486
		S 11 11 1:5(51) () ()	0.0001	6.9	1	809-888
1614	SAM_PN	Sterile alpha motif (SAM)/Pointed	0.0021	0.9	1	009-000
1614	T	domain	0.023	20.6	1	822-885
1614	SAM	SAM domain (Sterile alpha motif) Protein of unknown function DUF52	4.7e-64	226.2	1	9-270
1615	UPF0103		6.8e-36	132.7	2	606-
1616	C2	C2 domain	0.86-30	132.7	2	695:755-
		•			1	842
1617	C2	C2 domain	7.8e-35	129.2	2	87-
101/	C2	C2 domain	7.00-55	127.2	1~	176:236-
	}				l	323
1618	C2	C2 domain	0.16	2.4	1	265-346
	7tm_1	7 transmembrane receptor (rhodopsin	3.9e-20	80.3	1	217-427
1619	/un_1	family)	3.70-20	00.5	1 *	21, 12,
1620	K tetra	K+ channel tetramerisation domain	1.1e-25	98.7	1	3-101
	BTB	BTB/POZ domain	9	-22.4	i	21-104
1620		Cyclin, N-terminal domain	0.057	-1.4	$\frac{1}{1}$	46-149
1623	cyclin zf-C2H2	Zinc finger, C2H2 type	8.9e-19	75.8	4	34-57:71-
1624	ZI-CZHZ	Zine inger, Czriż type	0.50-15	73.0		93:112-
•	ļ					134:143-
					1	165
1607	PDZ	PDZ domain (Also known as DHR or	4.2e-16	66.9	1	66-149
1627	FUL	GLGF)	7.20-10	00.7	•	
1628	MttA Hcf	mttA/Hcf106 family	2.5	-14.8	1	54-107
1025	106	I HIMPATICITOO IGIIIIIY	2.5	1	1	1
1629	Tropomyo	Tropomyosin	4	-114.1	1	74-272
1628	sin	Tropomyosiii	"	11.1	1	
1629	Syntaxin	Syntaxin	5.7	-103.5	1	82-402
1628		Phosphatidylinositol 3- and 4-kinase	8.5	-118.0	 	125-342
1628	PI3_PI4_	rnosphandynnositor 5- and 4-kinase	0.5	-110.0	1	123-342
1628	kinase	HlyD family secretion protein	9.4	-64.2	1	129-400
ID/X	HlyD		10	-132.7	1	150-338
1628	UPF0089	Uncharacterised protein family				

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						142:156-
1632	D.".		<u> </u>	ļ <u></u>	<u> </u>	226
	Ribosoma l_L10	Ribosomal protein L10	4.2	-31.6	1	70-173
1632	Ribosoma 1_L10	Ribosomal protein L10	4.2	-31.6	1	70-173
1635	death	Death domain	1.5	2.0	1	261-348
1636	death	Death domain	1.5	2.0	1	73-160
1637	Gelsolin	Gelsolin repeat	4.1e-92	319.4	6	27-76:148- 188:265- 307:398- 451:523- 564:626- 668
1639	TBC	TBC domain	2e-08	15.3	1	98-293
1640	TBC	TBC domain	2e-07	1.3	1	98-297
1641	homeobox	Homeobox domain	0.0097	7.0	1	83-135
1646	transmem brane4	Tetraspanin family	1.6e-75	264.3	1	18-264
1652	LacY_sy mp	LacY proton/sugar symporter	4.9	-335.5	1	66-299
1652	oxidored_ q1	NADH-Ubiquinone/plastoquinone (complex I)	7.6	-169.3	1	53-279
1653	Colipase_ C	Colipase, C-terminal domain	4.3e-24	93.5	1	21-65
1654	SH2	SH2 domain	0.0091	3.5	1	1-83
1658	SUI1	Translation initiation factor SUI1	4.4e-46	166.5	1	50-149
1661	jmjC	jmjC domain	0.00052	13.9	1	308-415
1663	SH3	SH3 domain	0.011	9.5	1	332-388
1664	UBA	UBA/TS-N domain	6.7e-06	33.0	<u>i</u>	194-233
1664	TUDOR	Tudor domain	0.2	-0.7	<u>i</u>	506-627
1665	Ribosoma 1_S21	Ribosomal protein S21	0.0039	11.7	1	10-62
1666	transmem brane4	Tetraspanin family	2.2e-71	250.6	1	23-264
1669	RuBisCO _small	Ribulose bisphosphate carboxylase, smal	2.8	-52.1	1	354-430
1671	LRR	Leucine Rich Repeat	2e-50	180.9	12	29-47:48- 71:72- 95:96-
		•				118:119- 142:143- 166:167- 189:190- 213:214- 235:236-
1671	74 1					259:260- 283:284- 307
1671	7tm_1	7 transmembrane receptor	0.0032	-43.2	1	439-688
	Cytidylylt rans	Phosphatidate cytidylyltransferase	7.1		1	520-617
1671	oxidored_ q1	NADH-Ubiquinone/plastoquinone	9.7	-171.5	1	475-685
1671	MerC	MerC mercury resistance protein	9.8	-87.5	1	534-632
1672	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	4e-28		1	292-364
1672	UCH-1	Ubiquitin carboxyl-terminal hydrolases	1.9e-14	61.4	1	35-66

SEQ ID	Model	Description	E-value	Score	Repeats	Position
		famil	0.0000	260		07.104
1673	F-box	F-box domain	0.00071	26.3	1	87-134
1674	Lamp	Lysosome-associated membrane glycoprotein	5.7	-191.1	1	351-653
1675	FGGY	FGGY family of carbohydrate kinases, N-termi	2.7e-45	163.9	1	20-282
1675	FGGY_C	FGGY family of carbohydrate kinases, C-termi	5.5e-23	89.8	1	285-491
1676	Keratin_B	Keratin, high sulfur B2 protein	7.4	-81.9	1	24-201
1678	S_100	S-100/ICaBP type calcium binding domain	8.3	-9.6	1	909-941
1680	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	7.4e-24	92.7	1	12-369
1681	WD40	WD domain, G-beta repeat	9.3e-14	59.1	6	305- 343:352- 389:395- 432:440- 476:487- 524:583- 621
1683	Ribosoma 1 L44	Ribosomal protein L44	1e-38	142.1	1	17-95
1686	WD40	WD domain, G-beta repeat	8.9e-14	59.2	2	8-43:50-86
1688	FliE	Flagellar hook-basal body complex protein Fl	5.1	-27.5	1	673-763
1690	dCMP_cy t deam	Cytidine and deoxycytidylate deaminase	2e-13	58.0	1	12-100
1691	G-gamma	GGL domain	5.1	-8.6	1	712-760
1692	cpn60_TC	TCP-1/cpn60 chaperonin family	0.012	-260.5	1	32-187
1693	Glycopho rin A	Glycophorin A	4.4	-43.1	1	16-149
1696	zf-C2H2	Zinc finger, C2H2 type	4.5e-15	63.5	6	92- 115:120- 143:174- 198:210- 233:329- 353:363- 386
1698	LRR	Leucine Rich Repeat	0.44	17.0	4	37-58:59- 80:81- 102:103- 125
1699	VHS	VHS domain	9.5e-60	211.9	1	5-146
1700	rrm	RNA recognition motif.	3.6e-23	90.4	3	128- 203:332- 402:413- 480
1701	ank	Ankyrin repeat	3.8e- 101	349.4	12	12-44:45- 77:79- 111:112- 144:145- 177:179- 211:212- 244:245- 277:278- 310:312-

1701 1702 1702 1705 1708	URO-D pkinase HEAT cyclin WD40	Uroporphyrinogen decarboxylase (URO-D) Protein kinase domain HEAT repeat Cyclin, N-terminal domain WD domain, G-beta repeat	7.8 0.00012 1.2 3.8e-11 1.5e-11	-229.7 -68.0 15.6 50.5 51.8	1 2 1 5	344:345- 374:375- 407 79-354 31-278 342- 380:499- 537 157-279 278-
1702 1702 1705 1708	pkinase HEAT cyclin WD40	(URO-D) Protein kinase domain HEAT repeat Cyclin, N-terminal domain	0.00012 1.2 3.8e-11	-68.0 15.6	1 2	407 79-354 31-278 342- 380:499- 537 157-279
1702 1702 1705 1708	pkinase HEAT cyclin WD40	(URO-D) Protein kinase domain HEAT repeat Cyclin, N-terminal domain	0.00012 1.2 3.8e-11	-68.0 15.6	1 2	79-354 31-278 342- 380:499- 537 157-279
1702 1702 1705 1708	pkinase HEAT cyclin WD40	(URO-D) Protein kinase domain HEAT repeat Cyclin, N-terminal domain	0.00012 1.2 3.8e-11	-68.0 15.6	1 2	31-278 342- 380:499- 537 157-279
1702 1705 1708	HEAT cyclin WD40	HEAT repeat Cyclin, N-terminal domain	3.8e-11	50.5	1	342- 380:499- 537 157-279
1705 1708	cyclin WD40	Cyclin, N-terminal domain	3.8e-11	50.5	1	342- 380:499- 537 157-279
1708 1709	WD40	Cyclin, N-terminal domain WD domain, G-beta repeat	3.8e-11	50.5	1	380:499- 537 157-279
1708 1709	WD40	Cyclin, N-terminal domain WD domain, G-beta repeat				157-279
1709		WD domain, G-beta repeat				
					1.	1 2/0"
	0					313:371- 407:413- 447:493- 529:535- 569
	SH2	SH2 domain	0.002	10.0	1	
1710	abhydrola se	alpha/beta hydrolase fold	2.2e-20	81.2	1	287-364 124-355
1710	abhydrola se 2	Phospholipase/Carboxylesterase	1.2	-84.9	1	179-359
1711	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.002	22.7	 	
1711	PHD	PHD-finger	1.9	23.7	1	280-320
1712	WD40	WD domain, G-beta repeat	3.2e-18	74.0	5	282-323 67-
						101:123- 157:164- 199:209- 246:253- 290
1714	Acyltransf erase	Acyltransferase	0.0011	14.0	1	83-217
1719	helicase_ C	Helicase conserved C-terminal domain	1.2e-19	78.7	1	397-475
1719	DEAD	DEAD/DEAH box helicase	4.6e-07	10.4	1	2-210
1719	IPT	Isopentenyl transferase	7.9	-160.7	1	17-172
1720	Na_Ca_E x	Sodium/calcium exchanger protein	8e-76	265.3	2	109- 249:471- 616
720	DUF205	Domain of unknown function DUF	5.3	-112.7	1	85-253
1720	Fumarate red_D	Fumarate reductase subunit D	8.4	-49.5	1	518-620
721	vwa	von Willebrand factor type A domain	9.6e-29	108.9	1	34-205
721	fn3	Fibronectin type III domain	3e-15	64.1	2	212- 287:332- 413
	pkinase	Protein kinase domain	1.6e-06	-41.3	$\frac{1}{1}$	40-359
725	BRCT	BRCA1 C Terminus (BRCT) domain	1e-15	65.6	3	3-93:642- 730:753-
727	BRCT	BRCA1 C Terminus (BRCT) domain	7.0			833
~~~	rrm	RNA recognition motif.	7.2 1.1e-05	32.4	2	45-130 545- 612:880-
720	-6.0000	7				942
	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.012	22.2	1	285-311
		PWI domain	0.047	-0.6	1	6-78
		PX domain	2.5e-31	117.5	1	94-211
	PMP22_C laudin	PMP-22/EMP/MP20/Claudin family	1.5e-56	201.3	i	1-157

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1733	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1733	Vac Fusi	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
	on _	•				
1733	CUT	CUT domain	8.5	-38.0	1	159-240
1734	homeobox	Homeobox domain	0.00037	21.6	1	268-339
1734	Vac_Fusi	Chordopoxvirus fusion protein	5.2	-21.5	1	286-364
1734	On CUT	CUT domain	8.5	-38.0	1	159-240
1738	efhand	EF hand	1.5e-16	68.4	2	40-68:76-
1730	Cinaiid					104
1742	trypsin	Trypsin	6.5	-55.6	1	33-255
1743	Exonuclea	Exonuclease	1.2e-36	135.2	1	39-213
1745	Se	Smr domain	0.0029	13.0	1	1594-1672
1745	Smr	RyR domain	1.5	-29.0	l <del>i</del>	1312-1403
1745 1745	RyR_ L27	L27 domain	3.6	5.1	i	1573-1626
1745	Smr	Smr domain	0.0029	13.0	i	1611-1689
1746	RyR	RyR domain	1.5	-29.0	1	1312-1403
1746	L27	L27 domain	3.6	5.1	1	1590-1643
1746	Smg4 UP	Smg-4/UPF3 family	9.7	-74.5	1	1379-1518
	F3					
1747	mito_carr	Mitochondrial carrier protein	1.3e-81	284.5	3	1-90:98- 198:200- 288
1748	OSCP	ATP synthase delta (OSCP) subunit	8.4	-94.4	1	67-213
1749	Oxysterol BP	Oxysterol-binding protein	3.4e-78	273.2	1	488-875
1749	PH	PH domain	2.2e-09	44.6	1	52-146
1750	lactamase B	Metallo-beta-lactamase superfamily	4.1	-28.9	1	1-153
1751	lipoxygen ase	Lipoxygenase	9.5e- 133	454.4	1	126-703
1751	PLAT	PLAT/LH2 domain	1.6e-33	124.8	1	2-116
1753	Rho_GDI	RHO protein GDP dissociation	3.2e-	389.5	1	1-187
1755	10.0_02	inhibitor	113			
1756	GRAM	GRAM domain	7.5e-17	69.4	1	110-177
1757	homeobox	Homeobox domain	3.6e-29	110.3	1	21-77
1758	lipocalin	Lipocalin / cytosolic fatty-acid binding	1.1e-24	95.4	1	38-168
1759	ig	Immunoglobulin domain	3.1e-13	57.4	2	35- 112:160- 234
1761	oxidored_	NADH-Ubiquinone/plastoquinone (complex I)	0.078	-128.7	1	16-259
1761	DUF250	Domain of unknown function, DUF250	0.45	-85.1	1"	162-337
1761	DUF6	Integral membrane protein DUF6	2.5	-14.8	1	192-328
1761	secY	eubacterial secY protein	7.2	-246.6	1	36-243
1761	FecCD	FecCD transport family	9.8	-221.2	1	120-328
1762	Keratin_B	Keratin, high sulfur B2 protein	3.3e-07	32.9	2	11- 113:114- 204
1763	sugar_tr	Sugar (and other) transporter	0.018	-119.2	1	43-449
1763	oxidored_	NADH-Ubiquinone/plastoquinone (complex I)	4.7	-165.1	1	146-442
1765	q1 VPS9	Vacuolar sorting protein 9 (VPS9) domain	4.5e-33	123.3	1	380-484
1765	RA	Ras association (RalGDS/AF-6)	0.73	-5.9	1	518-607

SEQ ID	Model	Description	E-value	Score	Repeats	Doniss
1766	SSF	Sodium:solute symporter family	5.9e-	697.6	1	Position 106-535
			206	077.0	'	100-333
1766	oxidored_	NADH-Ubiquinone/plastoquinone	4.8	-165.2	<del> </del>	216-521
<u></u>	q1	(complex I)			-	210-321
1766	MIP	Major intrinsic protein	5.8	-121.9	1	112-364
1766	DsbD	Cytochrome C biogenesis protein	8.6	-97.3	1	195-425
1505	<del> </del>	transmemb				
1767	Peptidase	Peptidase family M3	1.3e-	689.8	1	251-701
1768	M3	COMP	203			1
1768	RasGAP PH	GTPase-activator protein for Ras-like	1.3e-26	101.9	1	449-621
1768	C2	PH domain	0.012	22.2	1	112-236
1768	Tymo_45	C2 domain	2.6	-10.9	1	249-332
1708	kd 70kd	Tymovirus 45/70Kd protein	4.2	-293.9	1	561-979
1768	RNA pol	DNA-dependent RNA polymerase	+		ļ	
1768	PHD	PHD-finger	5.1	-234.7	1	381-1225
1770	rrm	RNA recognition motif.	6.9	-17.6	1	214-273
		14 77 1000gintion motif.	0.48	5.6	2	238-
	,		1	1		323:352-
1772	zf-C2H2	Zinc finger, C2H2 type	1.6e-87	304.2	13	422
	1	\$-, \$p	1.00-07	304.2	13	49-71:197- 219:225-
						247:253-
						275:281-
		,		ł		303:309-
		i .				331:337-
			1			359:365-
						387:393-
	1				,	415:421-
		·				443:449-
		·				471:477-
				ľ		499:505-
1772	zf-BED	BED zinc finger	8.9	<del></del>	<del></del>	527
1773	ATP-	ATP synthase subunit C	5.4e-08	-6.9 40.0	1	490-528
_	synt C	Symmass Sastaint C	3.46-00	40.0	1	62-127
1774	zf-B_box	B-box zinc finger	7.2e-14	59.5	1	00 121
1774	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.6e-10	48.4	1	90-131 15-58
1774	PHD	PHD-finger	1.1	-10.3	i	14-61
1774	zf-AN1	AN1-like Zinc finger	1.4	-3.2	1	15-53
1774	zf-UBR1	Putative zinc finger in N-recognin	7.6	-23.6	î	93-146
1775	FH2	Formin Homology 2 Domain	5.4e-50	179.5	ī	21-455
1775	WH2	WH2 motif	0.0058	23.3	1	441-456
1777	PHD	PHD-finger	8.7	-18.6	1	493-522
1779	Branch	Core-2/I-Branching enzyme	3.9e-05	-52.8	1	175-516
1780	TFIIS	Transcription factor S-II (TFIIS)	3.9	-3.7	1	295-344
1781	SH3	SH3 domain	1.3e-13	58.6	1	454-508
1782	filament	Intermediate filament protein	3.9	-200.0	1	134-406
1783	SET	SET domain	2e-53	190.9	1	3878-4006
1783	PHD	PHD-finger	4.7e-28	106.6	3	20-71:72-
			. [		j	118:147-
1702	TD/C 1	In (O () i	1	[		200
1783	HMG_bo	HMG (high mobility group) box	0.0047	12.3	1	710-773
1702	X DC1	POI I				
1783	DC1	DC1 domain	8.5	1.7	3	19-50:69-
1784	at DUITO	DIHIC -t- C				98:146-176
1785	zf-DHHC	DHHC zinc finger domain		97.7	1	90-154
1703	zf-C2H2	Zinc finger, C2H2 type	9.3e-14	59.1		18-40:64-
			•			86:92-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						115:178- 200
<u> </u>			100 10	72.6	1	438-672
1788	ion trans	Ion transport protein	8.3e-18	34.8	2	77-
1788	ank	Ankyrin repeat	1.9e-06	34.0	4	108:163-
						195
1788	Srg	C.elegans Srg family integral	8.1	-222.4	1	418-669
1/00	Sig	membrane prot	5			1
1791	ubiquitin	Ubiquitin family	0.0036	24.0	1	124-195
1792	Gag_p10	Retroviral GAG p10 protein	4e-23	90.2	1	1-89
1798	Ribosoma	Ribosomal protein S12	0.003	-14.2	1	7-66
	I_S12	-			ļ	
1799	efhand	EF hand	1.1c-07	39.0	3	281-
	İ					309:318- 346:353-
•						340:333-
		A 14 C	0.0001	26.8	1	18-203
1799	Acyltransf	Acyltransferase	0.0001	20.6	1	16-203
1801	zf-C2H2	Zinc finger, C2H2 type	3.2e-79	276.6	12	160-
1001	21-02112	Zino migor, CZ112 typo	0			182:188-
•			- 1			210:216-
	İ				1	238:244-
	<u> </u>			1		266:272-
				,		294:300-
						322:355-
			ľ			377:431-
			]	]		453:459-
		•				481:487-
					ŀ	509:515-
			j			537:543- 565
1001	<del>                                     </del>	I IN A domestic	4.7	-17.4	1	433-487
1801	LIM	LIM domain	1.4e-25	98.4	1	143-250
1802	lectin_c	Lectin C-type domain Lectin C-type domain	1.4e-25	98.4	1	143-250
1802 1804	lectin_c efhand	EF hand	2.5e-08	41.1	2	16-44:56-
1004	Ciliand	151 manu	2.55	1	]	82
1806	LRR	Leucine Rich Repeat	1.5e-07	38.5	5	130-
1000					1	151:152-
			ŀ			173:174-
			.		į.	195:196-
			İ	1	1	217:221-
				<u> </u>	<u> </u>	243
1807	COX3	Cytochrome c oxidase subunit III	3.5	-233.2	1	51-219
1807	CbiM	CbiM	9.2	-93.3	1	114-249
1807	oxidored_	NADH-ubiquinone oxidoreductase	9.8	-59.5	1	89-169
1865	q5_N	chain 4	6.6	-108.5	1	39-282
1808	Sulfotrans	Sulfotransferase protein	0.0	-108.3	1	33-202
1017	fer	Calcineurin-like phosphoesterase	0.23	14.3	<del>                                     </del>	36-241
1814	Metalloph os	Calcineurin-like phosphoesierase	0.23	5	1	55 2.1
1815	rrm	RNA recognition motif.	0.67	4.1	1	201-269
1816	filament	Intermediate filament protein	1.5	-188.9	1	1-253
1817	MAGE	MAGE family	4.2e-17	70.3	2	14-
1017	1,11,00					613:655-
						867
1817	Atrophin-	Atrophin-1 family	9.5	-684.8	1	4-783
	1			<u> </u>		
1818	Tropomod	Tropomodulin	8.1	-168.0	1	362-653

SEQ ID	Model	Description	E-value	Score	Repeats	Position
1010	ulin					
1819	Hydrolase	haloacid dehalogenase-like hydrolase	3.4e-21	83.8	1	28-282
1820	Fe_hyd_l g_C	Iron only hydrogenase large subunit, C-te	1.3e-92	321.1	.1	204-516
1820	Fe_hyd_S SU	Iron hydrogenase small subunit	8.3	-13.1	1	529-576
1821	filament	Intermediate filament protein	1e-143	490.8	†1	55-366
1822	Keratin_B 2	Keratin, high sulfur B2 protein	0.082	-51.3	1	12-174
1824	metalthio	Metallothionein	5.7e-17	69.8	1	48-108
1824	AFP	Insect antifreeze protein	2.6	14.5	1	61-72
1825	C2	C2 domain	4.7e-53	189.7	2	373- 462:528- 617
1825	RPH3A_e ffector	Rabphilin-3A effector domain	0.035	-127.1	1	1-237
1825	zf-MIZ	MIZ zinc finger	0.4	-10.5	1	80-111
1825	PHD	PHD-finger	0.97	-9.7	i	62-108
1825	LIM	LIM domain	2.2	-14.6	1	80-128
1825	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1	-4.0	1	63-105
1828	efhand	EF hand	8.4e-08	39.4	3	106- 134:142- 170:407- 435
1829	60s_ribos omal	60s Acidic ribosomal protein	7.4	-38.2	1	163-291
1831	Tektin	Tektin family	1.6	-227.3	1	1-150
1833	EGF	EGF-like domain	1.1e-32	122.0	5	26-54:57-
1833	laminin_E	Lawlei- FOR III CO.				85:92- 124:156- 187:194- 226
	GF	Laminin EGF-like (Domains III and V)	1.6	-5.9	1	29-63
1833	Bowman- Birk_leg	Bowman-Birk serine protease inhibitor	4.8	-16.7	1	37-85
1833	metalthio	Metallothionein	5.5	-10.1	1	59-117
1834	7tm_1	7 transmembrane receptor (rhodopsin family)	4.8e-05	-0.8	1	31-273
1834	7tm_2	7 transmembrane receptor (Secretin family)	5.5	-151.6	1	9-248
1835	rrm	RNA recognition motif.	0.05	15.7	1	75-141
1835	Met_10	Met-10+ like-protein	0.065	-100.4	ì	333-583
1835	UPF0020	Putative RNA methylase family UPF0020	0.073	-53.8	1	410-566
1835	PCMT	Protein-L-isoaspartate(D-aspartate) O-	0.2	-114.1	ī	391-543
1835	Methyltra nsf_4	Putative methyltransferase	2.1	-82.0	1	424-566
1835	notch	Notch (DSL) domain	6.1	-10.5	1	233-271
1836	Kelch	Kelch motif	3e-33	123.9	4	242- 288:290- 331:333- 378:380- 435
1836	BTB	BTB/POZ domain	2.3	-15.2	ī	1-129
1837	tsp_1	Thrombospondin type 1 domain	0.0014	23.3	5	139- 196:203- 256:257-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
•			·			313:320-
	<b>.</b>			. :		370:374-
				10.5		432
1837	EB	EB module	6.4	-10.5	1	330-399
1838	adh_zinc	Zinc-binding dehydrogenase	7.3e-55	195.7	1	44-369
1838	Lipase_G DSL	Lipase/Acylhydrolase with GDSL-like motif	5.5	-20.4	1	103-189
1839	pkinase	Protein kinase domain	2.4e-05	-58.0	1	81-333
1841	zf-C2H2	Zinc finger, C2H2 type	4.4e-30	113.4	7	141-
·.	1				•	163:169-
						191:197-
			N			219:225-
						247:350-
						372:378-
						400:406-
1041	777 4 5	TEN A D I	51-22	90.0	1	434 44-84
1841	KRAB	KRAB box	5.1e-23	89.9	1	144-179
1841	TFIIS	Transcription factor S-II (TFIIS)  Lentiviral Tat protein	4.9	-1.9 -23.0	1	35-125
1841	Lentiviral	Lenuvirai Tat protein	+.7	-23.0	1	33-143
1841	_Tat zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.2	-7.1	1	352-411
1841	rubredoxi	Rubredoxin	7.4	-11.1	1	403-433
	n					•.
1842	E2F_TDP	Transcription factor E2F/dimerisation partne	1.5	-95.1	1	18-229
1843	V_ATPas e sub a	V-type ATPase 116kDa subunit family	0	1258.7	1	26-831
1843	UCR_14k	Ubiquinol-cytochrome C reductase compl	3.2	-40.4	1	6-112
1843	FliP	FliP family	4.8	-148.9	1	533-661
1843	PsbH	Photosystem II 10 kDa phosphoprotein	7.1	5.1	1	751-803
1844	aa_perme	Amino acid permease	5.6e-08	-125.3	1	28-529
	ases	•				
1844	Aa_trans	Transmembrane amino acid transporter pro	0.71	-178.9	1	30-408
1844	BPD_tran sp_2	Branched-chain amino acid transport syst	3.3	-116.9	1	175-440
1844	MVIN	Virulence factor MVIN	3.5	-240.9	1	87-515
1844	FecCD	FecCD transport family	5.3	-216.0	i	311-521
1844	ion trans	Ion transport protein	6.2	-11.7	1	288-495
1844	7tm_5	7TM chemoreceptor	7.1	-168.6	1	238-498
1848	sugar_tr	Sugar (and other) transporter	0.0072	-107.9	1	12-407
1848	xan_ur_pe	Permease family	5.6	-196.7	1	38-359
1848	rmease FecCD	FecCD transport family	6.3	-217.4	1	56-287
1848	Nucleosid	Nucleoside transporter	8.1	-162.4	1	82-365
20.10	e tran					
1848	PUCC	PUCC protein	9.8	-283.2	1	51-403
1849	Filamin	Filamin/ABP280 repeat	2.3e-20	81.1	1	396-494
1849	zf-B_box	B-box zinc finger	9.3e-11	49.2	2	130- 176:186- 227
1849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0016	24.4	1	29-62
1853	ank	Ankyrin repeat	1.1e-98	341.3	10	485-
-000						517:518-
						550:551-
						583:584-
	İ				į	616:617-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
						650:651-
	1 .					683:684-
	1			1		716:717-
	1			1		749:750-
	1		-			780:782-
1853	pkinase	D. A. C. L.				814
1854		Protein kinase domain	1.6e-50	181.3	1	22-286
1855	ras Acyltransf	Ras family Acyltransferase	1.4e-13	17.8	1	5-194
1033	erase	Acytransierase	3e-34	127.2	1	92-289
1856	wap	WAP-type (Whey Acidic Protein)	0.0005	100		ļ
		'four-disulfi	0.0025	18.7	1	31-72
1857	arf	ADP-ribosylation factor family	2.5e-11	24.6	<del>                                     </del>	7-193
1857	GTP EFT	Elongation factor Tu GTP binding	1.6	-82.5	1	+
	ับ	domain	1.0	-02.5	1	19-198
1858	zf-C2H2	Zinc finger, C2H2 type	2.1e-09	44.7	5	82-
				''''		104:110-
					j	132:138-
	1					161:364-
						386:392-
1050	77770					416
1858 1859	PHD	PHD-finger	7.7	-18.1	1	365-400
1009	zf-C2H2	Zinc finger, C2H2 type	7.2e-20	79.4	4	119-
	I	·				141:147-
	* .	•		1 .		169:175-
					•	198:214-
1860	ВТВ	BTB/POZ domain	1.7- 20	111.4		237
1860	zf-C2H2	Zinc finger, C2H2 type	1.7e-29 5.1e-14	60.0	3	22-126
	]		3.16-14	00.0	3	373-
						395:401- 423:429-
						423:429-
1860	K_tetra	K+ channel tetramerisation domain	0.44	-30.2	1	34-124
1860	zf-BED	BED zinc finger	8.9	-6.9	1	363-396
1861	SNF2 N	SNF2 and others N-terminal domain	2.1e-72	254.0	1	137-473
1861	helicase_	Helicase conserved C-terminal domain	1.4e-24	95.1	1	559-632
10(1	C					· · · ·
1861 1861	DEAD SEC-C	DEAD/DEAH box helicase	0.26	-59.6	1	124-337
1862		SEC-C motif	0.43	13.8	1	426-446
1862	ras arf	Ras family	2.4e-69	243.8	1	19-217
1864	rrm	ADP-ribosylation factor family	4.1e-05	-53.5	1	1-182
1867	T-box	RNA recognition motif. T-box	0.053	15.4	1	129-191
1870	F-box	F-box domain	4.3e-09	29.9	1	1-92
1871	PH	PH domain	1.8	15.0	1	124-171
1872	isodh	Isocitrate/isopropylmalate	1.1e-13	58.9	1	170-273
		dehydrogenase	1.4e- 123	423.9	1	10-383
1873	ank	Ankyrin repeat	1.8e-08	41.5		20.51.55
			1.06-00	41.5	2	39-71:72-
1874	ank	Ankyrin repeat	1.8e-08	41.5	2	104
			1.00-00	L.17	_	67-99:100-
1875	PAP2	PAP2 superfamily	0.0034	13.0	1	132
1876		Protein of unknown function DUF51	5.7e-13		1	107-261
1877		Zinc finger, C2H2 type	1.5e-72			285-
		2.				307:313-
				1		335:341-
	1					363:369-
						391:397-

SEQ ID	Model	Description	E-value	Score	Repeats	Position
			• .			419:425-
				- 1	]	447:451-
		•				473:479-
	·				ļ	501:507-
						529
1877	KRAB	KRAB box	2.7e-21	84.2	1	49-89
877	zf-BED	BED zinc finger	0.74	2.7	1	344-392
1877	TFIIS	Transcription factor S-II (TFIIS)	1.5	-0.0	1	369-407
1877	GATA	GATA zinc finger	2.1	-7.1	1	477-524
877	LIM	LIM domain	2.5	-15.1	1	371-435
1877	E6	Early Protein (E6)	5.7	-66.7	1	315-402
1878	AAA	ATPase family associated with various	1.3e-62	221.4	1	217-409
1878	Sigma54	Sigma-54 interaction domain	4.6	-165.4	1	184-365
1070	activat	Digina 5 ( interpolation domain				
1879	SSF	Sodium:solute symporter family	4.8e-	578.3	1	58-460
			170			
1880	SSF	Sodium:solute symporter family	1.3e-	673.2	1	58-487
			198			
1881	perilipin	Perilipin family	6.7e-53	189.2	1	12-369
1882	aminotran	Aminotransferase class I and II	7.5e-07	25.0	1	165-515
	_1_2				1	
1883	DSPc	Dual specificity phosphatase, catalytic	2.5e-30	114.2	1	54-199
	<u> </u>	doma			<u> </u>	-
1884	ig	Immunoglobulin domain	7.2e-14	59.5	2	34-
		•		]	1	111:155-
			4 6 10	(0.2		229
1885	MCM	MCM2/3/5 family	4.6e-12	-67.3	6	106-391
1886	Kelch	Kelch motif	1.8e-63	224.3	0	262-
			1			306:309-
						356:358- 403:405-
				İ		453:455-
					Į	495:497-
				]	ļ	544
1006	D	DWD MOZ I	5 20 22	119.7	1	26-134
1886	BTB	BTB/POZ domain	5.3e-32 1.9e-05	31.5	1	726-765
1887	UBA	UBA/TS-N domain	<del></del>		1	1342-140
1887	rrm	RNA recognition motif.	0.00026	27.8	1	270-571
1887	MARCKS	MARCKS family	4.3	-90.8		726-765
1888	UBA	UBA/TS-N domain	1.9e-05	31.5	1	
1888	rrm	RNA recognition motif.	0.00026	27.8	1	1303-136
1888	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	UBA	UBA/TS-N domain	1.9e-05	31.5	1	726-765
1889	rrm	RNA recognition motif.	0.00026	27.8	1	1245-131
1889	MARCKS	MARCKS family	4.3	-90.8	1	270-571
1889	Atrophin-	Atrophin-1 family	6.9	-676.1	1	237-986
1000	I TY TY	Sadium /hadas and and a Cartin	2 45 10	74.4	<del> </del>	119-520
1890	Na_H_Ex	Sodium/hydrogen exchanger family	2.4e-18	74.4	1 *	119-520
	changer	<u> </u>	-	12.6	<del>                                     </del>	270-384
1890	Na_Ca_E	Sodium/calcium exchanger protein	3.1	-43.6	1	2/0-364
1000	7tm_5	7TM chamoracantar	3.8	-163.7	1	259-503
1890		7TM chemoreceptor		-25.8	1	309-401
1890	Abi	CAAX amino terminal protease family	5.9		+	251-502
1890	oxidored_	NADH-Ubiquinone/plastoquinone	7.9	-169.7	1	251-302
1001	q1	Cytosolic long-chain acyl-CoA thioeste	8 00 70	251.9	2	26-
1891	Acyl-	Cytosonic long-chain acyl-CoA infoeste	8.9e-72	231.7	*	168:200-
	CoA_hydr					336
	0					

SEQ ID	Model	Description	E-value	Score	Repeats	Position
	i .				1	
1892	zf-DHHC	DHHC zinc finger domain	8.6e-18	72.5	1	145-207
1894	SPRY	SPRY domain	4.5e-11	50.2	1	353-474
1894	fn3	Fibronectin type III domain	0.054	17.6	1	165-258
1895	dsrm	Double-stranded RNA binding motif	1.5e-12	55.1	.2	229- 293:337- 401
1895	i ww	WW domain	0.00016	28.5	1	20-49
1896	SPRY	SPRY domain	9.9e-26	98.9	1	186-301

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PDB annotation		SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN	SIGNALING PROTEIN CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND, EH DOMAIN, SIGNALING PROTEIN		CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEINPEPTIDE)
Coumpound		EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	EPS15; CHAIN: NULL;	EPS15; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL	D score								
PMF	score	1.00	0.88	0.22	1.00	66.0	86.0	0.23	0.15
Verify	score	0.77	-0.14	-0.02	0.58	0.72	0.33	-0.21	-0.39
Psi Blast		5.7e-21	1.7e-07	3.8e-05	1.1e-31	6.8e-11	1.3e-05	1.5e-05	3.8e-05
END	AA	369.	86	345	369	24	348	345	345
STAR	TAA	279	4	293	278	m	280	284	293
CHAI	A E	<b>∢</b>	Ą					∢	4
PDB	a	1c07	1c07	lcll	leh2	1eh2	1rro	ltrc	lvrk
SEQ	ВÖ	951	951	951	951	951	951	951	951

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PDB annotation	METAL BINDING PROTEIN CALCILIM BINDING PROTEIN		CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCITM RINDING	HYDROLASE CALCINEURIN:	HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	MUSCLE PROTEIN MDE; MUSCLE	PROTEIN	CALCIUM BINDING CALCIUM BINDING	SIGNALING PROTEIN CALCIUM	BINDING, SIGNALING DOMAIN, NPF BINDING FW BINDING 2 FE HAND	EH DOMAIN, SIGNALING PROTEIN	SIGNALING PROTEIN CALCIUM	BINDING, SIGNALING DOMAIN, NPF BINDING, FW BINDING, 2 EF-HAND,	EH DOMAIN, SIGNALING PROTEIN			STRUCTURAL PROTEIN HELIX-	CALCIUM BINIVING EH2,	EPIDERMAI, GROWTH FACTOR
Coumpound	PARVALBUMIN; CHAIN: A;	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	PARVALBUMIN; CHAIN: A, B	TROPONIN C; CHAIN: NULL;	SERINE/THREONINE	PHOSPHATASE 2B; CHAIN: A, B;	MYOSIN; CHAIN: A, B, C, D, E,	r, c, H;	CALCIUM-BINDING PROTEIN; CHAIN: NULL;	EPIDERMAL GROWTH FACTOR	RECEPTOR PATHWAY CHAIN: A:		EPIDERMAL GROWTH FACTOR	RECEPTOR PATHWAY CHAIN: A;	CALCITIM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	1CLL 3	CARDIAC TROPONIN C;	EPS15; CHAIN: NULL;	
SEQFOL D score																				
PMF score	0.25	0.47	0.05	0.17	0.13		0.18		0.05	1.00			0.00		0.22			0.18	1.00	
Verify score	-0.13	-0.13	-0.81	0.02	-0.03		-0.05		-0.24	0.77			0.10		-0.02			-0.16	0.58	
Psi Blast	3.8e-05	5.7e-06	0.00095	5.7e-05	0.00038		0.0019	0000	0.0038	5.7e-21			5.1e-12	, 4,	3.8e-05			0.0038	1.1e-31	-
END	348	345	389	377	377		377	000	389	369			66		345			389	369	
STAR T AA	293	283	310	280	280		282	0.0	310	279			4		293			280	278	
CHAI N ID	А	Ą	¥.		В		<u>—</u>			<			┫					∢		
PDB UD	2pvb	2scp	la75	1aj4	1ani		1br1	,		1c07		_	ੇ ਤੋਂ		Icli		1	Ħ Ħ	1eh2	
SEQ EQ	951	951	952	952	952		952	220	725	952			706		952			352	952	

PDB annotation		RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF BINDING, EF-HAND, EH 2 DOMAIN	CALCIUM BINDING EH2, EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CALCIUM BINDING, SIGNALING DOMAIN, NPF	BINDING, EF-HAND, EH 2 DOMAIN GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	METAL BINDING PROTEIN CALCIUM BINDING PROTEIN		
Coumpound		,	EPS15; CHAIN: NULL;	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	CALCIUM-BINDING PROTEIN RAT ONCOMODULIN IRRO 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	CALMODULIN; CHAIN; A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	PARVALBUMIN; CHAIN: A;	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	
SEQFOL	D score										
PMF	score		66.0	0.80	0.98	0.23	0.49	0.15	0.25	0.47	
Verify	score		0.81	0.64	0.33	-0.21	-0.23	-0.39	-0.13	-0.13	
Psi Blast			1.7e-13	1.7e-08	1.3e-05	1.5e-05	0.00038	3.8e-05	3.8e-05	5.7e-06	
END	AA		76	97	348	345	377	345	348	345	
STAR	T AA		3	14	280	284	280	293	293	283	
CHAI	QIN			¥.		¥	Ą	<	¥.	A	
PDB	<b>a</b>		1eh2	1qjt	Irro	1trc	lvrk	Ivrk	2pvb	2scp	
SEO	βġ	į	952	952	952	952	952	952	952	952	

PDB   CBA   STAR   Ext)   Fel Blast   Vortify   Fortify   Store   Store   District   Coumpound   PDB annotation	سنسم	<del></del>	<u> </u>				1
EQ         PDB         CHAI         STAR         END         PSi Blast         Verify         PMF         SEQFOL           3.         1a09         A         319         413         3.8e-17         0.34         0.98         D score           3.         1ab1         A         255         413         1.5e-18         0.27         0.72         0.72           3.         1ab2         319         417         3.8e-17         0.02         0.63         0.63           4.         1aot         F         319         413         1.7e-17         0.46         0.99         1.00           1aya         A         317         412         7.6e-18         0.18         1.00         1.00           1bfi         319         418         3.8e-19         0.36         0.82         1.00	PD B annotation	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK,	KINASE, SH2 DOMAIN, ITAM	COMPLEX (PROTO- ONCOGENE/BARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/BARLY	PROTEIN)	SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2
EQ         PDB         CHAI         STAR         END         Psi Blast         Verify         PMF         SEOPE           3.         1a09         A         319         413         3.8e-17         0.34         0.98           3.         1ab1         A         255         413         1.5e-18         0.27         0.72           3.         1ab2         319         417         3.8e-17         0.02         0.63           4.         1aot         F         319         413         1.7e-17         0.46         0.99           4.         317         412         7.6e-18         0.18         1.00           4.         319         418         3.8e-19         0.36         0.82	Coumpound	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C,	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN: B, D, F, H, J, L;	TRANSFERASE(PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (B.C.2.7.1.112) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4	(NMK, 20 STRUCTURES) 1AB2 5 FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	HYDROLASE(SHZ DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SHZ DOMAIN) 1AYA 3 (PTP1D, SHPTPZ) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4	P85 ALPHA; CHAIN: NULL;
EQ         PDB         CHAI         STAR         END         Psi Blast         Verify Score           3         1a09         A         319         413         3.8e-17         0.34         0           3         1a81         A         255         413         1.5e-18         0.27         0           3         1ab2         319         417         3.8e-17         0.02         0           1aot         F         319         413         1.7e-17         0.46         0           1aya         A         317         412         7.6e-18         0.18         1.0           1bf         319         418         3.8e-19         0.36         0.8	SEQFOL D score						
EQ         PDB         CHAI         STAR         END         Psi Blast         Verify           3         1a09         A         319         413         3.8e-17         0.34           3         1a81         A         255         413         1.5e-18         0.27           3         1ab2         319         417         3.8e-17         0.02           1         1aot         F         319         413         1.7e-17         0.46           1aya         A         317         412         7.6e-18         0.18           1bfi         319         418         3.8e-19         0.36	PMF score	0.98	0.72	0.63	0.99	1.00	0.82
EQ         PDB         CHAI         STAR         END         PSi Blast           3         1a09         A         319         413         3.8e-17           3         1ab2         A         255         413         1.5e-18           1ab2         319         417         3.8e-17           1aot         F         319         413         1.7e-17           1aya         A         317         412         7.6e-18           1bfi         319         418         3.8e-19	Verify score	0.34	0.27	0.02	0.46	0.18	
EQ         PDB         CHAI         STAR         END           3         1a09         A         319         413           3         1a81         A         255         413           3         1ab2         319         417           4         1aot         F         319         412           1aya         A         317         418           1bfi         319         418	Psi Blast	3.8e-17	1.5e-18	3.8e-17			
EQ PDB CHAI STAR  O: ID NID TAA  3 1a09 A 319  3 1a81 A 255  3 1ab2 319  1 aot F 319  1 aba A 317	END	413	413	417	413	412	418
EQ PDB CHAI O:	STAR T AA	319	255	319	319	317	
EQ PDB O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID O: ID	CHAI N ID	<	4		Ľ.		
	PDB U	1a09	1a81	1ab2		a a	1b£i
	SEQ NO.	953	953	953	953		

PDB annotation	DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)	STRUCTURAL PROJEIN 1 WO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	GENE REGULATION SH2 DOMAINS	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES	
Coumpound		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	ALPHA SPECTRIN; CHAIN: A, B, C;	SAP SH2 DOMAIN; CHAIN: A, B, C, D;	T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C- TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029: ASP- ASN-ASP-PTYR-ILE-ILE- 2PLD 6
SEQFOL D score						58.62	
PMF		0.82	90.0	0.49	0.75		0.49
Verify		0.33	0.05	0.04	0.22		0.32
Psi Blast		3.8e-19	0.00013	5.7e-18	1.9e-19	0.0017	9.56-19
END		416	228	413	413	425	417
STAR T		319	140	320	319	312	319
CHAI N ID		<b>∀</b>	¥	В	A		∢
PDB		1csy	lcun	1d1z	1d4t	1 ffns	2pld
SEQ ID	:ÖZ	953	953	953	953	953	953

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PD B annotation			COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	COMPLEX (TRANSFERASE/PEPTIDE) ITAM PEPTIDE; COMPLEX (TRANSFERASE/PEPTIDE), SYK,	KINASE, SHZ DOMAIN, ITAM	COMPLEX (PROTO-ONCOGENEZARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION, PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENEZARLY PROTEIN)	
Coumpound	PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C,	SYK KINASE; CHAIN: A, C, E, G, I, K; T-CELL SURFAGE GLYCOPROTEIN CD3 EPSILON CHAIN; CHAIN; B, D, F, H, J, L;	TRANSFERASE(PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR. 20 STR IUCTI IRFS) 1AR2 5	FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P	HYDROLASE(SH2 DOMAIN) TYROSINE PHOSPHATASE SYP (N-TERMINAL SH2 DOMAIN) 1AYA 3 (PTP1D, SHPTP2) (E.C.3.1.3.48) COMPLEXED WITH THE PEPTIDE 1AYA 4
SEQFOL D score							
PMF score			86.0	0.72	0.63	0.99	1.00
Verify score			0.34	0.27	0.02	0.46	0.18
Psi Blast			3.8e-17	1.5e-18	3.8e-17	1.7e-17	7.6e-18
END			440	440	444	440	439
STAR T AA			346	282	346	346	344
CHAI N ID			∢	¥	·	ц	4
EDB ID			1a09	1a81	1ab2	laot	laya
SEQ ID NO:			954	954	954	954	954

PDB annotation		SH2 DOMAIN PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY ALPHA SH2 DOMAIN, P85ALPHA, PI 3-KINASE, NMR, C TERMINAL SH2 2 DOMAIN	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SHZ DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)	GENE REGULATION SH2 DOMAINS	SIGNALING PROTEIN SLAM; SH2 DOMAIN, TYROSINE KINASE, SIGNAL TRANSDUCTION, PEPTIDE 2 RECOGNITION	
Coumpound	PDGFR-1009 1AYA 5	P85 ALPHA; CHAIN: NULL;	SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	SAP SH2 DOMAIN; CHAIN: A, B, C, D;	T CELL SIGNAL TRANSDUCTION MOLECULE SAP; CHAIN: A; SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE; CHAIN: B;	PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA-1 (E.C.3.1.4.11) (C- TERMINAL SH2 2PLD 3 DOMAIN COMPRISING RESIDUES 663 - 759) COMPLEXED WITH A 2PLD 4 PHOSPHOPEPTIDE FROM THE PLATELET-DERIVED GROWTH FACTOR 2PLD 5 RECEPTOR (RESIDUES 1018 - 1029: ASP- ASN-ASP-PTYR-ILE-ILE- 2PLD 6 PRO-LEU-PRO-ASP-PRO-LYS) (NMR, MINIMIZED AVERAGE STRUCTURE) 2PLD 7
SEQFOL D score						
PMF score		0.82	0.82	0.49	0.75	0.49
Verify score		0.36	0.33	0.04	0.22	0.32
Psi Blast		3.8e-19	3.8e-19	5.7e-18	1.9e-19	9.5e-19
END		445	443	440	440	444
STAR T AA		346	346	347	346	346
CHAI N ID			4	В	A	4
PDB ID		1bfi	lcsy	1d1z	1d4t	2pld
SEQ ID	NO:	954	954	954	954	954

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PDE annotation	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE I:XCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING FROTEIN HEADER	TER GUANINE NUCLEOTIDE EXCHANGE FACTOR RCCI; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER		AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS	CAMPESIRIS HYDROLASE TILACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONAIJACFAF	OXYANION, CIS-PEPTIDE, HYDROLASE	HYDROLASE ALPHA/BETA	LIPASE LIPASE, ULYCOPROTEIN LIPASE LIPASE, LIPASE, HYDROLASE	PSEUDOMONAI) ACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE	ANALOGOE, ENAMINOSELECTIVII Y	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION
Coumpound	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;		PALMITOYL PROTEIN THIOESTERASE 1: CHAIN: 4:	TRIACYL-GLYCEROL- HYDROLASE; CHAIN: D. E.			UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;
SEQFOL D score	150.38										
PMF score		1.00		0.05	0.49		0.57	0.23			1.00
Verify score		0.69		-0.16	-0.67		0.14	-0.60			0.57
Psi Blast	1.7e-77	1.7e-77		0.0076	0.00038		7.6e-05	0.0048			3.8e-38
END	427	423		183	204		204	204			121
STAR T AA	35	51		82	991		86	165			2
CHAI	∢	∢		∢			∢	Ω			<b>√</b>
PDB CI	1a12	1a12		MZe	1cvl	_		4lip		$\dashv$	ıayz
SEQ D	955	955	1,00	3	957	250	/6%	957		+	705

PDB annotation	UBIQUITIN-CONJUGATING ENZYME	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	UBIQUITIN CONJUGATION UBCI; UBIQUITIN CONJUGATION, LIGASE	UBIQUITIN CONJUGATION UBCI; UBIQUITIN CONJUGATION, LIGASE	TELOT HERE! CONTINGATION LIBCO.	UBIQUITIN CONJUGATION OBCZ, UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME		UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST	LIGASE UBIQUITIN, UBIQUITIN-
Coumpound		UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C,	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	CA CASA	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING
SEQFOL D score		124.83			70.02		141.95				162.79		102.58
PMF score			1.00	1.00		1.00			1.00	1.00		1.00	
Verify score			0.63	0.62		0.59			1.15	0.91		0.63	
Psi Blast		3.8e-38	5.1e-37	3.4e-40	3.4e-40	3.4e-37	3.4e-37		1.5e-46	1.9e-48	1.9e-48	1.5e-50	1.5e-50
END		121	121	119	120	119	120		136	136	136	134	135
STAR T AA		2	2	-	E.		1		7	7	2	-	3
CHAI N ID			4	A	A				V	¥.	4	A	A
PDB ID		layz	layz	1qcq	1qcq	2aak	2aak		layz	layz	layz	1qcq	lqcq
SEQ	Ö	962	362	962	962	962	962		963	963	963	963	963

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PD'B annotation		CONJUGATING ENZYME, YEAST	UBIOLITIN CONJUGATION UBCI;	UBIQUITIN CONJUGATION UBC1; UBIOUITIN CONJIGATION LIGASE		MOTOR PROTIZIN MOTOR PROTEIN, ATPASE, MICROTUBULE	MOTOR PROTEIN SOUTH	ATPASE, MICROTUBULE	ASSOCIATED	CI APET SECRED TO THE	PROTEIN: NCT CBYSTAI	STRIICTURE MICROTURE	MOTOR VINERAL SIBERTANII	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN NCD	CLARET SEGRISGATIONAL	PROTEIN: NCD CRYSTAL	STRUCTURE MICROTUBILE	MOTORS, KINESIN 2 SUPERFAMILY	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN NCD.	CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	STRUCTURE, MICROTUBULE	MOTORS, KINESIN 2 SUPERFAMILY,	CONTRACTILE PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	TRANSCRIPTION INHIBITOR BETA-
Coumpound	ENITYME: CHARLA	LIBIOLITINI COMILIO ATRIC	ENZYME; CHAIN; NULL:	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;		KINESIN; CHAIN: NULL;	KINESIN: CHAIN: NIII 1.	the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	MICBOTTIBLE MOTOR	PROTEIN NCD: CHAIN: A B C	D:				MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C,	ä				MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C,	'n				SYNTAXIN BINDING PROTEIN	I; CHAIN: A; SYNIAXIN IA; CHAIN: R.	TRANSCRIPTIONAL
SEQFOL D score				179.88		207.35									139.50									<del></del>				-	
PMF score		1 00	2			,	1.00		1 30	3											1.00	•				,	-0.18		0.98
Verify score		0.88					0.39		0.33	)								_			0.34					1	CI.0		0.54
Psl Blast		3.4e-48		3.4e-48		o o	0		1.7e-81						1.7e-98					,	1./e-98					1 30 15		_	1.7e-78
END		134		135		37.1	371		372						372						7/5					308	<del></del>		1643
STAR T AA		-				0	7		5																	647			1269
CHAI N ID									A						∢					-	ς .					4	—- 1		A
PDB ID		2aak		Zaak	2,1	7301	1bg2		lcz7				,		lcz/					1000						Idni	_		1erj
SEQ	ö	963	0,0	963	071	1/2	971		971						7.7					071	:					971			971

			•									<u> </u>					_	
PDB annotation		PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2	SIGNAL TRANSDUCTION	COMPLEX (GIP- BINDING/TRANSDUCER) BETA1,	GAMMA1, TRANSDUCIN GAMMA	SUBUNII; COMPLEX (GIF- BINDING/TRANSDUCER), G	PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1,	TRANSDUCIN BETA SUBUNIT;	GAMMAI, IKANSDOCIIN GAMMA SUBUNIT; COMPLEX (GTP-	BINDING/TRANSDUCER), G	PROTEIN, RETEROTIONSIGNAL TRANSDUCTION	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON	CONTRACTILE PROTEIN AMESIN, MICROTUBULE-BASED MOTOR,
Coumpound		REPRESSOR TUP1; CHAIN: A, B. C:	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-	BEIA; CHAIN: B; GI-GAMMA; CHAIN: G;			GT-ALPHA/GI-ALPHA CHIMERA: CHAIN: A: GT-	BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;			KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	TO TAKE	KINESIN MOTOR NCD; CHAIN: A;
SEQFOL	D score		115.67							<u> </u>				135.00				
PMF	score			-	1.00				1.00						1.00	0.99		1.00
Verify	score				0.88				0.42						0.09	-0.48		0.34
Psi Blast			1e-98		1e-98		J.,		3.4e-46					1.5e-71	1.5e-71	1.7e-36		le-81
END	<b>AA</b>		1600		1640				1660					260	281	380	3	370
STAR	T AA		1229		1317				1429					3	7	296	}	5
CHAI	N IS		В		В				В					A	A	ď	à	A
PINR	a		1got		1got				Igot					2kin	2kin	27:10	7 P	2ncd
SEO	ខ្លួ	SO.	971		97.1				971					126	971	120	1/2	116

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PDI3 annotation	NCD CONTRACTILE PROTEIN	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR,	CONTRACTILE PROTEIN	KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN ATPAST P.	LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN.	MOTOR 2 PROTEIN, ATPASE, P.	PROTEIN	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN, KAR3, KINESIN-RELA IED PROTEIN	MOTOR 2 PROTEIN, ATPASE, P-	LOOP, MICROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN,	MOTOR PROTEIN MOTOR PROTEIN,	CYLOSKELETON	GENE REGULATION POZ DOMAIN;	PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE PROMYPT OCYTIC
Coumpound		KINESIN MOTOR NCD; CHAIN: A;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NITT.	(770)		KINESIN-LIKE PROTEIN KAR3;	CITATIVI NOLLI,			KINESIN-LIKE PROTEIN KAR3;	CHAIN: NULL;			KINESIN HEAVY CHAIN; CHAIN: A B C D.	KINESIN HEAVY CHAIN;	CHAIN: A, B, C, D,	PROMYELOCYTIC LEUKEMIA	CHAIN: A;		
SEQFOL D score		132.55	165.99					. ,												
PMF score						1.00				1.00				90:	1.00		1.00			
Verify score			-			0.30				0.19				-0.23	-0.39		0.20		-	
Psi Blast		1e-81	1.9e-91			1e-83				1.9e-91		-		3.8e-35	6.8e-28		1.7e-20			
END		371	370			370				370				380	405		125			
STAR T AA		7 .	<b>&amp;</b>			<b>x</b> 0				,				867	298				-	
CHAI N ID		∢											(	ŋ	В		∢.			
PDB ID		Zucd	3kar		ī	экаг			31502	3Kar				3KIII	3kin		1buo			
SEQ NO:		97.	971			1/6			071	711				1/6	971.		975			

PDB annotation	LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	GENE REGULATION FOL DOMALY, PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION			MOTOR PROTEIN MOTOR PROTEIN,	ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE
Coumpound		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAN: A:		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	Variation, Out Ini. Mill 1.	KINESIN, CITAIN, INCLES,	KINESIN; CHAIN: NULL;	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;
SEQFOL D score				58.76				220.57		160.51
PMF		0.99			0.19	-0.02		-	1.00	
Verify score		0.41			0.10	0.03			0.74	
Psi Blast		3.8e-28		3.8e-28	0.0022	5.1e-10		6.8e-81	6.8e-81	8.5e-69
END		128		130	464	385		352	352	352
STAR T AA		5		S	251	288		1	2	3
CHAI N ID		A		∢						A
PDB ID	+	1buo		1buo	lgof	1gof		16g2	1bg2	1cz7
SEQ	NO:	975	,	975	975	975		7176	776	21.6

PD)3 annotation	MOTORS, KINISIN 2 SUPERFAMILY,	CONTRACTILE PROTEIN NCD,	CLARET SEGREGATIONAL	STRUCTURE, MICROTTIBILE	MOTORS, KINESIN 2 SUPERFAMILY,	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	MEMBRANE PROTEIN FOILIR HELLY	BUNDLE, ALPHA HELIX	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	MOTOR PROTEIN MOTOR PROTEIN	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	MOTOR PROTEST SOTOR	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN,	CONTRACTIUE DE CONTRACTION VENEGES	MICROTUBULE RASED MOTOR	NCD, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN KINESIN,	MICROTUBULE-BASED MOTOR,	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN, KAR3, CONTRACTILE PROTEIN, KAR3,
Coumpound		MICROTUBULE MOTOR	PROTEIN NCD; CHAIN: A, B, C, D:			SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	SSOI PROTEIN; CHAIN: A:		KINESIN; CHAIN: A, B;	Valroni Citini	AINESIN; CHAIN: A, B;	KINESIN, CHAIN: A. B.		KINESIN; CHAIN: A, B;	KINESIN: CHAIN: A B.	ATTENDED STREET, D, D,	KINESIN; CHAIN: A, B;	KINESIN MOTOR NCD: CHAIN:	A;		KINESIN MOTOR NCD; CHAIN:	Ý.	KINESIN-LIKE PROTEIN KAR3:	CHAIN: NULL;
SEQFOL D score										151.15	151 15	51.151							157.70			_		185.54	
PMF		1.00				0.16		0.10					1.00	;	1.00	1.00		1.00			,	3			
Verify score		0.58				0.21		-0.00					0.38	,	0.45	-0.24		-0.22				90.04			
Psi Blast		8.5e-69				5.7e-05		0.0057		27-97.5	5.7e-72	1	1.2e-55	1	5.7e-72	1.7e-17	7	1.9e-36	1.2e-68	<del></del>	9			3.4e-66	***************************************
END		354				430		992	9,0	627	259		258	030	607	366	3,6,1	304	352		346	2		351	
STAR T AA		5				365		282		-	_		2	,	,	272	72.0	7/4	6		,	`		4	
CHAI N ID		∢.				m m		∀	<	τ	¥		∀		ζ	Д	٥	9	∢		4				
PDB ID		lcz7				ldnl		Iffio	2bin	ZVIII	2kin		2kin	2kin	Tuna	2kin	. Viin	T T T	2ncd		2ncd			3kar	
SEQ ID NO:		216				7.16		977	077	:	21.6		977	220		977	227		126		226			11/6	

PDB annotation	MOTOR 2 PROTEIN, ATPASE, P- LOOP, MICROTUBULE BINDING PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P- LOOP, MICROTUBULE BINDING PROTEIN	CYTOSKELETON CYTOSKELETON CYTOSKELETON	CYTOSKELETON	COMPLEX (BLOOD	COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA;	HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING 2 GLYCOPROTEIN,	COMPLEX (BLOOD COAGULATION/INHIBITOR)	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA;	HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN,	COMPLEX (BLOOD COAGULATION/INHIBITOR)	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN I, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR
Coumpound		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	Comment of the Company of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comments of Comm	CHAIN: C, L; D-PHE-PRO-MAI;			ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;			MEROZOITE SURFACE PROTEIN I; CHAIN: A;
SEQFOL D score												
PMF		1.00	0.99	1.00		-0.19			0.41			0.16
Verify score		0.58	-0.10	-0.19		0.03			0.36			-0.11
Psi Blast		3.4e-66	1.5e-34	1e-16		1.5e-10			1.1e-24			1.9e-20
END		348	364	366		670			823			820
STAR T AA		2	276	276		597			745			740
CHAI			В	В		1			H			∢
PDB		3kar	3kin	3kin		laut			laut			1cej
SEQ	Ö	27.1	116	716		982			982			982

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PDB annotation	PROTEIN, SUR FACE 2 ANTIGEN, MALARIA VACCINE COMPONENT,	GLYCOPROTEIN MEMBRANE	COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT	COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR. MEASLES VIRUS	GLYCOPROTEIN	APOPTOSIS TRAIL; DRS; LIGAND-	JELLY-ROLL TNF-R 2	SUPERFAMILY, APOPTOSIS	BLOOD COAGULATION, SERINF	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	rroleASE/COFACTOR/LIGAND)	BLOOD COAGULATION SERINE	PROTEASE, COMPLEX, CO-FACTOR	2 RECEPTOR ENZYME, INHIBITOR	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COF/ACTOR/LIGAND)		HYDROLASE/HYDROLASE	INHIBITOR PROTEIN-PEPTIDE	COMPLEX
Coumpound		CD46; CHAIN: A, B, C, D, E, F;				TNF-RELATED APOPTOSIS	DEATH RECEPTOR 5; CHAIN:	A;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE HISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG.	CHLOKOMETHYLKETONE  (DEEP CAR) WITH CITABLE	PI COR CO	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SULUBLE HISSUE FACTOR;	CHLOROMETHYI KETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA	(HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT
SEQFOL D score									•									7		_	<del></del>						_	
PMF score		0.17			3,5	-0.12	•		0.11					027	/7.0					0.00					- 6	00.0		
Verify score		0.22			000	67.0		,	0.13					10	(1:0					-0.16					1	01.0-	Ţ	
Psi Blast		1.9e-16			5 70-00	2.75-03		710.5	0.06-10	,				1.1e-24					7	3.8e-24			_		2 02 73			
END		107			889	3		67.0	670					831	}				27,0	840					821			
STAR T AA		<u>г</u>			556	}		739	967					741					750	601					734	-		
CHAI N ID		∢			A	1		-	3					7						1					1	1		
PDB ID		Icki			1d4v			Idan			-			Idan					1dan				_		Idva		_	
SEQ B SO SO SO SO SO SO SO SO SO SO SO SO SO		782			982			982						982					987	3					982			

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PDB annotation		HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX	COMPLEMENT INHIBITOR VCP, SP35, COMPLEMENT, NMR, MODULES, PROTEIN STRUCTURE, VACCINIA VIRUS	MATRIX PROTEIN EXTRACELLULAR MATRUX, CALCIUM-BINDING,	GLICOFROIEUS, Z PER EACT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE
Coumpound	CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PFFTIDE E-76; CHAIN: X, Y;	COMPLEMENT CONTROL PROTEIN; CHAIN: A;	FIBRILLIN; CHAIN: NULL;		FIBRILLIN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VII; CHAIN: A;
SEQFOL D score					·			
PMF score		0.13	0.33	-0.19		0.00	0.01	0.75
Verify score		-0.02	0.18	60.0		-0.22	0.07	0.15
Psi Blast		6.8e-16	3.8e-17	1.7e-11		3.46-15	1.9e-10	5.7e-17
END		823	96	337		808	672	781
STAR T AA		738	3	257		738	533	741
CHAI N ID		ı	4				4	<
PDB ID		Idva	le5g	lemn		lemn	1ext	1f7e
SEQ	NO:	982	982	982		982	982	982

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PD)3 annotation	DOWAIN BIOOD 2 OF CHARLES	DOWNER, BEOOD & CLOI I ING	COMPLEX (BL.)OD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	GLYCOPROTEIN SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	COMPLEMENT INHIBITOR SP35, VCP, VACCINIA VIRUS SP35; COMPLEMENT INHIBITOR, COMPLEMENT MODULE, SCR,	SUSHI DOMAIN, 2 MODULE PAIR GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SIRINE PROTEASE, PLASMA, BLOOD 2 COAGULATION	FACTOR BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
Coumpound		GLYCOPROTEIN FACTOR H, 15TH AND 16TH C-MODULE PAIR (NMR, MINIMIZED 1HFHA 1 AVERAGED STRUCTURE)	IHTH 4 IHTHA 3 FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	VACCINIA VIRUS COMPLEMENT CONTROL PROTEIN; CHAIN: NULL;	COAGULATION FACTOR X; CHAIN: NULL;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score							
PMF score		0.23	0.11	0.05	-0.09	0.11	-0.13
Verify score		0.03	-0.03	0.01	0.18	-0.30	0.04
Psi Blast		9.5e-16	1.3e-32	3.8e-29	1.7e-14	1.10-19	5.1e-10
END		%	840	830	96	814	441
STAR T AA		8	741	741	7	744	369
CHAI N ID			니	J			L
PDB ID		Ihfh	1pfx	Iqfk	lvvc	1 whe	Ixka
SEQ ID NO:		982	982	982	982	982	982

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PDB annotation	HOLD TRANSPORT	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN		COMPLEX	(TRANSMEMBRANE/GLYCOPROTEI N) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEI N)	COMPLEX (TRANSMEMBRANE/GLYCOPROTEI N) MHC GLYCOPROTEIN, COMPLEX (TRANSMEMBRANE/GLYCOPROTEI N)	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN	MMUNE SYSTEM HLA-DRZ, MYELIN BASIC PROTEIN, MULTPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM	IMMUNE SYSTEM HLA-DRZ,
Coumpound		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	E 10 cd 1 cd 1 cd 1 cd 1 cd 1 cd 1 cd 1 c	HLA-DK3; CHAIN: A, B; CLLF; CHAIN: C;	HLA-DR3; CHAIN: A, B; CL.P; CHAIN: C;	HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I,	H.A-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L;	HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	HLA-DR2; CHAIN: A, D; HLA-
SEOFOL	D score				61.03		57.96		95.88	
PMF	score	0.06	0.07			0.39		0.58		0.58
Varify	score	0.05	-0.46			-0.06		-0.34		-0.11
Dei Dlact	Lor Diagr	1.9e-27	1.4e-09		1.4e-46	1.4e-46	1.4e-46	1.4e-46	8.5e-61	8.5e-61
ENG.	AA A	831	617		202	201	201	201	202	202
4,45	TAA	741	557		77	25	16	45	22	28
,	NID	<u>-</u>			æ	æ	æ	æ	4	A
	10 E	1xka	4mt2		1a6a	1a6a	1aqd	laqd	1bx2	1bx2
	) (1) (1)	NO:	982		986	986	986	986	986	986

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PDE annotation	MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNEY, IMMINE SYSTEM	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 ALITOMAM INITY MAN INE SYSTEM	IMMUNE SYSTEM HA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 ALITOMAN INTY IMAN INE SYSTEM	IMMUNE SYSTISM MHC CLASS II DR2A		IMMUNE SYSTIM MHC CLASS II DR2A		IMMUNE SYSTEM RING6, HLA- DMA; RING7, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM		HISTOCOMPATIBILITY ANTIGEN I- AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
Coumpound	DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	HLA-DR2; CHAIN: A, D; HLA- DR2; CHAIN: B, B; HLA-DR2; CHAIN: C, F;	HLA-DR2; CHAIN: A, D; HLA- DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN;	CHAIN: B, E; MYELIN BÁSIC PROTEIN; CHAIN: C, F;	MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E: MYFLIN RASIC	PROTEIN; CHAIN: C, F;	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN: A; CLASS II	HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN: B:	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE
SEQFOL D score		59.12						282.05		106.84
PMF score		·	0.46	0.90		0.39				
Verify score			-0.39	-0.31		-0.50				
Psi Blast		1.7e-45	1.7e-45	3.4e-60		1.7e-46		3.4e-43		16-61
END		204	201	202		201		207		202
STAR T AA		20	45	29		29		20		20
CHAI N ID		Д	В	¥		<b>m</b>		∢		∢
PDB ID		1bx2	1bx2	1fv1		ĮĘv]	;	mpu1		liak
SEQ ID NO:		986	986	986		986	, 60	88		986

PDB annotation	HISTOCOMPATIBILITY ANTIGEN I- AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX	HISTOCOMPATIBILITY ANTIGEN I- AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX	MHC II MHC II, CLASS II MHC, I-A, OVALBUMIN PEPTIDE	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN HISTOCOMPATIBILITY ANTIGEN	MHC II MHC II, CLASS II MHC I-AD	MHC II MHC II, CLASS II MHC I-AD	MHC II MHC II, CLASS II MHC I-AD	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,
Coumpound	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	MHC CLASS II I.AD; CHAIN: A, B;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-EK; CHAIN: A, B, C, D;	MHC CLASS II I-AD; CHAIN: A, B;	MHC CLASS II I-AD; CHAIN: A, B;	MHC CLASS II I-AD; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score		59.46	58.50	100.86		53.16	58.75		109.34		59.80	·	
PMF score	1.00				0.95			0.21		00.1		09:0	0.89
Verify score	-0.12				-0.28			-0.34		60.0		-0.43	-0.29
Psi Blast	le-61	1.5e-43	1.2e-43	5.1e-59	5.1e-59	3.4e-45	3.4e-45	3.4e-45	3.4e-61	3.4e-61	3.4e-44	1.9e-11	3.8e-15
END	202	201	201	203	203	199	199	199	207	206	201	214	130
STAR T AA	37	23		21	27	7	-	51	20	37	2	22	49
CHAI N ID	A	æ	В	₹	¥	В	В	æ	A	A	æ	<b>∀</b>	<b>V</b>
PDB ID	liak	liak	liao	lica	liea	liea	lieb	lieb	2iad	2iad	2iad	1a4y	1a9n
SEQ ID NO:	986	986	986	986	986	986	986	986	986	986	986	786	286

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PDI annotation	SNRNP RIBONI ICI EOPROTEIN	COMPLEX (NUCLEAR PROTEIN'RNA) COMPLEX (NUCLEAR PROTEIN'RNA), RNA,	SNRNP, RIBONIJCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNKNP, KIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE. RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYI INDEP
Coumpound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	TROPOMYOSIN; CHAIN: A, B, C, D	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN:	B, U; OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;
SEQFOL D score									
PMF		0.40	0.94	0.35	0.03	86.0	0.66	0.52	0.55
Verify score		0.10	0.07	0.05	-0.72	0.33	0.27	-0.19	-0.08
Psi Blast		3.8e-14	3.8e-15	5.7e-14	5.1e-19	1.2e-18	1.2e-14	le-14	3.8e-15
END		199	145	661	493	162	151	150	155
STAR T AA		25	49	52	231	'n	34	48	50
CHAI		∢	U	ပ	<b>A</b>	A	<b>4</b>	⋖	A
PDB ID	,	layn	la9n	la9n	1clg	1d0b	1dce	lds9	1ds9
SEQ NO:	100	) 8	987	286	987	987	286	987	987

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PDB annotation	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSCRIPTION RNA 1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNA 1P, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	MENOREDAY	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SER/THR PROTEIN KINASE, 2 ZN FINGER	TRANSFERASE CASEIN KINASE BETA SUBUNIT (1-182), SERTHR PROTEIN KINASE, 2 ZN FINGER		OXIDOREDUCTASE FERROCYTOCHROME C.:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE	TO A CITATOL AND THE COMMENT OF THE	TRANSCRIPTION IKANSFERASE, TRANSCRIPTION, DNA-DIRECTED RNA POLYMERASE, 3D- 2 STRUCTURE
Coumpound	$\sqcap$	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;		CASEIN KINASE II; CHAIN: A, B;	CASEIN KINASE II; CHAIN: A, B;		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,		DNA-DIRECTED RNA POLYMERASE; CHAIN: A, B; DNA-DIRECTED RNA POLYMERASE; CHAIN: C; DNA- DIRECTED RNA POLYMERASE; CHAIN: D; DNA-DIRECTED
SEQFOL D score		72.54								
PMF			0.13		1.00	1.00		0.07		0.96
Verify score			-0.14		0.46	0.46		0.10		-0.22
Psi Blast		7.66-07	1.96-12		3.8e-56	6.8e-51		8.5e-29		0
END		491	210		123	123		141		1076
STAR T AA		236	57		7	7		73		-
CHAI		A	<b>∀</b>		¥	A		н		U
PDB U		1quu	lyrg		1qf8	1qf8		2000	1	1ddq
SEQ	NO:	287	786		991	991		993		994

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PD]3 annotation		TRANSCREPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCREPTION PEGLII A TOX			LIGASE CBL, UBCH7, ZAP-70, E2,	UBIQUITIN, E3, PHOSPHORYI & TION 3 TWBOSPHE	KINASE, UBIQUITINATION, PROTEIN DEGRADATION,		LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3,	PHOSPHORYLATION, 2 TYROSINE KINA SE IBIOLUTINA TION	PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC-	BINDING PROTIZIN, XNF7, BBOX,	DEVELOPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING	FINGER PROTEIN MATI; RING	FINGER (C3HC4) DNA-BINDING PROTEIN V(D)1
Coumpound	RNA POLYMERASE: CHAIN: E:	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1 CHC 3 (NMR, 1 STRUCTURE) 1 CHC 4	SIGNAL TRANSDUCTION	70 PEPTIDE: CHAIN: A; ZAF-	UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7;	CHAIN: C;	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-	70 PEPTIDE; CHAIN: B; UBIOUITIN-CONILIGATING	ENZYME E12-18 KDA UBCH7; CHAIN: C:	NUCLEAR FACTOR XNF7;	CHAIN: NULL;		CDK-ACTIVATING KINASE	ASSEMBLY FACTOR MATI;	RAGI; CHAIN: NULL:
SEQFOL D score		-				-				-							
PMF score		0.05	0.59	0.47	0.52			,	0.30			0.03			0.46		0.49
Verify score		-0.39	0.29	-0.45	-0.04			,	-0.46			-0.11	-		-0.33		0.13
Psi Blast		1.4e-08	1.7e-12	5.7e-12	5.1e-10	-		1	3.8e-09			3.4e-05			0.00017		i.le-16
END		50	51	09	51			5	2			134			57	-	100
STAR T AA		2	10	9	10				رر			86			9		4
CHAI N ID				-	A				€						∢		
PDB		1bor	1chc	1chc	1fbv			167:				lfre		-	<u>23</u>		1rmd
SEQ NO:		995	995	995	995			200	3			995			35		995

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PDB annotation	PECCAMENA TION ACTIVATING	RECOMBINATION ACTIVATION PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD. RING FINGER, 2 ZINC	BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA) SREBP-1A;	STEROL REGULATORY ELEMENT BINDING PROTEIN, 2 BASIC-HELIX-	LOUP-HELLY-LEUCLNE ZIFFER, SREBP, TRANSCRIPTION 3 FACTOR, COMPLEX (TRANSCRIPTION BEGIT A FIGURANA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) MYN PROTEIN; MAX, DNA BINDING, BASIC-HELIX-	LOOP-HELIX-LEUCINE ZIPPER, 2 TRANSCRIPTION FACTOR,	COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (TRANSCRIPTION	FACTOR MAXIONA)	DNA BINDING, COMPLEX 2	(TRANSCRIPTION FACTOR MAX/DNA)	COMPLEX (TRANSCRIPTION	FACTOR MAX/DNA)   TRANSCRIPTIONAL REGULATION,	DNA BINDING, COMPLEX 2 (TRANSCRIPTION FACTOR	MAX/DNA)
Coumpound				STEROL REGULATORY	ELEMENT BINDING TROTEIN 1A; CHAIN: A, B, C, D; DNA; CHAIN: E, F, G, H;		MAX PROTEIN: CHAIN: A. C.	DNA; CHAIN: B, D;			TRANSCRIPTION FACTOR	MAX; CHAIN: A, B; DNA (5'-	D(*CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF CFAFCF		TRANSCRIPTION FACTOR	MAX; CHAIN: A, B; DNA (5'-	P*GP*GP*T)-3', CHAIN: C, D;	
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	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT,	TRANSPORT PROTEIN TC4; GTPASE, NICLEAR TRANSPORT	TRANSPORT PROTEIN	SIGNALING PROTEIN GTP-BINDING	PROTEIN RHOA, GTPASE RHOA;	RHO GDI 1; RHO GTPASE, G-	SIGNAL ING PROTEIN PROTEIN.	PROTEIN COMPLEX.	ANTIPARALLEL COILED-COIL	ENDOCYTOSIS/EXOCYTOSIS G-	PROTEIN, GTPASE, RAB6,	VESICULAR TRAFFICKING	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI;	BETA SANDWHICH, PROTEIN-	PROTEIN COMPLEX, G-DOMAIN, 2	IMMUNOGLOBILIN FOLD,	WALKER FOLD, GTP-BINDING PROTEIN	SMALL GTPASE KARYOPHERIN	BETA, P95 SMALL GTPASE,	NUCLEAR TRANSPORT RECEPTOR	GTP-BINDING GTP-BINDING,	GTPASE, SMALL G-PROTEIN, RHO	FAMILY, RAS SUPER 2 FAMILY	GTP-BINDING GTP-BINDING,	GTPASE, SMALL G-PROTEIN, RHO	FAMILY, RAS SUPER 2 FAMILY	COMPLEX (SMALL
	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;		TRANSFORMING PROTEIN	KHOA; CHAIN: A, C; RHO GDP	DISSOCIATION INHIBITOR ALPHA; CHAIN: E. F.	HIS-TAGGED TRANSFORMING	PROTEIN RHOA(0-181); CHAIN:	A; PKN; CHAIN: B;	RAB6 GTPASE; CHAIN: A;			RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN:	A; RHO GDP-DISSOCIATION	INHIBITOR 2; CHAIN: B;		-	RAN; CHAIN: A, C; IMPORTIN	BETA SUBUNIT; CHAIN: B, D;		RAC1; CHAIN: NULL;			RACI; CHAIN: NULL;			KAN; CHAIN: A, C; NUCLEAR
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		1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN;           CHAIN: A, B;         CHAIN: A, B;	1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN;           CHAIN: A, B;         CHAIN: A, B;         CHAIN: A, B;         CHAIN: A, B;         CHAIN: A, B;	1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN;           1byu         B         13         1.2e-46         0.17         0.72         GTP-BINDING PROTEIN RAN;           CHAIN: A, B;         CHAIN: A, B;         CHAIN: A, B;	1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: B           1byu         B         13         1.2e-46         0.17         0.72         GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B;           1cc0         A         23         140         3.4e-47         -0.23         0.96         TRANSFORMING PROTEIN	1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: B           1byu         B         13         1.2e-46         0.17         0.72         GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, C; RHO GDP	1byu A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; CHAIN: A, B;   139   1.2e-46   0.17   0.72   GTP-BINDING PROTEIN RAN;   150   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RAN;   RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHBITOR ALPHA; CHAIN: B, F:	1byu         A         17         139         5.1e-46         -0.02         0.64         GTP-BINDING PROTEIN RAN; CHAIN: A, B;           1byu         B         13         1.2e-46         0.17         0.72         GTP-BINDING PROTEIN RAN; CHAIN: A, B;           1cc0         A         23         140         3.4e-47         -0.23         0.96         TRANSFORMING PROTEIN RAN; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR           1cxz         A         23         140         1e-47         -0.14         0.98         HIS-TAGGED TRANSFORMING	1byu A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, F; CHAIN: B, F; CHAIN: B, F; CHAIN: B, F; CHAIN: B, F; CHAIN: CHAIN: B, F; CHAIN: CHAIN: B, F; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN:	1byu A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; 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CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, F; CHAIN: B, B; CHAIN: B, B; CHAIN: B, B; CHAIN: B, B; CHAIN: B, B; CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: B, CHAIN: A, CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN:	1byu A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; 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    1byu   B   13   139   1.2e-46   0.17   0.72   GTP-BINDING PROTEIN RAN;     1cc0   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RIPHORICAL AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND	1byu   A   17   139   5.1e-46   -0.02   0.64   CTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, F; PROTEIN RHOA(0-181); CHAIN: B, B; PROTEIN RHOA(0-181); CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, B; PROTEIN RHOA(0-181); CHAIN: A, B; PROTEIN RHOA(0-181); CHAIN: B, B; PROTEIN RHOA(0-181); CHAIN: B, B; PROTEIN RHOA(0-181); CHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; PROTEIN SCHAIN: B, B; 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    1byu   B   13   139   1.2e-46   0.17   0.72   CHAIN: A, B;     1cc0   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RAN;     1cx2   A   23   140   1e-47   -0.14   0.98   TRANSFORMING PROTEIN IN;     1dsc   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1ds6   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B;     1dsf   A   22   24   24   24   24   24   24	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN;	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN;     1byu   B   13   139   1.2e-46   0.17   0.72   GTP-BINDING PROTEIN RAN;     1cc0   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RING, CHAIN: A, E; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E, ENCHAIN E	1byu   A   17   139   5.1e-46   -0.02   0.64   CHAIN: A, B;     1byu   B   13   1.2e-46   0.17   0.72   CHAIN: A, B;     1cc0   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RAN;     1cx1   A   23   140   1e-47   -0.14   0.98   TRANSFORMING PROTEIN RHOGOP DISSOCIATION INHIBITOR ALPHA; CHAIN: B, F.     1dsc   A   22   140   8.5e-49   -0.05   0.88   RAB6 GIPASE; CHAIN: A; RAB6 GIPASE; CHAIN: B, F.     1dsc   A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B, F.     1dsc   A   20   145   1.4e-45   RAB6 GIPASE; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   145   1.4e-45   RAB6 BETA SUBUNIT; CHAIN: B, D, III     1dsc   A   20   20   20   20   20   20   20	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, B; GHAIN; A, C, CHAIN; A, C, CHAIN; A, C, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN; B, CHAIN	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: A, B; GTAIN: B, B; GTAIN: B, B; GTAIN: B, B; GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B, GTAIN: B,	1byu A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: B, B; CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: B, CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: C	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: A, B; GHAIN: B, B; GHAIN: B, B; GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: B, GHAIN: GHAIN: B, GHAIN: GHAIN: B, GHAIN: GHAIN: B, GHAIN: GHAIN: B, GHAIN: GHAIN: B, GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHAIN: GHA	1byu A   17   139   5.1e-46   -0.02   0.64   CTP-BINDING PROTEIN RAN;     1byu B   13   139   1.2e-46   0.17   0.72   CTP-BINDING PROTEIN RAN;     1cc0 A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RAN;     1cx1 A   23   140   1e-47   -0.14   0.98   TRANSFORMING PROTEIN RHOA; CHAIN: A, B;     1cx2 A   23   140   1e-47   -0.14   0.98   HIS-TAGGED TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR A; PROTEIN RHOA; CHAIN: B, B;     1dsc A   22   143   1.4e-49   0.14   0.84   RAB6 GTPASE; CHAIN: A, C; IMPORTIN A;     1dsc A   22   140   8.5e-49   -0.05   0.88   TOXIN SUBSTRATE 2; CHAIN: B, B;     1mhl   17   145   1.4e-45   68.78   RAN; CHAIN: A, C; IMPORTIN B;     1mhl   17   145   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1mhl   22   24   24   24   24   24   24   2	1byu   A   17   139   5.1e-46   -0.02   0.64   CTP-BINDING PROTEIN RAN;     1byu   B   13   139   1.2e-46   0.17   0.72   CHAIN: A, B;     1cc0   A   23   140   3.4e-47   -0.23   0.96   TRANSFORMING PROTEIN RAN;     1cx2   A   23   140   1e-47   -0.14   0.98   RHOACHENS EARLY CHAIN: B, B;     1dsc   A   22   140   8.5e-49   -0.05   0.84   RAS-RELATED C3 BOTULINUM A; RUGGED C3 BOTULINUM A; RUGGED C3 BOTULINUM A; RUGGED C3 C3 C4 C4 CAIN: B;     1dsc   A   22   140   8.5e-49   -0.05   0.88   RAS-RELATED C3 BOTULINUM A; RUGGED C3 C4 CAIN: B;     1mhi   17   145   5.1e-50   -0.12   0.87   RACI; CHAIN: A, C; IMPORTIN B, B, D;     1mhi   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1dsc   A   22   140   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1dsc   A   20   145   1.4e-45   RACI; CHAIN: MULL;     1dsc   A   20   145   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1dsc   A   20   145   1.4e-45   RACI; CHAIN: NULL;     1dsc   A   20   145   5.1e-50   -0.12   0.87   RACI; CHAIN: NULL;     1dsc   A   20   20   20   20   20   20   20	1byu   A   17   139   5.1e-46   -0.02   0.64   GTP-BINDING PROTEIN RAN;     1byu   B   13   139   1.2e-46   0.17   0.72   GTP-BINDING PROTEIN RAN;     1cc0   A   23   140   3.4e-47   -0.23   0.96   RANSFORMING PROTEIN RAN;     1cx2   A   23   140   1e-47   -0.14   0.98   REALFIELD RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RANSFORMING PROTEIN RA

PDB annotation	GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	HYDROLASE CDC42/CDC42/GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE	HYDROLASE O'TROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G FRO IEM, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	
Coumpound	PORE COMPLEX PROTEIN GT NUP358; CHAIN: B, D; GT GT SIW	RABPHILIN-3A; CHAIN: B; BI PR PR PR PR	RAB-3A; CHAIN: A; CX RABPHILIN-3A; CHAIN: B; BI PH BI EE EE EE	TEIN (G25K); TEIN (RHG);	RAB3A; CHAIN: A; H V V V H H H H H H H H H H H H H H H	RAB3A; CHAIN: A; H	
SEQFOL D score		54.15				64.11	
PMF			0.78	0.89	0.88		
Verify			0.17	-0.07	0.19		
Psi Blast		1.7e-53	1.7e-53	3.4e-46	5.1e-55	5.1e-55	
END		144	143	141	143	145	
STAR T AA		17	18	77	17	17	
CHAI N ID		4	∢	∢	4	₹	
PDB ID		1zbd	1zbd	2ngr	3rab	3rab	
SEQ	NO:	766	997	266	766	. 166	

		7		_	_			_					_				_					_					_		_		
PD]3 annotation	KINASE KINASE, SIGNAL TRANSDUCTION,	CALCIUM/CALMODULIN												•								TRANSFERASE KINASE DOMAIN	AUTOINHIBITORY FRAGMENT.	HOMODIMER			KINASE KINASE, TWITCHIN,	INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN,	INTRASTERIC REGULATION	KINASE RABBIT MUSCLE PHOSPHORYT ASE KINASE.
Coumpound	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: MIII 1.	TP ANSTER A SECULTORS TO THE	IKANSFERASE(PHOSPHOTRA NSFERASE) &C-/AMP&	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	(CATALYTIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/S139A\$) COMPLEX WITH	THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE	DETERGENT MEGA-8 1APM 6	PHOSPHOTRANSFERASE	CAMP-DEPENDENT PROTEIN	KINASE CATALYTIC SUBUNIT	ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA	NSFERASE) CAMP.	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (CAPK) 1CTP 3	(CATALYTIC SUBUNIT) 1CTP 4	SERINE/THREONINE-PROTEIN	KINASE PAK-ALPHA; CHAIN:	A, B; SERINE/THREONINE-	PROTEIN KINASE PAK-ALPHA;	CHAIN: C, D;	TWITCHIN; CHAIN: NULL;		TWITCHIN; CHAIN: A, B;		PHOSPHORYLASE KINASE; CHAIN: NULL;
SEQFOL D score														•													-				
PMF score	0.16	0.53	2										0.47				0.78					0.51					0.37	1	0.72	000	0.80
Verify score	-0.20	-0.21									•		-0.17				-0.02	•	-			-0.02					-0.02		-0.02	0.13	
Psi Blast	1.7e-50	5.1e-66	)					_				,	5.1e-66		-	,	09-97:1				,	3.4e-53				†	1.2e-38	1 25 40		3 40 54	╗
END	174	175	}		_								175			:	<u>.</u>					091				5	9	1,60	<u> </u>	140	
STAR T AA												-					_		_				_			1.	-			-  -	
CHAI N ID		E										E	긔			-	្ន				,	ر						<b> </b>			
PDB ID	1a06	Iapm										1	Yurs	-		†					153.22		-			1600		1koh		Iphk	
SEQ NO:	866	866										800	220			800					800	000		_		866	?	866	!	866	

																	_					T		
PDB annotation	ANY TOTAL PROPERTY.	GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	TV 101 C	INSECT IMMUNITY INSECTIONMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	IKANSDOCTION, 2 DIMENTERTION,	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	TE ANSPIRCTION 2 DIMERIZATION.	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	CELL ADHESION NCAM; NCAM,	
Coumpound			TITIN; CHAIN: A, B;	TITIN; CHAIN: A, B;		HEMOLIN; CHAIN: A, B;	AXONIN-1; CHAIN: A;	FIREORI AST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH  EACTOR RECEPTOR 1: CHAIN:	C.D.		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	(၁.၁)	ETRROBI AST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CREAM.	J.	NEURAL CELL ADHESION	
SEQFOL	D score																							
PMF	score		0.75	0.25		0.40	0.10	0.16	21.0				0.21	7.0				60.0	50.0				-0.13	
Verify	score		0.18	-0.12		0.28	0.09	000	8 0.0				0.15	3				8	0.03				0.11	
Psi Blast			1.7e-34	1.9e-34		1.7e-27	3.4e-34	,	3.46-23				51236	5.16-30					1.2e-26				3 de-18	
END	AA		149	186		283	283	,	199				300	284					199				282	7,3
STAR	T AA		1	1		01	29		21				(;	1112					21				193	1257
CHAI	E Z		A	A		Α.	A		ပ					Ω					Ω					4
PDB	a		1tki	1tki		1bih	1cs6		Icvs					lcvs					Icvs				,	lepi
SEO	i i	Ö	866	866		1000	1000		1000					1000					1000				900	3

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PDI3 annotation	IMMUNOGLOFIULIN FOLD,	GLYCOPROTEIN CELL ADHESTON NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE.	BINDING 2 PROTEIN IMMUNE SYSTEM FC-EPSILON RI- ALPHA, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-	BINDING 2 PROTEIN IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE	ANTIBODY, IGB-FC IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE	ANTIBODY, IGIS-FC IMMUNE SYSTISM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE,	CD32 IMMUNE SYSTI:M, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE,	CD32 IMMUNE SYSTEM RECEPTOR BETA
Coumpound	MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	LOW AFFINITY
SEQFOL D score				·	·				
PMF score		-0.09	0.31	0.22	0.57	0.12	-0.12	0.41	90.0
Verify score		0.11	0.12	0.00	0.31	-0.04	0.15	0.23	0.05
Psi Blast		3.46-24	1.7e-19	3.4e-28	le-17	1.4e-27	1.7e-19	5.16-29	3.4e-17 (
END		201	281	208	281	207	281	205	281
STAR T AA		33	117	28	116	56	115	56	114
CHAI N ID		₹	Ą	4	∢	A	A	4	A
PDB ID		lepf	1 <u>12</u> q	1f2q	1f6a	1f6a	1fcg	lfeg ,	1fn1 ,
SEQ ID NO:		1000	1000	1000	1000	1000	1000	1000	1000

PDB annotation	14 11140 2000 5 5	SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN- LIKE, RECEPTOR	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION,	TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD,	ALIEKNATIVE SPLICING, SIGNAL, S MUSCLE PROTEIN	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL	KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN	INHIBITORY RECEPTOR KILLER	CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL	RECEPTORS, IMMUNOGLOBULIN FOLD	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL	KILLER CELLS, IMMUNOULOUCAL 2 RECEPTORS, IMMUNOULOBULIN FOLD	NHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR;
Coumpound		IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	LOW AFFINITY IMMUNOGLOBULIN GAMMA FOREGION CHAIN: A:	TWITCHIN; CHAIN: NULL;	TITIN; CHAIN: NULL;			P58-CL42 KIR; CHAIN: NULL;		DSS_CT 42 KTR: CHATN: NULL:			P58-CL42 KIR; CHAIN: NULL;		P58-CL42 KIR; CHAIN: NULL;
SEQFOL	D score										-		71.59		
PMF	score		0.58	0.33	-0.15			0.76			0.22		·		0.87
Verify	score		. 0.07	0.35	0.47			0.20		130	-0.51				0.22
Psi Blast			1.5e-24	5.1e-12	3.4e-13			3.4e-29			6.8e-13		1e-30		1e-30
END	AA		206	284	284			282			113		216		204
STAR	T AA		24	207	213			117	<u>.</u> ,				27		. 28
CHAI	O Z		Α,												
PDB	А		1fnl	1koa	1nct			Inkr			Inkr		Inkr		Inkr
SEO	e ș	Š	1000	1000	1000			1000			1000		1000		1000

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PDE annotation	INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD		IMMUNOGLOBULIN ANTI- NITROPHENOL, LAMBDA LIGHT	CHAIN, IMMUNOGLOBULIN IMMUNE SYSTIM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RICEPTOR, 2	IMMUNOGLOBULIN IMMUNE SYSTIM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY <u>RECEPTOR</u> , 2	IMMUNOGLOBULIN IMMUNE SYSTIM CD32; RECEPTOR,	FC, CD32, IMMUNE SYSTEM IMMUNE SYSTEM CD32, RECEPTOR, FC, CD32, IMMUNE SYSTEM	HYDROLASE C2 DOMAIN, PHOSPHOTIDYI,INOSITOL, PHOSPHOTASH HYDROI A SE	HYDROLASE C2 DOMAIN, PHOSPHOTIDYI INOSITOL, PHOSPHOTASE, HYDROLASE
Coumpound	-	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM	FAB FRAGMENT; CHAIN: NULL;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;	PHOSPHOINOSITIDE PHOSPHOTASE PTEN; CHAIN: A;
SEQFOL D score			54.09		,				
PMF score		-0.18		0.51	0.74	-0.08	0.55	0.07	0.07
Verify		0.37		0.22	0.23	0.26	0.03	-0.64	-0.64
Psi Blast		3.40-13	8.5e-07	3.4e-29	5.1e-29	5.1e-20	3.40-29	0.0019	0.0019
END		284	236	282	203	281	206	344	262
STAR T AA		213	28	117	56	115	26	291	209
CHAI N ID			н	∢	4	V	4	· V	V V
PDB ID		Itmm	1 yufı	2dli	2dli	2fcb	2fcb	1dSr	1dSr ,
SEQ ID NO:	000	99	1000	1000	1000	1000	1000	1001	1003

PDB annotation	HYDROI ASE CO DOMAIN	PHOSPHOTIDYLINOSITOL, PHOSPHOTASE, HYDROLASE	Ond identified it manoritation	STRUCTORAL PROTEIN 1 WO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECIKIN, ALPHA	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, erpiicht BAI PROTEIN	ENDOCYTOSIS/FXOCYTOSIS	NSECT PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	COMPLEX (DNA-BINDING	PROTEIN/DNA) TUS; TER; DNA-	BINDING, DNA REPLICATION, 2	COMPLEX (DNA-BINDING	PROTEIN/DNA)	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX	BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,
Coumpound	TULLENGLING	PHOSPHOINGSLIDE PHOSPHOTASE PTEN; CHAIN: A;		ALPHA SPECTRIN; CHAIN: A, B. C:			ALPHA SPECTRIN; CHAIN: A,	B, C;			ALPHA SPECTRIN; CHAIN: A,	В, С;			SATE AND DISTRIBUTED BEATERN	1. CHAMIN BINDING FROIDING	CHAIN: B:	REPLICATION TERMINATOR	PROTEIN; CHAIN: A; DNA	16MER DUPLEX REPLICATION	TERMINATOR; CHAIN: B, C;		SSOI PROTEIN; CHAIN: A;	SSOI PROTEIN: CHAIN: A:		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;
SEQFOL D score																										
PMF score		0.07		-0.03			0.13				0.23					10.0		900	<u>_</u>				0.00	61.0	-0.12	0.05
Verify		-0.64		0.04			-0.08				-0.12			<u>.</u>		-0.32		-0.61	5				0.00	800	0.02	-0.31
Psi Blast		0.0019		5.7e-16			1.5e-16				1.7e-13					5.7c-18		0.0013					3.8e-11	: 0	7.96-11	1.1e-22
END		344		396			429				505	}				470		200	907				329		401	370
STAR T AA		291		164			213				203	3				236		17	<u>.</u>				133		217	75
CEAI N ID		A		¥			4				•	¢		•		В			. ←				Ą		∢	A
PDB ID		1d5r		lcnn			1cm				1 cin	III)				1dn1		-	1201				1fio		1fio	Iquu
SEQ TO		1004		1010			1010	2			1010	0101				1010			2101				1010		1010	1010

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PDI: annotation	CONTRACTILE PROTEIN					TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORWATION.	TRANSMEMBRANE 2 PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKIR REGION, 22	TANDEM 3-HELIX COLLED-COLLS,	STRUCTURAL PROTEIN	SIRUCTURAL PROTEIN TWO PERFATS OF SPECTED A 1 PLIA	HEI ICAL I INKIR REGION 22	TANDEM 3-HELIX COILED-COILS	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	KEPEAIS OF SPECIRIN, ALPHA	HELICAL LINKER REGION, 22	STRICTINALIX COLLED-COLLS,	STRUCTURAL PROTEIN TWO
Coumpound		DEFENSIN DEFENSIN /HNP\$-3 IDFN 3	DEFENSIN DEFENSIN /HNP\$-3	DEFENSIN DEFENSIN /HNP\$-3 IDFN 3		COLICIN IA; CHAIN: NULL;		ALPHA SPECTRIN; CHAIN: A, B, C;			AT DATA COMPOSITOR ATTACK	ALFHA SFECIKIN; CHAIN: A, B. C.	ĵ.			ALPHA SPECTRIN; CHAIN: A,	ည်း				ALPHA SPECTRIN; CHAIN: A,				ALPHA SPECTRIN; CHAIN: A,
SEQFOL D score		59.97			1	148.75																		-	
PMF score			1.00	1.00				-0.09			113					0.04				5	-0.02				0.30
Verify score			-0.35	-0.35				0.12	_	•••••	700	00.0				0.11				77	<del>-</del> -				-0.09
Psi Blast		1.1e-12	1.1e-12	3.4e-11	00	5./6-59		3.8e-15			1 00 15		•			3.8e-21	_			1 00 10					1.9e-09
END AA		138	138	138	100	930		394			447					583				634	<u> </u>				284
STAR		109	110	110	7.	<del>*</del>		061			218					345				419	}				50
CHAI N ID		<	Ą	∢				∢	•		A	:				∢				A	-				A
PDB ID		1dfn	1dfn	1dfn	101	3	1	Icun			1cm		-		1	unoi		-,		Icin					lcun .
SEQ ID NO:		1013	1013	1013	101	<u> </u>		1014			1014			-	7101	1014				1014			_		1014

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PDB annotation	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN 1 WO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	SIGNALLING FRO LEIN CORNILLY, NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS  NSEC1; PROTEIN-PROTEIN  COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOOK HELIX BUNDLE, ALPHA HELIX	CHAPERONE ARCHAEAL PROTEIN	CHAPERONE ARCHAEAL PROTEIN	CHAPERONE ARCHAEAL PROTEIN
Coumpound	В, С;	ALPHA SPECTRIN; CHAIN: A, B, C;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SSOI PROTEIN; CHAIN: A;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B;
SEQFOL D score										
PMF score		0.12	0.17	-0.07	0.23	99.0	-0.17	0.01	0.15	0.22
Verify		-0.06	-0.16	0.07	-0.04	0.02	0.01	0.08	0.00	0.26
Psi Blast		5.7e-10	0.0057	1.5e-18	5.7e-26	1.7e-09	1.9e-11	1.9e-05	3.8e-07	1.9e-05
END		741	307	509	598	733	518	422	513	578
STAR T AA		525	55	297	370	484	361	308	391	472
CHAI		. ∀	A	В	æ	В	∢	ပ	U	U
PDB		Icun	1483	1dn1	1dn1	1dn1	1fio	1fxk	1fxk	1fxk
SEQ	S S S S S S S S S S S S S S S S S S S	1014	1014	1014	1014	1014	1014	1014	1014	1014

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	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE. HELLY COULED COIL, CONTRACTILE PROTEIN		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA)
PREFOLDIN; CHAIN: C:	PREFOLDIN; CHAIN; A; PREFOLDIN; CHAIN; B; PREFOI DIN; CHAIN; C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSK ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	GGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONICLEOTIDE BINDING	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
									·		
	0.11	0.07	0.01	0.15	0.03	0.03		0.62	-0.06	0.03	0.28
	0.21	0.15	0.48	0.20	-0.05	-0.06		-0.31	0.01	0.11	-0.37
	0.00057	1.1e-24	1.3e-32	7.6e-27	3.8e-17	3.8e-15	,	1.2e-23	1.7e-24	1.7e-26	1e-27
	635	549	580	630	746	398	90,	429	468	498	555
	552	272	321	359	471	81	,	24¢	378	405	472
	ပ	¥	A	⋖	⋖	А	\ 	¢	∢	A	4
	1fxk	1quu	lquu	1quu	lquu	Iquu	4101			laih	lalh ,
	1014	1014	1014	1014	1014	1014	1015	Cio	1015		1015
		1fsk         C         552         635         0.00057         0.21         0.11         PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	1fkk         C         552         635         0.00057         0.21         0.11         PREFOLDIN; 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CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; CHAIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREFOLIDIN; C; PREF

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PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
SEQFOL D score								
PMF score		0.10	0.87	0.18	0.81	0.72	0.82	0.95
Verify score		0.34	0.10	-0.65	-0.12	-0.01	-0.01	-0.25
Psi Blast		3.4e-30	3.4e-30	1.7e-10	1.7e-41	1.7e-42	1.7e-45	5.1e-47
END		981	1010	554	429	468	496	527
STAR T AA		901	929	505	349	374	404	443
CHAI		4	₹		U	U	ပ	O
PDB		la1h	lalh	1bbo	Imey	Imey	Imey	lmey
SEQ	:ON	1015	1015	1015	1015	1015	1015	1015

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PD)3 annotation	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	CAMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	FINGER, PROTISIN-DNA INTERACTION PROTESTING	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTIIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRISIAL SIR()CIURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	CRYSTAL STRICTINE COMPLEY	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	COVERACTION, PROTEIN DESIGN, 2	(ZINC FINGER/INA)	COMPLEX (ZINC FINGER/DNA) ZINC
Соптроинд	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEEN: CHAPL C. C.	INOIEIN, CRAIN: C, F, G;	DNA: CHAIN: A B D E:	CONSENSUS ZINC FINGER PROTEIN: CHAIN: C. F. G.			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C F G.	() (1.5) (mm) (mm)		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	INOTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;
SEQFOL D score																			_		
PMF score		0.90	2.0	4		-0.20			0.16	 			0.51				88.0				0.39
Verify score		-0.26	100	10.0		0.02			0.13	71.0			0.25			200	) (0.0)				-0.05
Psi Blast		3.46-46	150.36	00000		6.8e-44			5 10.45	f .			3.46-50			2 42 50	3.46-20			$\exists$	3.4e-12
END		556	612			778			953	}			100			1010	2	·,		7	/75
STAR T AA		471	530	3		869			840	2			100			908	077				200
CHAI N ID		ပ	S	)		၁			C			c	<u></u>			0	)		-	,	
PDB ID		Imey	lmev	Ì		lmey			Imev	•		-	, integ		_	Imev			·,	+	TIMES
SEQ NO:		1015	1015			1015			1015			1015				1015				1015	7701

PDB annotation		FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGENDINA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
Coumpound		CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION REGULATION YEAST TRANSCRPTION FACTOR ADRI (RESIDUES 130- 159) 1PAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH 1PAA 4 PRO 133 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 1PAA 5 REPLACED BY ALA (P131A,P133A,C140A)
SEQFOL	D score	,	·				
PMF	score		0.24	-0.18	0.42	0.65	0.96
Verify	score		-0.71	0.22	-0.03	0.23	-0.38
Psi Blast			5.1e-11	1.5e-11	le-12	8.5e-12	1.7e-05
END	AA.		556	865	953	1010	1013
STAR	T AA		528	839	926	286	985
CHAI	e z		O	D	ō	ڻ ن	
PNR	9		Imey	1mey	Imey	1mey	Ipaa
OAS	ខ្ពុំ១ខ្		1015	1015	1015	1015	1015

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PDB annotation		ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION A CHIVATION SERVER	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER,	ZINC FINGER TRANSCRIPTION FACTOR SPI, ZINC FINGER, TRANSCRIPTION A CTIVA TON CONTROL OF THE ANSCRIPTION A CTIVA TON	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	GENE, NMR, TFIIIA, PROTEIN, DNA,	IKANSCRIF 110N FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE, MARK, TRILIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGULATION (DNA)
Coumpound	(NMR, 10 STRUCTURES) 1PAA 6	SP 1F3; CHAIN: NULL;	SP IF2; CHAIN: NULL;	SPIF2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	CHAIN: E, F;			TRANSCRIPTION FACTOR IIIA;	CHAIN: E, F;		,		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 3S KNA GENE;	(True, 1)		•	
SEQFOL D score											<del></del>				_				
PMF score		0.70	0.27	0.90	0.05				0.23					0.03					
Verify score		-0.10	-0.77	-0.54	-0.11	,			0.15					-0.17					
Psi Blast		0.00051	0.00017	1.9e-05	6.8e-17				3.4e-18					1.7e-18					
END AA		1010	375	1010	468				496					551					$\exists$
STAR T AA		985	349	586	377				405				_	472					
CHAI N ID					¥				∢					∢					
PDB ID		Ispl	1sp2	1sp2	1143				£					<del></del>				_	
SEQ ID NO:	,	1015	1015	1015	1015				1015					1015	_				

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
Coumpound	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF score	0.64	0.47	0.00	0.29	0.28
Verify score	-0.17	-0.42	-0.65	-0.56	-0.39
Psi Blast	1.5e-21	8.5e-34	1.7e-28	7.6e-17	8.5e-31
END	1010	565	593	496	468
STAR T AA	929	405	472	351	354
CHAI N ID	<b>4</b>	⋖	<b>4</b>	ပ	U
PDB U	EB	1tf6	1tf6	1ubd	1ubd
SEQ B	1015	1015	1015	1015	1015

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PDB annotation	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRÁNSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRÁNSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/IDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/IDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF		0.47	0.54	0.57	-0.18
Verify score		-0.13	-0.38	-0.26	0.04
Psi Blast		1.7e-31	5.1e-30	16-31	6.8e-28
END AA		497	527	584	953
STAR T AA		384	412	479	813
CHAI N ID		ပ	ပ	U	v
PDB ID		1ubd	1ubd	1ubd	1ubd
SEQ ID NO:		1015	1015	1015	1015

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PDB annotation	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION, TRANSCRIPTION REGULATION,
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	ADRI; CHAIN; NULL;	ADR1; CHAIN: NULL;
SEQFOL D score			·				
PMF score		0.00	0.84	0.81	0.19	0.39	60.0
Verify score		0.13	0.22	-0.56	-0.66	-0.80	0.39
Psi Blast		3.46-30	3.46-34	5.16-27	6.8e-12	8.5e-15	3.4e-16
END		981	1006	1086	403	558	955
STAR T AA		848	806	933	349	503	901
CEAI N ID		ပ	v	v			
PDB ID		1ubd	Iubd	Iubd	2adr	2adr	2adr
SEQ NO.		1015	1015	1015	1015	1015	1015

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PDB annotation	ADRI. ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR. ZINC PRICER, NAR	A TORREST OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S										COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI:	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTIEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GIT
Coumpound		ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION	TO A MITTO A CIV. BROTTETAL CITIZO	ZINC-FINGER PEPTIDE)	COMPLEXED WITH 2DRP 3	DNA 2DRP 4	COMPLEX(TRANSCRIPTION	TO A MEDION ACT DE CHESTS (THE COMPANY)	TRIC EDICED DEPTITION	COMPI EXED WITH JOBB 3	DNA 2DRP 4	ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		ZDIO ERICER PROGRESSI OF 11	CHAMILA: DNA: CHAMILO D.	Chain: A; DNA; Chain: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		The state of the state of the	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA: CHAIN: C. D:
SEQFOL D score						. 10			·		,				•.														
PMF score		0.80	0.11					0.01					0.21				0.10			12.0	<u>.</u>			000	0.28			21.0	0.15
Verify score		-0.01	-0.30					-0.47					-0.36				-0.44			0.34	t ( )		-	000	-0.29			230	-0.07
Psi Blast		6.8e-18	3.4e-06					8.5e-10					3.4e-18				1.5e-26	-		6 80-33	55.5		-	0 60 27	0.36-33			5 10 20	3.1e-20
END		1015	428					556					428			1	467			556	3			503	200		•	503	373
STAR T AA		957	372					501					354				358			404		_		151	<u>.</u>			470	214
CHAI N ID			∢					∢					∀			1	<			<b>A</b>	:				ς.			4	
PDB ID		2adr	2drp					Zdrp Zdrp					2gli			:	ııg7	-		2pli	į,			2ali				20li	$\neg$
SEQ ID NO:		1015	1015					1015					1015				5101			1015				1015	3			1015	

und PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	TEIN GLII; HAIN: C, D; CLI, ZINC FINGER, COMPLEX (DNA-BINDING) GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	A BINDING AGER (ZFY- TRUCTURES)	OXIDASE; OXIDOREDUCTASE E, F, G, H, I, I, FERROCYTOCHROME CLOXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE	٦	THETASE 1; PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, S; CHAIN: C, ADENYLATE FORMING	AIN: NULL; OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE	TIDE; NDING	I, D, E; COMPLEX (ZINC FINGER/DNA) ZINC FINGER FINGER, PROTEIN-DNA
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY- SWAP) (NMR, 12 STRUCTURES) 7ZNF 3	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,		GRAMICIDIN SYNTHETASE 1; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D:	LUCIFERASE; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
SEQFOL D score		·				139.53	133.28	76.54	97.35
PMF score		96.0	0.31	-0.17					
Verify score		-0.18	-0.23	10.0					
Psi Blast		1e-33	3.4e-05	3.4e-88		0	0	3.4e-29	1.7e-50
END		1010	1013	299		610	808	184	239
STAR T AA		901	985	1		48	59	86	157
CHAI N ID		Α ,		<b>4</b>		<b>⋖</b>		4	၁
PDB ID		2gli	7znf	20cc		lamu	Ilci	lalh	lmey
SEQ ID		1015	1015	1021		1023	1023	1028	1028

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PDE annotation	CRYSTAL STRIJCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATIONA) COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGIL ATIONALY YING-YANG 1	TRANSCRIPTION INITIATION, INITIATOR ELEMENT VY1 2INC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION(I)NA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOBHIT ICA PHESTONI	TOWN THE CONTROLL	•		COMPLEX	IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A. B:			ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		HEMOLIN; CHAIN: A, B;	CATALYTIC ANTIBODY 17E8	(1-N-	SUCCINYLAMINO)PENTYLJ IEAP 3 PHOSPHONATE IEAP 4	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1	RECEPTOR; CHAIN: B;
SEQFOL D score		106.38		89.78				87.54		65.92	55.72			51.71	
PMF score												•			
Verify score			·			<del>,</del>									
Psi Blast		1.4e-36		6.8e-35				3.4e-31		6.8e-48	1.7e-10			1.7e-34	
END		269		239				240		351	348			353	
STAR T AA		6		130				8		peni	133			<del>2</del>	
CHAI N ID		∢	ì	ပ				∢		∢	В			n,	
PDB ID		1446		lubd				Zgli		Ibih	leap			<u> </u>	
SEQ NO:		1028		1028			000,	1028		1029	1029		000	1029	

PDB annotation	GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T. CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)		TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS	TRANSFERASE FPS, TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS				COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	+
Coumpound		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	IMMUNOGLOBULIN ANTIGEN- BINDING FRAGMENT (FAB) (1GG2B, KAPPA) IMAM 3	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	DEFENSIN DEFENSIN /HNP\$-3 1DFN 3	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: O.
SEQFOL D score		59.81	56.22		70.74	58.55				
PMF score				0.11			1.00	1.00	0.35	0.78
Verify score				-0.31			-0.35	-0.35	 -0.15	0.44
Psi Blast		1.7e-08	1.2e-11	5.1e-66	5.1e-66	1.1e-12	1.1e-12	5.1e-11.	5.7e-22	3.8e-24
END		351	349	398	397	191	161	161	224	208
STAR T AA		133	139	57	99	132	133	133	99	89
CHAI N ID		Ħ	н			4	⋖	Ą	¥	Ą
PDB ID		1kb5	lma m	1uby	1uby	1dfm	1dfn	1dfn	la4y	190n
SEQ EQ		1029	1029	1031	1031	1032	1032	1032	1034	1034

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PDB annotation	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONI/CLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRND RIRONI (CT BORDOTEN)	SOUPLEX (NUCLEAR PROTEIN PROTEIN/SOUPLEX (NUCLEAR PROTEIN/RNA), RNA, SOUPLE STRONG PROTEIN/RNA), RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RNA, SOUPLE STRONG PROTEIN/RN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	CELL ADHESION NEURAL CELL	GROWTH FACTOR/GROWTH FACTOR RECEIPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR PROFITOR	GROWTH FACTOR/GROWTH FACTOR/GROWTH IMMUNOGLOBULN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Coumpound	R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B", CHAIN: B, D;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;
SEQFOL D score									
PMF score	-	0.57	0.80	0.62	0.05	0.22	0.25	0.74	0.58
Verify score		0.15	0.52	0.21	0.12	0.27	0.15	0.22	0.13
Psi Blast		1.3e-21	1.1e-23	9.5e-21	3.8e-06	7.6e-07	1.5e-06	8.5e-19	1.9e-24
END		249	208	249	363	364	367	186	223
STAR T AA		8	89	93	279	283	283	39	44
CHAI N ID		∢	ပ	ပ	Ą	O	Д	A	4
PDB ID		1a9n	1a9n	la9n	1cs6	lcvs	lcvs	1d0b	140b
SEQ ID NO:		1034	1034	1034	1034	1034	1034	1034	1034

		VSFERASE,	LPHA			NSFERASE,	LPHA		LEUCINE-	טייים אייים	GELLA	LEUCINE-	A-ALPHA	GELLA	NCAM,	<u> </u>	/TH	2; FGFR2;	CIKE	OTHEL	N IG-LIKE	VTH 2; FGFR2;
PDB annotation	ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA	SUBUNIT, BELA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE-	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, Z CHLAMYDOMONAS, FLAGELLA	CELL ADHESION NCAM; NCAM,	IMMUNOGLOBULIN FOLD GLYCOPROTEIN	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SEL 2 SUBGROUP WITHIN IG-LIKE   DOMAINS B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;
Coumpound		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE	KASE BELA SUBUNIL; CITALIN: B, D;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C, NAB GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN: B. D:	OUTER ARM DYNEIN; CHAIN:	A;		OUTER ARM DYNEIN; CHAIN:	A;		NEURAL CELL ADHESION	MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;
SEQFOL D score			-											· .				_				
PMF score		0.03			-0.01				0.10			0.04			86.0		0.33					0.77
Verify score		-0.25		•	0.05				-0.76			-0.56			0.10		0.15			· 		0.12
Psi Blast		1e-09			1.9e-16				1e-08			7.6e-21			5.7e-07		1.5e-06					3.8e-06
END		218			235				245			208			358		373					358
STAR T AA		106			38				104			45			279		276	; i				283
CHAI		Ą			V				A			A			A	 	E	1				Ð
PDB 1D		ldce			1dce				6sp1			1ds9			Jepf	4	lev2					lev2
SEQ ID		1034			1034				1034			1034			1034		1034					1034

T	<del>.</del>	T	<del></del>	<del></del>	<u> </u>	·
IMMUNOGLORIUIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) ADD LEUCINE-RICH-	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-	INMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN 1G REPEAT 27; MUSCLE PROTEIN,	TWING COROLOGY OF THE DOMAIN	NERVE GROWTH FACTORTRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LER, LEUCINE- 2 RICH REPEAT PROTEIN TWINING
FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	TITIN, 127; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 1TNM 50	NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
	0.25	0.05	0.01	0.34	-0.19	0.24
	-0.40	-0.61	0.21	0.23	0.25	-0.34
·	0.0013	0.00076	5.7e-06	1.7e-06	1.7e-09	7.6e-19
	230	236	356	358	490	198
	183	183	280	279	394	44
-	Ą	В			×	4
	1fo1	1601	1tit	1tnm	lww w .	lyrg
	1034	1034	1034	1034		1034
		FIBROBLAST GROWTH   FACTOR RECEPTOR 2; CHAIN: E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H;   E, F, G, H	1fol A   183   230   0.0013   -0.40   0.25   PACTOR RECEPTOR 2; CHAIN: E, F, G, H;   FACTOR RECEPTOR 2; CHAIN: E, F, G, H;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A, B;   FACTOR 1; CHAIN: A,	1fo1   A   183   230   0.0013   -0.40   0.25   E, F, G, H;     1fo1   B   183   236   0.00076   -0.61   0.05   PACTOR I; CHAIN: A, B;     1ft1   280   356   5.7e-06   0.21   0.01   TITIN, 127; CHAIN: NULL;	1fol   A   183   230   0.0013   -0.40   0.25   FACTOR RECEPTOR 2; CHAIN: E, F, G, H;     1fol   B   183   236   0.00076   -0.61   0.05   FACTOR 1; CHAIN: A, B;     1fit   280   356   5.76-06   0.21   0.01   TITIN, 127; CHAIN: NULL;     1lm   279   358   1.76-06   0.23   0.34   MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN)     1TNM 3 (NMR, MINIMIZED A VIENA GE STRUCTURE) ITNM 4 1 NUM 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1fo  A   183   230   0.0013   -0.40   0.25   NUCLEAR RNA EXPORT

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PDB annotation	HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN		TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE,, TRANSFERASE	TRANSFERASE TRANSFERASE	TRANSFERASE APS KINASE; APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC
Coumpound		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	-	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	GLYCEROL-3-PHOSPHATE CYTIDYLYLTRANSFERASE; CHAIN: A, B;	ADENOSINE- SPHOSPHOSULFATE KINASE; CHAIN: A, B;	TRIACYLGLYCEROL ACYL- HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	RP2 LIPASE; CHAIN: NULL;
SEQFOL D score							112.24	107.65
PMF score		0.46		0.12	0.18	0.35		
Verify score		0.40		-0.10	0.18	-0.55		
Psi Blast		9.5e-07		0.0019	1.1e-11	1.9e-05	0	0
END		358		519	312	393	319	316
STAR T AA		279		360	193	359	1	2
CHAI		¥		<b>V</b>	4	Α	<b>4</b>	
PDB ID		3ncm		1cke	1coz	146j	1eth	1gpl
SEQ ID	Ö	1034		1035	1035	1035	1038	1038

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PDB annotation			HYDROLASE FRYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE			COMPLEX (DNA-BINDING PROTEINDNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEINING HOMEODOMAIN, PROTEINING HOMEODOMAIN, PROTEIN PROTEINING	TRANSCEILING TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL TO THE TRANSCEIL THE TRANSCEIL THE TRANSCEIL TO THE TRANSCEIL THE TRANSCEIL TO THE TRANSCEIL THE TRANSCEIL THE TRANSCEIL THE TRANSCEIL THE TRANSCE
Coumpound	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROI ASE) 14P1 3	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED 11.PB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO	PANCREATIC LIPASE RELATED PROTEIN I; CHAIN: NULL;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D: DNA CHAIN: F:	UL TRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN
SEQFOL D score	107.77	109.40	100.01		·			
PMF score					1.00	0.65	1.00	1.00
Verify					0.19	-0.39	0.20	0.33
Psi Blast	0	0	0		3.46-34	3.8e-26	1.7e-27	5.1e-29
END AA	318	316	316		219	213	215	212
STAR T AA	-	-	2		154	145	158	158
CHAI N ID	Ą	Ф			<b>1</b> 4	<	<b>∀</b>	A
PDB ID	1hpl	11pb	lrpl		land		01	198i
SEQ ID NO:	1038	1038	1038	104	1044	1044	1044	1044

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PDB annotation	HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	DNA BINDING PROTEIN TTF-1 HD; IFTT 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR IFTT 19		COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEOBOX, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEOBOX, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA) HELIX	
Coumpound	EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	THYROID TRANSCRIPTION FACTOR I HOMEODOMAIN; IFTT 6 CHAIN: NULL; IFTT 7	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	HOMEOBOX PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	HOMEOBOX PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	DNA-BINDING PROTEIN
SEQFOL D score						50.85		
PMF score		1.00	1.00	0.96	0.99		1.00	0.99
Verify		0.16	0.09	0.03	0.16		0.26	0.30
Psi Blast		7.6e-26	1.9e-23	1.9e-23	5.1e-29	6.8e-20	1.96-25	8.5e-32
END		213	211	216	212	223	215	219
STAR T AA	·	153	155	155	153	146	153	160
CHAI		Ą	B			D.	d.	
EDB EDB		151	191	1fft	1ftz	Ink2	1nk3	Isan
SEQ D SEQ	2	1044	1044	1044	1044	1044	1044	1044

PDB annotation		COMPLEX (INFIBITOR/NUCLEASE) COMPLEX (INFIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE., TRANSFERASF	TRANSFERASE APS KINASE; APS KINASE, APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL ?! TRANSFER, TRANSTION SITATE ANALOG	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN TRANSFERASE	
Coumpound	ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	ADENOSINE- S'PHOSPHOSULFATE KINASE; CHAIN: A, B;	URIDYLMONOPHOSPHATE/CY TIDYLMONOPHOSPHATE KINASE; CHAIN: A;	SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4)
SEQFOL D score				į			
PMF score		0.46	0.40	0.33	0.99	0.84	0.64
Verify score		0.27	-0.08	0.08	0.34	-0.06	0.35
Psi Blast		0.0095	6.8e-22	3.4e-23	1.7e-21	1.7e-20	1.4e-19
END		214	187	187	185	186	185
STAR T AA		41	9	3	9	1	9
CHAI N ID		A	V V	A	∢	¥	
PDB UD		la4y	1cke	1d6j	1qf9	1shk	lukz
SEQ D NO:		1046	1048	1048	1048	1048	1048

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PDB annotation		TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE		(aotamiento), aotamiento (aotamiento)	HOH; HOHBP; COMPLEX (HORMONE/RECEPTOR)	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,	PECEPTOR DECEDED SIGNAL	TP ANSTITCEP OF II A TVPF	CYTOKINES THIRD 2 N. TERMINAI	DOMAIN, TRANSMEMBRANE,	GLYCOPROTEIN	RECEPTOR RECEPTOR, SIGNAL	TRANSDUCER OF IL-6 TYPE	CYTOKINES, THIRD 2 N-TERMINAL	DOMAIN, TRANSMEMBRANE,	GLYCOPROTEIN	RECEPTOR RECEPTOR, SIGNAL	I KAINSDUCER OF IL-0 I I FE	CYTOKINES, THIRD 2 N-TERMINAL	DOMAIN, TRANSMEMBRANE,	GLYCOPROTEIN	RECEPTOR RECEPTOR, SIGNAL	IKANSDUCER OF IL-6 1 IFE	CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,
Coumpound	COMPLEXED WITH ADP AND AMP IUKZ 3	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	CDOMETITION COME. CITABL	A; GROWTH HORMONE RECEPTOR; CHAIN: B;	HEMOLIN; CHAIN: A, B;	Chiao. Cuv Ni. viii I.	OF 150; CHAIN: NOLL;				GP130; CHAIN: NULL;					GP130; CHAIN: NULL;					GP130; CHAIN: NULL;		
SEQFOL D score																								
PIMF score		0.12	0.22	97.0	0.40	-0.14	40	74.7				0.33				1	0.01			-		0.35		
Verify score		0.01	-0.02	010		0.21	200	0.33				0.07					0.27					0.25		
Psi Blast		1.7e-21	8.5e-22	1 72 10	1.76-10	6.8e-21	10, 14	1.36-14				3.8e-09					8.5e-12					5.7e-19		
END AA		187	184	240	747	338 ·	036	000				461					208					674		
STAR T AA		9	3	25.	707	2	250	607				360					477					573		
CHAI N ID		4			<b>a</b>	A																		
PDB ID		2cmk	3adk		Z Z	16ih	11:0	ofor -				1bj8					15)8					1bj8		
SEQ NO:		1048	1048	9,01	£	1049	1040	1049				1049				3	1049					1049		

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GLYCOPROTEIN	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN	CONNECTIN A 71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A 71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BE'IA SUBUNIT, SIGNAT ING PROTEIN	SIGNATURE PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BEYA SUBUNIT, SIGNATURE PROTEIN	SIGNATURE PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	GP130; CHAIN: A, B;	GP130; CHAIN: A, B;	GP130; CHAIN: A, B;
	0.05	0.77	0:30	0.25	0.15	0.55	-0.09	0.21	0.03
	0.14	0.12	0.59	-0.02	0.09	0.28	0.02	-0.07	0.25
	1.2e-21	3.8e-1 <i>5</i>	3.8e-12	5.1e-11	9.5e-14	3.8e-17	8.5e-19	1.9e-20	3.8e-12
	354	259	351	572	578	675	363	347	479
	158	651	257	479	479	577	158	159	256
,	<b>a</b>						∢	∢	<b>4</b>
	1bp3	Ibpv	1bpv	1bpv	lbpv	Ibpv	16qu	Ibqu	1bqu
3,	1049	1049	1049	1049	1049	1049	1049	1049	1049
		1bp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN: CHAIN: B.           CHAIN: B:         CHAIN: B.	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN:           A; PROLACTIN RECEPTOR;         CHAIN: B;         CHAIN: B;           1bpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN:           lbpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;           lbpv         257         351         3.8e-12         0.59         0.30         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;           lbpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;           lbpv         257         351         3.8e-12         0.59         0.30         TITIN; CHAIN: NULL;           lbpv         479         572         5.1e-11         -0.02         0.25         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;           lbpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;           lbpv         479         572         5.1e-11         -0.02         0.25         TITIN; CHAIN: NULL;           lbpv         479         578         9.5e-14         0.09         0.15         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN: CHAIN: BL           lbpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;           lbpv         257         351         3.8e-12         0.59         0.30         TITIN; CHAIN: NULL;           lbpv         479         572         5.1e-11         -0.02         0.25         TITIN; CHAIN: NULL;           lbpv         577         675         3.8e-17         0.28         0.55         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE; CHAIN: CHAIN: DCTIN RECEPTOR; CHAIN: B;           lbpv         159         259         3.8e-15         0.12         0.77         TiTIN; CHAIN: NULL;           lbpv         479         572         5.1e-11         -0.02         0.25         TITIN; CHAIN: NULL;           lbpv         479         578         9.5e-14         0.09         0.15         TITIN; CHAIN: NULL;           lbpv         577         675         3.8e-17         0.28         0.55         TITIN; CHAIN: NULL;           lbpu         A         158         3.5e-19         0.02         0.55         TITIN; CHAIN: NULL;	lbp3         B         158         354         1.2e-21         0.14         0.05         GROWTH HORMONE, CHAIN:           lbpv         159         259         3.8e-15         0.12         0.77         TITIN; CHAIN: NULL;           lbpv         257         351         3.8e-12         0.59         0.30         TITIN; CHAIN: NULL;           lbpv         479         572         5.1e-11         -0.02         0.25         TITIN; CHAIN: NULL;           lbpv         479         578         9.5e-14         0.09         0.15         TITIN; CHAIN: NULL;           lbqu         A         158         36-17         0.28         0.55         TITIN; CHAIN: NULL;           lbqu         A         158         3.5e-19         0.02         -0.09         GP130; CHAIN: A, B;           lbqu         A         159         347         1.9e-20         -0.07         0.21         GP130; CHAIN: A, B;

PDB annotation	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN		CYTOKINE G-CSF; G-CSF-R; CLASS1 CYTOKINE, HEMATOPOIETIC OR; RECEPTOR, SIGNAL TRANSDUCTION	NT WO	
Coumpound	GP130; CHAIN: A, B;	GP130; CHAIN: A, B;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN:	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN:	GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) ICFB 5	NET ID AT A DHESTON
SEQFOL D score								
PMF score	0.10	0.09	0.35	-0.12	0.24	0.06	0.55	000
Verify score	-0.05	0.04	0.36	0.28	0.17	0.14	-0.07	020
Psi Blast	1.7e-14	6.8e-23	3.8e-13	7.6e-09	9.5e-27	7.6e-16	1.1e-34	1 00-73
END	581	. 189	352	457	356	564	350	156
STAR T AA	358	479	256	359	159	360	156	255
CHAI	4	∢	A	A	æ	æ		
PDB	1bqu	Ibqu	1c8p	lc8p	1cd9	1cd9	1cfb	100
SEQ ID	NO: 1049	1049	1049	1049	1049	1049	1049	10/0

PDB annotation											CELL ADHESION NET BAT CELT	ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL	ADHESION CELL ADHESION NEURAL CELL ADHESION
Coumpound	MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL	TENCHECINI LIFE III REPEATS ICFB 4 (RESIDUES 610 - 814) ICFB 5	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL	FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES	NEURAL ADHESION	MOLECULE DROSOPHILA NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO	AMINO PROXIMAL FIRRONFCTIN TYPE III	REPEATS ICFB 4 (RESIDUES	AXONIN-1; CHAIN: A;		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
SEQFOL D score	·														
PMF score		0.42	0.47			90.0					-0.20	000	-0.08	-0.17	0.10
Verify score		0.17	ì.			0.35					00.00	0.16	0.10	0.12	-0.08
Psi Blast		3.8e-31	10-20:0		·	le-18					6.8e-23	170.35		3.4e-15	6.8e-30
END		675	)			670					671	340	}	06/	464
STAR T AA		475				479					272	2		320	29
CHAI											Ą			ť	V
PDB CI		1cfb				lcfb					lcs6	1036	$\dashv$	0831	1036
SEQ NO:	· · · · · · · · · · · · · · · · · · ·	1049				1049					1049	1049	1040	104	1049

PDB annotation	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROW1H FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	COMPLEX (CYTOKINE/RECEPTOR)
Coumpound	GRANULOCYTE COLONY- STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	GRANULOCYTE COLONY- STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	GRANULOCYTE COLONY- STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2, CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	ERYTHROPOIETIN; CHAIN: A;
SEQFOL D score								
PMF score	0.04	0.09	-0.09	0.42	-0.15	0.19	0.51	0.13
Verify score	-0.16	0.12	0.47	0.25	0.02	-0.01	-0.03	0.08
Psi Blast	7.6e-13	3.8e-13	7.6e-10	6.8e-31	1,5e-15	5.7e-20	1.7e-28	1.5e-07
END	247	350	585	250	135	153	250	555
STAR T AA	157	259	479	74	2	61	47	474
CHAI				U	Q	Ω	Ω	В
PDB	1cto	1cto	Icto	lcvs	lcvs	lcvs	lcvs	leer
SEQ	1049	1049	1049	1049	1049	1049	1049	1049

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PD 8 annotation	EPOBP; ERYTIROPOIETIN, ERYTHROPOIITIN RECEPTOR, SIGNAL 2 TRANSDUCTION, HEMATOPOIETIC CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, CYTOKINE, C	CTIONINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINE/RECEPTOR) CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOEULIN FOLD, GLYCOPPOTEIN	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B TATELL	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTOR/GROWTH FACTOR RECEITOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP FOR THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS BELONGING TO THE I- DOMAINS TO TH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS REI CNGING TO THE I
Coumpound	ERYTHROPOIETIN RECEPTOR; CHAIN: B, C;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1: CHAIN:
SEQFOL D score							
PMF		0.27	0.07	0.65	0.12	0.58	0.63
Verify score		0.02	0.13	-0.02	-0.14	-0.08	0.05
Psi Blast		3.8e-14	6.8e-13	1.7e-26	3.4e-30	5.7e-20	1.7e-26
END		222	234	250	254	213	250
STAR T AA		19	71	74	74		74
CHAI N ID	,	A	¥	ш	ර	U .	U
au au		lepf	lepf	lev2	1ev2	levt	levt
SEQ ID NO:		1049	1049	1049	1049	1049	1049

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PDB annotation	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL		
Coumpound	C, D;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	TELOKIN; CHAIN: A	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3
SEQFOL D score							
PMF		0.51	0.03	0.71	-0.20	0.16	-0.20
Verify		0.28	-0.23	-0.11	0.18	0.23	0.38
Psi Blast		3.4e-24	1.7e-16	7.6e-10	5.1e-08	1.7e-13	6.8e-09
END		354	253	352	572	565	866
STAR T AA		160	70	192	475	486	179
CHAI N ID		В	В	U	Ą		
PDB		.1 <i>f</i> 6 <i>f</i>	1f6f	1f6f	Ifhg	1fna	1fna
SEQ		1049	1049	1049	1049	1049	1049

PDB annotation		CELL ADHESION PROTEIN RGD,	CELL ADHESION PROTEIN RGD.	EXTRACELLULAR MATRIX 1FNF 18	CELL ADHESION PROTEIN RGD,	CELL ADHESION PROTEIN POD	EXTRACELLUI, AR MATRIX 1 FNF 18	CELL ADHESION PROTEIN RGD,	EXIRACELLULAR MATRIX 1FNF 18 HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRAL BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	HEPAKIN AND INTEGRIN BINDING	CELL ADHESION PROTEIN CELL	AUHESION PROTEIN, RGD,	EAIRACELLULAR MATRIX, 2	ALL AKIN-BINDING,	GLYCOPROTEIN	CELL ADHESION PROTEIN CELL	AUTESION FROIEIN, KGD,	EXIKACELLULAR MATRIX, 2	GLYCOPROTERS	CELL ADHESION PROTEIN CELL ADHESION PROTEIN CELL	MEDICINI INCITETIN, ROLL,
Coumpound		FIBRONECTIN; IFNF 6 CHAIN:	4; 1FNF 6 CHAIN:	_	FIBRONECTIN; 1FNF 6 CHAIN:   C	+		FIBRONECTIN; 1FNF 6 CHAIN:	V; CHAIN: A;		FIBRONECTIN; CHAIN: A;		ribronectin; CHAIN; A; H	FIBRONECTIN: CHAIN: A: H		FIBRONECTIN; CHAIN: A; H		FIBRONECTIN; CHAIN: A;	FIBRONECTIN: CHAIN: NITH I.		4 6	<b>d</b> 5	<b>G</b> (	†	THE CHAIN: NOLL; C.	-	₫ E	년 년 -	FIBRONECTIN; CHAIN: NULL; CE	200
SEQFOL D score		-	166.16															•		` <u> </u>		<del>- ,,,-</del>							μ.	
PMF score		86.0		500	0.23	0.76		-0.20	0.55	100	0.0	-0.07	}	-0.19		0.98	6	-0.20	8:				-	8					0.49	
Verify		0.25		00.0	0.29	0.24		0.08	0.22	200	07.0	0.12		0.01		0.29	90		0.21				-	0.03		•	_		-0.04	
Psi Blast	, ,	3.1e-36	5.1e-36	2 10 22	2:46-33	1.7e-26	1	21-24-17	1.7e-20	3 40 27		3.4e-23	_	8.5e-25	7	1.4e-18 (	3 40-20		1.1e-27		•			3.4e-14 0		•		7	1.1e-20	
END	202	202	575	866	335	459	077	///	564	664	5	751		855		333	226		343					343	-	-		7	420	
STAR T AA	150	901	159	470	<u>}</u>	89	777	7//	272	361	;	482		280	6	?	774		157					162					239	
CHAI N ID									¥	<b>▼</b>		A		∀		<	\   											1		
PDB UD	1Enf		Ju I	1faf		I fift	1finf		1fnh	Ifnh		1fnh	7	<u></u>	151		1fnh	-	lmfn					Imfn		_		1 1 6 1		
SEQ	1040 1040		1049	1049		1049	1049		1049	1049		1049	355	1049	10/10	}	1049		1049					1049				1040	$\dashv$	

PDB annotation	EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GL YCOPROTEIN	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
Coumpound		FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;
SEQFOL D score		·					·
PMF score		0.45	0.13	0.17	-0.05	1.00	0.99
Verify		0.13	0.05	0.24	0.20	0.16	0.19
Psi Blast		6.8e-11	3.4e-20	1.9e-27	6.8e-25	9.5e-23	1.2e-15
END		459	565	999	599	152	352
STAR T AA		272	360	482	482	2	160
CHAI							₹.
PDB ID		1mfh	1mfn	Imfn	Infi	Inct	1923
SEQ EQ		1049	1049	1049	1049	1049	1049

			<del></del>					
PDE annotation	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2	FRUIEIN STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2	PROTEIN STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2	PROTEIN STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN 1 YPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN,	STRUCTURAL PROTEIN STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN,	STRUCTURAL PROTEIN STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN	STRUCTURAL PROTEIN IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN 1G REPEAT 27: MUSCI E PROTEIN
Coumpound	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TITIN, 127; CHAIN: NULL;
SEQFOL D score		103.51						L
PMF score	0.59		0.43	0.66	0.43	-0.20	-0.20	0.15
Verify	0.11		0.23	0.29	0.24	0.09	0.08	0.70
Psi Blast	3.4e-19	5.1e-26	5.1e-26	3.4e-17	6.8e-12	3.4e-08	3.46-11	1.1e-19
END	695	677	663	248	564	862	971	150
STAR T AA	361	479	481	89		711	776	89
CHAI N ID	∢	V	<b>∢</b>	¥	∢	4	4	
PDB ID	1983	Iqg3	1983	1983	1qr4	1qr4	1qr4	1tit
SEQ ID NO:	1049	1049	1049	1049	1049	1049	1049	1049

PDB annotation	IMMUNOGLOBULIN-LIKE DOMAIN			MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D- DOMAIN SWAPPING, 2 TRANSFERASE	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
Coumpound		MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;
SEQFOL D score										
PMF score		0.84	-0.20	-0.09	0.59	0.01	0.68	0.16	0.10	0.04
Verify		0.39	0.39	99.0	0.18	-0.00	0.55	0.76	0.02	-0.12
Psi Blast		1.9e-22	1.7e-09	1.9e-22	1.1e-21	9.5e-13	1.5e-14	9.5e-14	9.5e-10	1.9e-13
END		152	998	152	163	251	250	345	465	570
STAR T AA		19	776	65	49	09	154	255	359	475
CHAI N ID					A	Ą	∢	Ą	4	A
PDB		1tmm	1#t	1wit	1wwc	2fcb	2fnb	2fnb	2fnb	2fnb
SEQ	Ö	1049	1049	1049	1049	1049	1049	1049	1049	1049

PD/8 annotation	PROTEIN BINI)ING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 RINDING			CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILLS 3 BINDING, CELL ADHESION PROTEIN	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION CELL ADHESION NEURAL CELL	GROWTH FACTOR/GROWTH FACTOR RECEIPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,
Coumpound	FIBRONECTIN; CHAIN: A;	HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN)	HORMONE/RECEPTOR HUMAN HORMONE/CORVITH HORMONE COMPLEXED WITH ITS RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN)	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	HEMOLIN; CHAIN: A, B;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:
SEQFOL D score							
PMF score	0.28	0.13	0.03	0.46	-0.06	0.07	-0.05
Verify score	0.10	0.16	0.24	0.45	60:0	0.02	0.12
Psi Blast	1.5e-16	le-10	3.8e-27	3.8e-23	3.4e-29	3.4e-34	3.4e-41
END	670	349	351	154	157	158	157
STAR T AA	574	162	162	59	20	4	3
CHAI N ID	<b>V</b>	æ	m	4	A	A	U
PDB ID		3hhr	3hhr	3пст	1bih	1cs6 /	lcvs
SEQ NO:	1049	1049	1049	1049	1050	1050	1050

PDB annotation	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,	GECTOR RECEPTOR CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	IMMUNE SYSTEM FC-EPSILON RI-	ALPHA; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM, MEMBRANE
Coumpound	C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	C, D; NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN: E, F, G, H;		FIBROBLAST GROWTH	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;	FIBROBLAST GROWTH	FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	HIGH AFFINITY	IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A;	FC RECEPTOR
SEQFOL D score																			
PMF score		0.33	0.64	0.05				-0.05				0.54				0.54			0.00
Verify score		0.22	-0.00	0.08				0.21				0.08				0.19		·	-0.02
Psi Blast		6.8e-42	6.8e-22	1.7e-36			1	8.5e-14				1e-41				1.7e-23			8.5e-24
END		157	143	157				162				157				162			159
STAR T AA		rn .	2	<u>س</u>	•			66				3				2	1		2
CHAI		Q	A	pi	l			ш				ပ				<b>∀</b>			A
PDB ID		lcvs	lepf	lev2				lev2				levt				1920			Ifcg
SEQ ID		1050	1050	1050				1050				1050				1050			1050

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PDB annotation	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA RARRET	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA RARBEI	IMMUNE SYSTISM RECEPTOR BETA SAMUNE SYSTISM RECEPTOR BETA TWE PROFESSIONAL TANKS BECKETON	MUSCLE PROTIJIN CONNECTIN, MUSCTARS; CELL ADHESION, GLYCOPROTEIN	TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3	MUSCLE PROTEIN MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN,	TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MISCI E DE OTTEN	Marion	
Соимроии	FC(GAMMA)RIIA; CHAIN: A;	TELOKIN; CHAIN: A	TELOKIN; CHAIN: A	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A	IIIIN; CHAIN: NULL;		TITIN; CHAIN: NULL;		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED 1TNM 4 (NMR, MINIMIZED	MUSCLE PROTEIN TITIN MODDLLE MS (CONNECTIN) 1TNM 3 (NMR, MINIMIZED
SEQFOL D score										
PMF score	·	0.63	-0.14	0.31	0.87		-0.09		0.54	-0.12
Verify score		-0.10	0.37	0.00	0.07		0.20		0.43	0.07
Psi Blast		1.2e-12	3.4e-17	1.9e-20	1.2e-12		1.70-16		1.2e-12	1.7e-16
END		75	157	147	75		158		75	158
STAR T AA		-	92	5	2		08		8	80
CHAI N ID		4	۷	∢						
PDB ID		lfhg	lfhg	E TE	Inct		Inct	,	Itnm	Itnm
SEQ ID NO:		1050	1050	1050	1050		1050		1050	1050

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PDB annotation	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR,	NATURAL KILLER RECEPTOR, 1 INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	COMPLEX (ANTIGEN/PEPTIDE) B35;	MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX	B8; B2M; PEPTIDE HLA B8, HIV,	HISTOCOMPATIBILITY COMPLEX		IMMUNE SYSTEM IMMINOGLOBILLIN FOLD			IMMUNE SYSTEM MHC, HLA,	CLASS 1, KIR, NK CELL RECEPTOR,	RECEPTOR/MHC COMPLEX				
Coumpound AVERAGE STRUCTURE) ITNM	4 1TNM 58 MHC CLASS I NK CELL RECEPTOR PRECURSOR;	CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	B*3501; CHAIN: A, B; PEPTIDE	VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	(GGKKKYKL - INDEX	PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D;	CHAIN: B, E; HTLV-1	OCTAMERIC TAX PEPTIDE;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	MICKOGLOBOLIN; CHAIN: B; PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	HISTOCOMPATIBILITY	ANTIGEN MURINE CLASS I
SEQFOL D score																			
PMF	0.09		69.0	0.30		0.25				0.22			0.28					69.0	
Verify	-0.26		0.14	-0.16		90.0				0.18			0.24					0.34	
Psi Blast	1.9e-19		6.8e-25	3.4e-43		3.4e-43				1.7e-42			5.1e-43					1.4e-42	
END	146		160	115		115				115			115					116	
STAR T AA	2		2	26		26				26			26					26	
CHAI N ID	A	,	A	A		A				Ą			¥					A	
PDB ID	2dli		2fcb	lain		lagd	)			Iduz			1efx					Ihoc	
SEQ ID NO:	1050		1050	1051		1051			•	1051			1051					1051	

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PD B annotation			MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-	CLASSICAL MIAC, CLASS IB MHC COMPLEX (MHC IPEPTIDE) VSV-8; MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC I/PEPTIDE)	COMPLEX (NK RECEPTORAMIC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-1, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY R2M 1 VAO
Coumpound	MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D===, B2- MICROGLOBULIN, AND A 9-	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3	H.A CLASS I H.A CLASS I HISTOCOMPATIBILITY ANTIGEN H.A-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MHC CLASS I H-2KB HEAVY CHAIN; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN;	CHAIN: C; MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2. MCROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;
SEQFOL D score					
PMF score		0.40	0.25	0.37	0.39
Verify score		0.08	0.13	0.13	0.10
Psi Blast		8.5e-44	8.5e-43	1.2e-43	3.46-42
END		115	115	115	1115
STAR T AA		26	56	56	26
CHAI N ID		∢		∢	4
PDB ID		1hsb	υ	losz	1403
S E S		1051			1051

PDB annotation	LY-49		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	
Coumpound		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALÇIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2
SEQFOL D score		·	100.26	108.39	89.55	68.22	97.42
PIMF score		0.52					
Verify score		0.43					
Psi Blast		8.5e-44	3.4e-49	8.5e-38	3.4e-34	5.1e-37	3.4e-44
END		115	650	762	466	291	283
STAR T AA		26	268	596	327	160	154
CHAI N ID		¥	U	<b>4</b>	V	<b>A</b>	
PDB		Itme	1mey	1466	2gli	1a25	Irsy
SEQ EL SEG		1051	1068	1068	1068	1070	1070

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PDB annotation			COMPLEX (G1P- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G	SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTI:IN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRIJCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (TRÁNSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION	REGULATIONINA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	COMPLEX (DNA-BINDING PROTFINDNA) FIVE FINGED CT 1.
Coumpound	DOMAIN) (CALB) IRSY 3		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAIMA; CHAIN: G;		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C. D:
SEQFOL D score			116.65		104.69		107.26	114.17		103.60
PMF score			·							
Verify score										
Psi Blast			5.1e-89		5.16-81		1.4e-48	le-37	<u> </u>	1.4e-33
END			322		345		412	913		441
STAR					ဇ		330	750		302
CHAI N ID			m .		g	1	ပ	∢		4
PDB UD			lgot		Igot	+	Imey	11166		2gli /
SEQ ID NO:			1075		1078	, ,	1084	1084		1084

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PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	CONTRACTILE PROTEIN WHI DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN	CELL MOTILITY AN INCOMPLEIE SEVEN STRANDED ANTI-PARALLEL BETA BARREL 2 CLOSED BY AN ALPHA HELIX, EVHI DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE	Village drawn and and and and and and and and and an	COMPLEX (ZINC FINGERIDAS) COMPLEX (ZINC FINGERIDAS), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2
Coumpound		MENA EVHI DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	EVHI DOMAIN FROM ENA/VASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE- PRO-PRO-PRO-THR-ASP- GLU-GLU; CHAIN: C, D;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score		82.80	62.71		84.85	110.38	120.65	98.51
PMF score								
Verify								
Psi Blast		3.4e-50	1.7e-44		1.7e-26	1.4e-45	3.4e-34	3.4e-33
END		122	121		473	500	530	444
STAR T AA		6	6		391	418	362	336
CHAI		∢	<b>∀</b>		4	U	A	U
PDB ID		1evh	19c6		lalh	Imey	14f6	pqnI
SEQ ID	NO:	0601	1090		1095	1095	1095	1095

PD)3 annotation	FINGER PROTISIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGII A TION/DNA)	COMPLEX (DNA-BINDING PROTEINIDNA) FIVE-FINGER GLI; GLI, ZINC FINCER, COMPLEX (DNA- BINDING PROTEIN/DNA)		CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECADI2; CADHERIN, CELL ADHESION PROTEIN, CALCIUM PENDANG PERCEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN		MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCHIM BINDING	HYDROLASE, PHOSPHATASE,	DAMOUNDS OF THE SOLON CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPICIFIC GUANYLATE	2 CYCLASE ACTIVATOR			· .	
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		E-CADHERIN; CHAIN: A, B;	N-CADHERIN; CHAIN: A;		TROPONIN C; CHAIN: NULL;	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B:	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN
SEQFOL D score		105.76		122.19	122.52		73.76	92.24	184.52	57.84		-		67.88
PMF											••			
Verify														
Psi Blast		6.8e-34	,	5.Ie-48	6.8e-50		8.5e-36	1.7e-39	1.7e-49	1.4e-55				3.4e-60
END		473	200	007	265		237	249	245	234			<u> </u>	235
STAR T AA		334	3	78	19		72	47		82				82
CHAI N ID		4	<	₹	∢			В	¥	A	•			
PDB ID		2gli	1001		Incj	+		laui	lbjf	lcdm				Ioll
SEQ ID NO:		1095	1011		1101	100	CO 1	1105	1105	1105	<del></del> -		+	1105

PDB annotation			CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCUIM-BINDING PROTEIN	T. D. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S. C. S.	CALCIUM-KEGULA I ED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)		COMPLEX (GTPASE-	ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING),	TRANSPORT PROTEIN TC4; GTPASE,
Coumpound		CALMODULIN (VERTEBRATE) 1CLL 3	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) 1REC 3	TROPONIN C; CHAIN: NULL;		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 170P 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	BINDING PROTEIN SARCOPLASMIC CALCIUM-BINDING PROTEIN 2SCP 3	PSO BHOGAP: CHAIN: A B C:	CDC42HS; CHAIN: D, E, F;	GTP-BINDING PROTEIN RAN;
SEQFOL	D score		160.57	143.82	73.38	<u>.</u>	96.69	73.36	68.28	53.97	20 02	)(r.80	74.78
PMF	score												
Verify	score					·							
Psi Blast			3.4e-39	1.7e-34	1.5e-39		.1e-38	8.5e-40	3.4e-59	3.4e-09	9	6.8e-48	8.5e-52
END	*		245	250	235		233	237	236	205		216	231
STAR	TAA		79	89	70		29	63	79	34		51	45
CHAI	N ID								A	A		Ω	A
aua	A		1 iku	1rec	1tcf		1tmx	Itop	lvrk	2scp		lam4	1byu
Cata	a e	Ö	1105	1105	1105	•	1105	1105	1105	1105		1114	1114

Ibyu   B   41   231   1.7e-52   69.65   GTP-BINDING PROTEIN RAN;     Ibyu   B   41   231   1.7e-52   69.65   GTP-BINDING PROTEIN RAN;     Icid   A   50   216   1.7e-63   75.99   TANNSFORMING PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICATE PROTEIN RAPRICA							•													
Part   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation	NUCLEAR TRANSPORT,	TRANSPORT PROTEIN TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT,	SIGNALING PROTEIN SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS		SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC	CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX,	ANTIPARALLEL COILED-COIL	PROTEIN TRANSPORT GDP. BINDING, MENIBRANE TRAFFICKIN,	NON-MYRISTOYLATED 1HUR 16	SWALL GIFASE KARY OPHERIN BETA, P95 SMALL GIPASE,	NUCLEAR TRANSPORT RECEPTOR	GTP-BINDING PROTEIN GTP. BINDING PROTEIN, SMALL G	PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO	FAMILY, RAS SUPER 2 FAMILY	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN)	COMPLEX (SMALL	GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF	Coumpound	CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE	SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN:	A; PKN; CHAIN: B;	FACTOR 1; 1HUR 5 CHAIN: A,	BAN CHAIN A C. IMBORTEN	BETA SUBUNIT; CHAIN: B, D;	D A DO A . CHIA PATTITITITITITI	NAFZA; CHAIN: NULL;	DACI: CHAIN: NITE	INC. I; CHAIN: NOLL;	DANI CITABLA CATIOTAL	PORE COMPLEX PROTEIN	NUP358; CHAIN: B, D;	
PDB   CHAI   STAR   END   Psi Blast   Verify   Score	SEQFOL D score		69.65	67.97		75.99		82.44	97.52	71.40	86.05	}	T		1					
PDB   CHAI   STAR   END   Psi Blast   TAA   AA   AA   TABBast   TAA   AA   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast   TABBast	PMF score																		·····	
PDB   CHAI   STAR   END   Psi B   N ID   TAA   AA   AA	Verify score									-			-				+			
PDB   CHAI   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   STAR   S	Psi Blast		1.7e-52	1.7e-63		1.7e-62		1.5e-54	\$ 10.17	71-21:5	3.4e-51		3.46-60	3	1.2e-54		3.4e-51			
PDB CHAI  IDD NID  Ibyu B  Ictq A  Ictq A  Ibr A  Ilbr A  Imhi  Imhi  Imhi  Irrp C  4	END	ļ 	231	216		217		777	218		221	-	217	<u>-</u>	222		231			
PDB	STAR T AA		41	50		99	ţ	<del>}</del>	37				50		49					
PDB  PDB  ID  Ictq  Ictq  Ictq  Ictq  Imhi  Imhi  Irrp	CHAI N ID		В	¥		∢		<	A		A						U		·	
~	PDB ID		1byu	lcly		l ctq		727	1		T		1kao		1mh1		+			
	SEQ NO:		1114	1114		4111		<u> </u>	1114		1114		1114		1114		1114		_	

PDB annotation	TRANSPORT	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE	ACTIVATION/FROTO-ONCOGENE,, GTPASE, 2 TRANSITION STATE, GAP	COMPLEA (OTF- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-	BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC	EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION	STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP	HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HIDROLAGE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE; HYDROLASE, ACETYLATION, TYROSINE PHOSPHATASE
Coumpound		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;			GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE	ACTIVATING PROTEIN (RHG);	RAB3A; CHAIN: A;			RIBONUCLEASE INHIBITOR; CHAIN: NULL;	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;
SEQFOL D score		70.72		93.30			77.06		102.45			56.47	214.70
PMF score													
Verify													
Psi Blast		1.4e-51		1.7e-63			3.4e-50		6.8e-65			1.7e-52	1.4e-54
END		216		226			230	<del></del>	221			324	140
STAR T AA		51		49			50		47			2	2
CHAI		m		A			A		Ą				
PDB		1tx4		1zbd			2ngr		3rab			2bnh	Spnt
SEQ	ÖN	1114		1114			1114		1114			1116	1120

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PDB annotation	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER,	COMPLEX (SERINE PROTEASE/INFIBITOR) (DELTAFEK)DSPAALPHAI; EGRCMK; SERINE PROTEASE, FIBRINOL YTIC ENZYMES,	PLASMINOGEN 2 ACTIVATORS COMPLEX (SERINE PROTEINASE/INHIBITOR)	COMPLEX (BLCOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COAGULATION/INHIBITOR) HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE
Coumpound	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A, B, C, D;	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	ALPHA-THROMBIN; 1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: 1. 1AUT 0	CHAIN: P;	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;
SEQFOL D score	51.65	100.75	106.52	91.53	99.33	89.82
PMF score						
Verify						
Psi Blast	5.1e-05	3.4e-76	5.1e-67	1.5e-73	5.1e-68	1.7e-76
END	280	741	739	744	739	739
STAR T AA	83	465	454	465	464	468
CHAI N ID	4	A	. ∢	Н	U	æ
PDB ID	lavi	1a01	1851	laht	laut	1ekb
SEQ ID NO:	1122	1127	1127	1127	1127	1127

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otation		ATION FACTOR ATION FACTOR TEASE, PPACK ETONE, SETONE, SETONE	EN, SERINE A, BLOOD COMPLEX	OENZYME) OENZYME), THROMBIN-2, ROTEASE	SX (ZYMOGEN NARY COMPLE NE PROTEINAS YTIDASE	3 (TC)-T-PA;	INGER/DNA) Z DNA OTEIN DESIGN URE, COMPLE
PDB annotation		COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (PROTEASE INHIBITE RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)	COMPLEX (BLOOD COAGULATIONPROENZYME) COMPLEX (BLOOD COAGULATIONPROENZYME), THROMBIN, 2 PRETHROMBIN-2, PLASMA, SERINE PROTEASE	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
			22225	••		2 2 E	OFHO
Coumpound	HYDROLASE(SERINE PROTEINASE) EPSILON- THROMBIN (E.C.3.4.21.5) NON- COVALENT COMPLEX WITH IETR 3 MQPA IETR 4	COAGULATION FACTOR XA- TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG- CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	ALPHA-THROMBIN; CHAIN: L, H; PRETHROMBIN-2; CHAIN: K;	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
of.	14701	07100					
SEQFOL D score	92.09	89.40	98.96	93.49	95.69	102.89	71.69
PMF score							
Verify score							
Psi Blast	1.5e-71	1.4e-76	3.4e-70	1.7e-72	1.5e-75	1.7e-68	6.8e-47
END	745	742	745	739	739	740	430
STAR T AA	465	463	465	425	454	467	342
CHAI	H	A	H	¥	Q	æ.	၁
PDB ID	1etr	lfxy	lkig	1mkx	lpyt	1rf	lmey
SEQ	NO:	1127	1127	1127	1127	1127	1135

PDB annotation	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR. 5S RNA 2	GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/JNA) YING-YANG 1; TRANSCRIPTION INITIATION	NITIATOR ELEMENT, YYI, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	REGULATION/DNA)	COMPLEX (DN/\-BINDING	FROIEINDNA) FIVE-FINGER GLI;	BINDING PROTEIN/DNA)		HYDROLASE A'IP SYNTHASE, FOF1. ATPASE, OXIDATIVE PHOSPHORY A TION 3	MITOCHONDRIA, HYDROLASE	
	(ZINC F	COMPL REGUL	GENE; 1 TRANS	GENE, 1 ZINC FI	REGUL	COMPL REGUL	(TRANS	POLYM	TRANSC	COMPLI	REGUL,	INITIAT	FINGER	PECOGE PANA	REGUL!	COMPLI	PROTEI	BINDIN		HYDRO ATPASE PHOSPH	MITOCH	
Coumpound		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE;	CIMIN: E, F;			TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE;	Chain: B, C, E, F;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;				ZINC FINGER PROTEIN GLII; CHAM: A: DNA: CHAM: C. D.	CIMIN: A, DIVA, CITAIN: C, U;			FI-ATPASE ALPHA CHAIN; CHAIN: A; FI-ATPASE BETA CHAIN: CHAIN: B: FI-ATPASE	GAMMA CHAIN; CHAIN: G;	
SEQFOL D score		67.88				105.09				80.44						202.77				64.40		
PMF																						
Verify score																						-
Psi Blast		1.5e-21				3.46-41				1.7e-30				•		1.46-00				1.7e-46		
END		433				404 404		,,,		400					121			1		183		1
STAR T AA		342				0/7				//7					277							
CHAI N ID		∢			-	₹			(	د.					4	<del></del>			1	n n		
PDB ID		£			7,462	071				pont		_		<u>-</u>	Joli				┿	Open	+	
SEQ ID NO:		1135			1126	CCII	-		1136	6511					1135	}		1	1130	6011	+	1

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PDB annotation	HYDROLASE ATP SYNTHASE, FOF1- ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN	
Coumpound	FI-ATPASE ALPHA CHAIN; CHAIN: A; FI-ATPASE BETA CHAIN; CHAIN: B; FI-ATPASE GAMMA CHAIN; CHAIN: G;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	GT-AIPHA/GI-AIPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	
SEQFOL D score	130.11						329.67		
PMF		0.17	0.94	0.18	0.40	1.00		1.00	
Verify		0.19	0.70	0.16	0.01	69.0		0.64	
Psi Blast	6.8e-66	1.6e-09	3.2e-29	3.2e-10	8e-22	1.4c-97	0	0	
END	264	122	127	79	122	326	339	334	
STAR T AA	51	3	11	3	9	43	36	9	
CHAI N ID	В	A	A	A	а	- A			
PDB	1mab	lorz	lerj	lerj	lgot	1ef1	1a06	1a06	_
SEQ	NO:	1148	1148	1148	1148	1149	1153	1153	ļ

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PD]3 annotation	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE		SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN		KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG	TRANSFERASE TRANSFERASE	(PHOSPHORYL) TRANSFERASE TRANSFERASE	(PHOSPHORYL)		
Coumpound	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;		URIDYLMONOPHOSPHATE/CY TIDYLMONOPHOSPHATE KINASE; CHAIN: A;	PHOSPHOGLYCERATE	MUIASE; CHAIN: A, B; PHOSPHOGLYCERATE	MUTASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE	KINASE (E.C.2.7.4.3) 3ADK 4
SEQFOL D score	82.01							63.00			
PMF		1.00		00.1		0.62	1.00			99.0	
Verify score		0.47		0.06		-0.03	0.47			-0.17	
Psi Blast	1e-28	1e-28		1.26-46		1.5e-19	5.1e-47	5.1e-47		3.4e-26	
END	203	203		96		239	424	449		736	
STAR T AA	51	52				23	249	250		9	
CHAI N ID				∢		∢	٧	A			
PDB ID	1cfe	1cfe		lds6		विप्रि	l 1qhf	1qhf	17.7	Sadk	
SEQ ID NO:	1155	1155		1156		6011	1159	1159	1150	6011	

								_																$\Box$
PDB annotation			-				KINASE KINASE, PHOSPHOTRANSFERASE	(). (d)	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMEKASE III, 2	I KANSCKIP TION INTITATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGILLATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-
Coumpound	The Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract of the Contract o	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE	MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	TRANSFERASE (PHOSPHORYL)	PHOSPHOGL YCERATE	MULASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		TFIIIA; CHAIN: A, D; 58 RIBOSOMAI, RNA GENE:	CHAIN: B, C, E, F;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	CHAIN: A B.	CIENTY, D,			ZINC FINGER PROTEIN GLII; CHAIN: A: DNA: CHAIN: C. D:	
SEQFOL	D score			58.96					100.83			108.88					86.63						98.31	
PMF	score	1.00					0.19									· <u>-</u>								
Verify	score	0.19					-0.13																	
Psi Blast		1.7e-48		1.7e-48			1.2e-29		4.8e-51			8e-38					5 IA-53						3.2e-34	
END	AA	441		441			237		442			437					442	Ì				,	443	
STAR	T AA	249		249			34		360			276					23.4	# 					304	
CHAI	e Z						A		O.			A					ر	ر					A	
PDB	<u>e</u>	3pgm		3pgm			3tmk		Imey			1tf6					1164	pont					2gli	
SEQ	АÖ	1159		1159			1159		1160			1160					9,	201					1160	

		1		<del></del>	<del></del>													_		
PDB annotation	BINDING PROTEIN/DNA)		KINASE KINASE, SIGNAL TRANSDUCTION,	TRANSFERASI: TRANSFERASE, SERINE/THRECONINE-PROTEIN KINASE, CASEIN KINASE, 2 SEP 7THD 2 THA SE	ACCULATION AND AND AND AND AND AND AND AND AND AN						PROTEIN KINA SE CDK2; PROTEIN	KINASE, CELL CYCLE,	PHOSPHORYLATION,	MITOSIS, INHIBITION	COMPLEX (KINASE/INHIBITOR) CDK6: P19NK4D: CYCI IN	DEPENDENT KINASE, CYCLIN	DEPENDENT KINASE INHIBITORY 2	PROTEIN, CDK, INK4, CELL CYCLE,	COMPLEX (KINASE/INHIBITOR) HEADER HELLY	COMPLEX (INFIBITOR PROTEIN/KINASE) INHIBITOR
Coumpound			CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: MIIIT:	PROTEIN KINASE CKZ/ALPHA- SUBUNIT; CHAIN: NULL;	TRANSFERASE (PHOSPHOTRA NSFERASE) \$C-/AMP\$-	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	CYCLIN-DEPENDENT PROTEIN	KINASE 2; CHAIN: NULL;			CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-	DEPENDENT KINASE	INHIBITOR; CHAIN: B, D;			CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:
SEQFOL D score			130.42	108.45	168.88						111.26				93.00					113.75
PMF																			_	
Verify																				
Psi Blast			3.2e-84	6.8e-54	0						4.8e-56				0.8e-56		-	_		6.8e-62
END			340	334	353				······		348			000	273			_		331
STAR T AA			43	18	81						20				1			•		47
CHAI N ID					ш										ζ					V
PDB ID		į	1a06	1a60	lapm						laq1	'		15:0					-	xiq i
SEQ D NO:			1163	1163	1163						1163			2711	3					1103

	Т	<del></del>	65	<i>t.</i>				
PDB annotation	THE CANOT IN DEBENDENT	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE			PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHOR YLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFKIR, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHOR YLATION, RECEPTOR, PHOSPHOTRANSFERASE	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN
Coumpound		<b>B</b> ;	C-TERMINAL SRC KINASE; CHAIN: A;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;
SEQFOL	D SCOLE		93.49	175.36	168.10	106.44	117.87	128.78
PMF	SCOI C							
Verify	score							
Psi Blast		·	1.3e-31	0	0	6.4e-31	1.3e-37	1e-66
END	¥¥		300	353	343	309	304	348
STAR	TAA		44	6	15	39	36	50
CHAI	E E N		V	ы	E	∢	Ф	
PDB	<u>e</u>		1byg	1cmk	lctp	1fgk	1fgk	lhcl
SEQ	A Š		1163	1163	1163	1163	1163	1163

150   10   10   10   10   10   10   10	г		<del></del>						·										
1   1   1   1   1   1   1   1   1   1	PD)3 annotation	KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS,	PHOSPHORYLATION COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL	IKANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINIASE/PEPTIDE SUBSTRATE/ATP ANALOG).	ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	TRANSFERASE JNK3; TRANSFERASE JNK3 MAP KINASE	SERINE/THREONINE PROTEIN 2	KINASE KINASE, TWITCHIN,	TRANSFERASE MITOGEN	ACTIVATED PROTEIN KINASE;	SERINE/THREONINE-PROTEIN	KINASE, 2 P38 KINASE RABBIT MUSCLE	PHOSPHORYLASE KINASE;	TRANSFERASE.	SERINE/THREONINE-PROTEIN, 2	CALMODULIN-BINDING	TRANSFERASE MAP KINASE,	SERINE/THREONINE PROTEIN	SERINE KINASE SERINE KINASE
Q PDB         CHAI         STAR         END         Fel Blast         Verify         PMF         SEOFOL           3         11r3         A         38         323         3.2e-26         99.07           1 ljnk         A         24         359         1.e-90         104.42           1 lphk         A         24         359         1.e-50         159.16           1 phk         49         305         1.1e-83         116.26           1 pme         44         389         9.6e-46         104.21           1 ltk         A         47         370         8e-57         131.84	Coumpound		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;			C-JUN N-TERMINAL KINASE; CHAIN: NULL;		TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN:	NULL;		PHOSPHORYLASE KINASE;	CHAIN: NULL;				ERK2; CHAIN: NULL;		
Q PDB         CHAI         STAR         END         Psi Blast         Verity           D D         In3         A         38         323         3.2e-26         score           1 lin3         A         38         323         3.2e-26         score           1 link         38         388         5.1e-64         score           1 lphk         A         24         359         1.6e-50           1 lphk         49         305         1.1e-83           1 lpme         44         389         9.6e-46           1 lti         A         47         370         8e-57	SEQFOL D score		99.07			104.42		159.16	109.88	-		156.26							П
Q         PDB         CEAI         STAR         END         Psi Blast           9.         ID         N ID         T AA         AA         AB         Psi Blast           3.         1ii3         A         38         323         3.2e-26         AB           1 link         A         24         359         1e-90         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB         AB	PMF score														<del></del>				
Q         PDB         CHAI         STAR         END         Psi Bi           9         ID         N ID         T AA         AA         38         3.2e-2c           3         1ii3         A         38         388         5.1e-6d           1 lpk         A         24         359         1e-90           1 phk         49         305         1.1e-83           1 pme         44         389         9.6e-46           1 lbis         A         47         370         8e-57	Verify										H								
9 PDB CHAI STAR 10 D NID TAA 31 lir3 A 38 31 38 31 31 31 31 31 31 31 31 31 31 31 31 31	Psi Blast		3.2e-26		5 10-64	10-21-0		16-90	1.6e-50			1.1e-83				77 - 77	2.06-40		8e-57
9 PDB CHAI STAR 9. ID NID TAA 33 lit3 A 38 1 livb A 24 1 lphk 49 1 lpme 44 1 lpme 44 1 ltki A 47	<del></del>		323		388	3		359	395			305				300	3		370
9 PDB CHAI  9 ID N ID  1 Jink 1 1pine 1 lpine 1 ltki A	STAR T AA		38		38	}	3	74	31			49				1			
9	CEAI N ID		<b>∀</b>										<u> </u>		-				
00 i	PDB ID		lir3		1ik		103-	n koo	1p38			1phk				1 nme	<u> </u>	7	7
	SEQ ID NO:		1163		1163		1163	3	1163			1163				+-	_	$\dashv$	٦.

PDB annotation	TITIN, MUSCLE, AUTOINHIBITION	ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	IMMUNE SYSTEM IMMUNOGLOBULN, IMMUNORECEPTOR, IMMUNE SYSTEM	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE	GLYCOPROTEIN	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM			IMMUNE SYSTEM HUMAN TCRPEPTIDE/MHC COMPLEX, HLA- A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM
Coumpound	CT HALLOW	EXTRACELLOLAR REGULATED KINASE 2; CHAIN: NULL;	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;		IGGI ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGGI ANTIBODY 58.2 (HEAVY CHAIN); CHAIN; H; EXTERIOR	MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT IFIG 3	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;
SEQFOL D score		116.38	50.07	50.90		51.50		51.43	50.17
PMF score									
Verify score									
Psi Blast		3.4e-69	1.6e-12	0.00034		4.8e-21		8e-19	6.4e-23
END		400	247	061		244		239	219
STAR T AA		36	17	22		17		17	14
CHAI N ID			A			н		H	D
PDB ID		3erk	1bw m	1cdy		1f58		1fig	19rn
SEQ ID	NO:	1163	1170	1170		1170		1170	1170

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PDB annotation		IMMUNOGLOBULIN IMMUNOGLOBULIN	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE		BLOOD COAGI ILATION FACTOR BLOOD COAGI ILATION, GLYCOPROTEIN, CALCIUM, PLATELET, PLASMA, 2 ALTERNATIVE SPLICING, SIGNAL, DISEASE MUTATION, 3	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN,	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN,	BLOOD COAGULATION BLOOD COAGULATION, FIBRINOGEN-420, ALPHAEC DOMAIN, 2 FIBRINOGEN RELATED DOMAIN, 2	BLOOD COAGULATION BLOOD COAGULATION, PLASMA,	BLOOD COAGULATION BLOOD
Coumpound	IMMUNOGLOBULIN IGGZA FAB FRAGMENT (CNI206) 2GFB	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;		GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT; CHAIN: NULL;	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	FIBRINOGEN-420; CHAIN: A, B, C, D, E, F, G, H;	FIBRINOGEN; CHAIN: A, B, C, D, E, F, S, T, M, N;	FIBRINOGEN: CHAIN: A. B. C.
SEQFOL D score	51.08	51.13			129.15	132.32	141.90	154.36	141.24	130.27
PMF score			0.04							
Verify score			-0.20							
Psi Blast	1.6e-17	9.6e-21	0.0017		1.7e-53	1.7e-63	3.4e-62	1.7e-57	1.1e-39	3.2e-39
END	240	239	245		418	416	422	419	419	416
STAR T AA	15	17	152		561	148	151	242	170	160
CHAI N ID	4	В				В	၁	¥	ပ	E
PDB ID	2gfb	2pcp	1a17		1fib	Ifzc	lfzc	1fzd	Ifzg	lfzg
SEQ ID NO:	1170	1170	1174		1180	1180	1180	1180	1180	1180

																				<del></del> -
PDB annotation	COAGULATION, PLASMA,	PLATELET, FIBRINOGEN, FIBRIN	CYTOKINE MACROPHAGE,	INFLAMMATORY RESPONSE, CYTOKINE	CYTOKINE MACROPHAGE,	INFLAMMATORY RESPONSE, CYTOKINE	CYTOKINE PHENYLPYRUVATE TAUTOMERASE; CYTOKINE,	MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE	M VMOI NOIL VERTICAL IN	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT	5000000	CALCIUM-BINDING PROTEIN CALSEQUESTRIN, CALCIUM-	BINDING PROTEIN, SAKCOFLASMIC 2 RETICULUM, RABBIT SKELETAL MISCI F	MOSCEE	UBIQUITIN CONJUGATION UBC2;	UBIQUITIN-CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL	STRUCTURE, ELONGATED SEALE,   F2 FRIOTITIN LIGASE. E2 2	UBIQUITIN CONJUGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN- CONJUGATING ENZYME, YEAST
Coumpound	N N H S d d N	L, E, E, S, 1, 195, 19,	MACBOBHAGE MIGBATION	INHIBITORY FACTOR; CHAIN:	GLYCOSYLATION-INHIBITING	FACTOR; CHAIN: A, B, C;	MACROPHAGE MIGRATION INHIBITORY FACTOR: CHAIN:	A, B, C;		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN;	CHAIN: A;	CALSEQUESTRIN; CHAIN: NULL			UBIQUITIN-CONJUGATING	ENZIME NADO, CITALIN 19, 5, 5,	UBIQUITIN-PROTEIN LIGASE	E3A; CHAIN: A, B, C;	ENZYME E2; CHAIN: D;	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;
SEQFOL	31036		20 37	143.02	180.54		170.94			76.43		91.59	<del>,,,,</del>		71.29		84.49			81.61
PMF	acore												·							
Verify	Score																			
Psi Blast				1.6e-43	1.6e-52		3.2e-52			1.2e-35		4.8e-25			3.2e-47		9.6e-40			3.2e-53
END	AA			104	115	}	115			450		723			190		161			193
STAR	T AA			7	-	•	2			195		382			31		47	:		44
CHAI	A B				\ <	4	¥			Ą					A			,		\d
PDB	<u>e</u>			1fim	45.	 ā	lmfi			1d2n		1a8y			layz		1047	3		1qcq
SEQ	ВŞ			1181	1101	1011	1181			1185		1195			1200		1200	1200		1200

PDB annotation	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN- CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE	UBIQUITIN CONJUGATION UBCI;	UBIQUITIN CONJUGATION, LIGASE UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN,	THIOESTER 2 BOND, LIGASE UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST		TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR	TRANSFERASE ATK, AMGXI, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA,	BIK, SH3 2 DOMAIN, TRANSFERASE TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL	IRANSDUCTION, 2 SH3 COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/IRAL ENHANCER), PROTO-ONCOGENE, 2 IRANSFERASE, TYROSINE-
Coumpound	UBC9; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME: CHAIN: NIII 1 .	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;		ITK; CHAIN: NULL;	BRUTON'S TYROSINE KINASE; CHAIN: NULL;	HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;
SEQFOL D score	74.19	71.32	67.54	64.54					
PMF score						90.0	0.58	0.21	0.82
Verify score						-0.35	0.55	0.03	0.12
Psi Blast	1.6e-43	3.2e-47	1.4e-41	3.2e-43	1	3.2e-15	1.16-13	4.8e-15 0	1.6e-17
END	193	193	193	193	1	31/	319	318	317
STAR T AA	24	31	26	33	1,70	741	250	258	258
CHAI N ID	¥							∢	4
PDB ID	1u9a	2aak	2e2c	2ucz	1	Tax I	laww	1buf /	lefn A
SEQ ID NO:	1200	1200	1200	1200	1204				1204

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PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GIP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTE	TRANSFERASE PRO I C-ONCOCENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)		COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN	
	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	C-SRC; CHAIN: C; NL1 (MN7- MN2-MN1-PLPPLP); CHAIN: N;	TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	PHOSPHOTRANSFERASE FYN
	0.58	0.63	69:0	0.43	0.31
	0.32	0.25	0.42	0.41	0.39
	6.46-19	4.86-12	1.3e-16	4.8e-13	8e-19
	318	322	316	318	318
	255	260	259	257	256
	A	∢	· O	<	4
	1fyn	1gbr	Inlo	1qly	Ishf
Ö	1204	1204	1204	1204	1204
		1fyn A 255 318 6.4e-19 0.32 0.58 PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	1fyn         A         255         318         6.4e-19         0.32         0.58         PHOSPHOTRANSFERASE FYN;           1fyn         A         255         318         6.4e-19         0.32         0.68         PHOSPHOTRANSFERASE FYN;           CHAIN: A; 3BP-2; CHAIN: B;         CHAIN: A; 3BP-2; CHAIN: B;         Signal: TRANSDUCTION PROTEIN: B;         PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 29 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR 4 (NIR, 20 STRUCTURES) IGBR	1fyn   A   255   318   6.4e-19   0.32   0.58   PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B; CHAIN: A   260   322   4.8e-12   0.25   0.63   SIGNAL TRANSDUCTION   RECEPTOR-BOUND PROTEIN 2 (GRB2 J. H-TERAINFAL 1GBR 3 SH3 DOMAIN) COMPLEXED   WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5   1.3e-16   0.42   0.69   C-SRC; CHAIN: C; NLI (MN7-MN2-MIN) PLPPLP); CHAIN: N;	15µ

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PDIs annotation		TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT			COMPLEX (HYDROLASE/INHIBITOR) LDTI; COMPLEX (HYDROLASE/INHIBITOR), HYDROLASE, INHIBITOR, 2 INFLAMMATION, TRYPTASE		CALCIUM-BIND ING PROTEIN CALMODULIN CERUM TRIC- DOMAIN, RESIDUES 1 - 75; CERUM- LOADED, CALCIUM-BINDING	METAL BINDING PROTEIN CAVE
Coumpound	PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	ABL TYROSINE KINASE; CHAIN: NULL;	HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	CYTOCHROME B5; CHAIN: A;		COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (/OMTKY3\$) 1CHO 5	TRYPSIN; CHAIN: T; TRYPTASE INHIBITOR; CHAIN: L;		CALMODULIN; CHAIN: NULL;	CALCIUM VECTOR PROTEIN;
SEQFOL D score										
PMF score		-0.15	0.55	0.19		0.58	0.86		0.05	0.23
Verify score		0.04	0.04	0.69		-0.30	-0.23		-0.15	-0.50
Psi Blast		9.6e-28	3.2e-15	0.0096		5.1e-07	1.7e-07		3.4e-05	6.8e-06
END		423	318	86		592	587		014	410
STAR T AA		251	255	38		554	655		356	349
CEAI				V			L			Ą
PDB ID		2abl	4hck	1cxy.		Icho	11dt		lak8	lc7w
SEQ ID		1204	1204	1205		1208	1208	,	5171	1215

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PDB annotation	ED HAND BAMILY CALCHIM	BINDING PROTEIN, NMR										STRUCTURAL PROTEIN HELIX-	TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	ANTIFREEZE PROTEIN INSECT	ANTIFREEZE PROTEIN, THERMAL	HYSTERESIS, TENEBRIO 2	MOLITOR, IODINATION, RIGHT	HANDED BEIA-FELIA, IMAFF	IRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX	BUNDLE	BLOOD CLOTTING	COMPLEX(SERINE	PROTEASE/COFACTOR/LIGAND),	BLOOD COAGOLATION, 2 SENINE	RECEPTOR ENZYME, 3 INHIBITOR,	GLA, EGF, COMPLEX (SERINE 4
Coumpound		CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	CALMODULIN-DEPENDENT	PROTEIN KINASE II ICDM 4	COMPLEX(SERINE PROTEINASE-INHIBITOR)	AI PHA-CHYMOTRYPSIN	(E.C.3.4.21.1) COMPLEX WITH	TURKEY ICHO 4 OVOMUCOID	THIRD DOMAIN (COMINISA)	CARDIAC TROPONIN C;	CHAIN: A;	CALMODULIN; CHAIN: A;	TITED MAI ELVETED DESIG	PROTEIN ISOFORM YL-1;	CHAIN: A, B;			CALMODULIN; CHAIN: A;	!	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR;	(1) (2) (2) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1
SEQFOL	21026						,																				
PMF	arore		0.09				0.65		٠			0.21	<u> </u>	0.05	,	0.13				69.0		-0.19					
Verify	score		-0.48				0.04					-0.26	2	0.15		0.21				0.10		0.07	<u> </u>				
Psi Blast			3.4e-05		-		5.1e-10					1 70-05	20.7.1	1.4e-05		3.2e-06				6.8e-05		4 8e-09	3			. •	
END	AA		418				84					410	2	414		305				410		302	3				
STAR	I AA		356				39		-			340	7+7	348		226				349		23.6	3				
CHAI	9		¥				I					<	∢	∀		∢				¥			1				
PDB	A		lcdm				1cho					1451	IIDI	lexr		1ezg				1411		1651	1191				
SEO	A 8		1215				1215					3,60	C171	1215		1215				1215		1016	CIZI				

PDB annotation	PROTEASE/COFACTOR/LIGAND), BLOOD CLOTING	EXTRACELLULAR MODULE OSTEONECTIN, SPARC, SECRETED	FROTEIN ACIINC AND EXTRACELLULAR MODULE, GI YCOPROTEIN AND A DIEGE	PROTEIN, ANII-ADHESIVE	SILE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODDES	GROWTH FACTOR EHI; EH	DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100	PROTEIN			COMPLEX (SEIUNE PROTEASE/INFIIRITOR) SGPR: 18GP	8 ALA18-OMTKY3; 1SGP 14 SERINE	PROTEINASE, PROTEIN INHIBITOR	CALCIUM-BINIDING PROTEIN BM.	40, OSTEONECITN; 1SRA 7	EXTRACELLUI, AR MATRIX	CALCHIA BRINES	40, OSTEONECTIN: 1SRA 7	EXTRACELLULAR MATRIX	PROTEIN ISRA 20	BLOOD COAGULATION FACTOR	COAGIII ATION FACTOR SERVICE	PROTEINAGE EDINEDAAAT
Coumpound		BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;				EPIDERMAL GROWTH FACTOR	CHAIN: A;		CALCIUM-BINDING PROTEIN	RAI UNCUMUDULIN IKKU 3	PROTEINASE B; 18GP 6 CHAIN:	E; ISGP 7 TURKEY	OVOMUCOID INHIBITOR; 1SGP	SPARC; 1SRA 4 CHAIN: NULL;	1SRA 5	-	SPARC: ISRA 4 CHAIN: NIII I	1SRA 5			BLOOD COAGULATION FACTOR XA: CHAIN: 1 C:	6) (1)	
SEQFOL D score		73.86															58.51						-
PMF score						0.01		9,	٠. الا	250	C			0.72						010	}		
Verify score						-0.05		22.0	, , ,	0.67	<u> </u>		-	0.43						00 0		,	
Psi Blast		1.7e-28				6.8e-07		3 40.05		1 70-08		,		1.5e-38	-		1.5e-38			4 8e-09			
END		426	<b>4.</b> "			419		410	?	84				423			426		_	313			
STAR T AA	Ş	707				348	_	348	2	43				279			279			240			
CHAI N ID		∢				<				I					_					1			
PDB ID	1	opur —				<u>p</u>		1TO		Isgp	i			Isra			1sra			1xka I			1
SEQ ID NO:	1215	CIŽI			3.6	5121		1215		1215			1	5121			1215			1215			1

PDB annotation	GROWTH FACTOR LIKE DOMAIN				PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN					
Coumpound		PROTEINASE INHIBITOR (KAZAL) OVOMUCOID THIRD DOMAIN CLEAVED RDI 30VO 3	CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) 5PAL 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	ANNEXIN V; CHAIN: NULL;	ANNEXIN V; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3
SEQFOL D score						75.48		170.55			75.25
PMF		0.21	0.13	-0.19	1.00		1.00		1.00	1.00	
Verify		0.76	-0.11	0.08	0.58		0.23		-0.02	0.42	
Psi Blast		1.7e-09	3.4e-05	3.2e-15	3.2e-51	3.2e-51	1e-68	1e-68	4.8e-67	3.2e-53	3.2e-53
END		84	410	286	217	217	222	223	222	214	214
STAR T AA		40	348	112		-	61	61	62		-
CHAI				А							
PDB		3000	5pal	9wga	1a8a	1a8a	1ain	lain	lain	1ala	1ala
SEQ	NO:	1215	1215	1215	1216	1216	1216	1216	1216	1216	1216

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PDB annotation	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I, 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II	CALCIUMPHOSPHOLIPID-BINDING PROTEIN 32.5 ICD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5 KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II	CALCIUM/PHOISPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, 1.POCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN	CALCIDARPIOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, I.IPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUMPHOSPHOI IPID-BINDING
Coumpound	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	ANNEXIN VI; CHAIN: NULL;	ANNEXIN VI; CHAIN: NULL;
SEQFOL D score		68.51			
PMF score	1.00		1.00	00.1	1.00
Verify score	0.42		0.46	0.24	0.48
Psi Blast	9.6e-51	3.2e-67	3.2e-67	1.6e-50	9.6e-78
END	215	216	219	216	221
STAR T AA	<b>=</b>	-	62	10	ر. ا
CHAI N ID					
PDB ID	lann	Iann	lann	lavc	lavc
SEQ ID NO:	1216	1216	1216	1216	1216

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PDB annotation	PROTEIN CALCILIM/BHOSPHOLIPID-BINDING	PROTEIN ANNEXIN FAMILY 1AXN 14	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14	CALCIUMPHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14					PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG,	CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN				
Coumpound	A A SALA OLIABI.	ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V	(LPOCORTIN V, ENDONEXIN II, PLACENTAL 1HVD 3	ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE)	MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G) 1HVD 5	ANNEXIN V; CHAIN: NULL;		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I. IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	CALCIUM/PHOSPHOLIPID- BINDING PROTEIN ANNEXIN V 1ALA 3
SEQFOL D score			84.90		69.28				-	·		403.43		
PMF score		1.00		1.00					1.00		1.00		1.00	1.00
Verify score		0.76		0.70					0.64		0.22		0.17	0.31
Psi Blast		9.6e-53	3.2e-67	3.2e-67	1.16-49				8e-39		8e-32	0	0	3.2e-38
END		216	223	222	212				189	<u> </u>	187	304	300	186
STAR T AA		4	53	59					<b>∞</b>		13	33	35	8
CHAI														
PDB ID		laxn	laxn	1axn	1hvd				la8a		1ain	1ain	1ain	1ala
SEQ ID	Ö	1216	1216	1216	1216				1217		1217	1217	1217	1217

1217   1840   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   187   18							
PDB CHAI STAR END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12.2 CHROMOBINDIN IV, PROTEIN II	1ANN 13 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN	4.	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN	MEMBRANE 2 BINDING PROTEIN PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT
Q PDB         CHAI         STAR         END         Psi Blast         Verify         PMF           1 Iann         8         187         3.2e-38         0.55         1.00           1 Iaxn         8         186         4.8e-26         0.28         1.00           1 Ihvd         8         187         1.6e-37         0.54         1.00           1 Iaxn         8         184         6.4e-38         0.31         1.00           1 Ia8a         31         195         3.2e-66         55           1 Ia8a         33         194         3.2e-66         0.68         1.00	Coumpound	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	ANNEXIN VI; CHAIN: NULL;	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL 1HYD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION 1HYD 4 WITH GLU IT? REPLACED BY GLY (E17G)	ANNEXIN V; CHAIN: NULL;	ANNEXIN V; CHAIN: NULL;
PDB   CHAI   STAR   END   Psi Blast   Verify score	SEQFOL D score						
PDB   CHAI   STAR   END   Psi Blast   Verify	PMF score	1.00	1.00	1.00	1.00		1.00
Q         PDB         CHAI         STAR         END         Psi Blast           7         Iann         8         187         3.2e-38           7         Iann         8         186         4.8e-26           1         Iaxn         8         187         1.6e-37           1         Ihvd         8         184         6.4e-38           1         1a8a         31         195         3.2e-66           1a8a         33         194         3.2e-66	Verify score	0.55	0.28	0.54	0.31		
O PDB CHAI STAR END T Iann 1 Iaxn 1 Ia8a 1 Ia8a 1 IBA 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a 1 Ia8a	Psi Blast	3.2e-38	4.8e-26	1.6e-37	6.4e-38	3.2e-66	
1 lawn lawn lawn lawa lawa lawa lawa 3		187	186	187	184	195	1-1
PDB CHAI  I lann  I lavc  I lasa  I la8a  I la8a	STAR T AA	<b>∞</b>	œ	8	∞	31	33
	CHAI						
0.5	PDB ID	lann	lavc	laxn	Ihvd	la8a	Ia8a
	SEQ EQ	1217	1217	1217	1217	1218	+

PDB annotation	BEOTEIN: BHOSPHOI IPID ANALOG	CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN			Oladian din tormooyas and	PROTEIN 32.5 KD CALELECTRIN,	ENDONEXIN I; IAMN / 32.3XJ CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II	CALCIUMPHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I; IANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II	CALCIUMPHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA- CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,
Coumpound			CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	ANNEXIN VI; CHAIN: NULL;	ANNEXIN VI; CHAIN: NULL;
SEQFOL D score				170.39		65.05				
PMF	3000		1.00		1.00			1.00	1.00	1.00
Verify	score.		0.23		0.15			0.54	0.30	0.61
Psi Blast			1e-68	1e-68	1.6e-65	3.2e-68		3.2e-68	1.6e-38	1.6e-71
END	AA		194	195	194	195		190	186	193
STAR	T AA		33	33	35	33		34	2	34
CHAI	Q N									
PDB	<u> </u>		1ain	1ain	1ain	1ann		lann	lavc	Javc Javc
SEQ	e ë		1218	1218	1218	1218		1218	1218	1218

PDB annotation	MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING DOCTEDIA	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNISXIN FAMILY 1AXN	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNI:XIN FAMILY 1AXN	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING	PROTEIN	. •								SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A
Coumpound		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	ANNEXIN III; IAXN 4 CHAIN: NULL; IAXN 5	ANNEXIN 24(CA32); CHAIN: A, B;	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V G IPOCORTIN V ENLONEYED	II, PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN)	COLCION IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU IT REPLACED BY GLY (E17G) IHVD 5	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V	(LIPOCORTIN V, ENDONEXIN II, PLACENTAL 1HVD 3	(CALCIUM IONS ARE VISIBLE)	MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G)	1HVD 5		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;
SEQFOL D score		85.90		·	68.02	-								120.56
PMF score			1.00	1.00				1.00			-			
Verify score			0.70	0.02				0.59						
Psi Blast		6.4e-67	6.4e-67	3.2e-19	9.66-68			9.6e-68		-				1.06-45
END		195	194	691	195			194			-		200	/70
STAR T AA		25	31	2	32								133	3
CHAI N ID				Ą										
PDB ID		Iaxn	laxn	Idk5	1hvd		,	paur	<u></u>				1,43,1	
SEQ NO:		1218	1218	1218	1218		9	8171					1210	

•																					_				7
PDB annotation	PHOSPHORYLATION, HEAT REPEAT	SCAFFOLD PROTEIN SCAFFOLD	PHOSPHORYLATION, HEAT REPEAT	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,	PHOSPHOKYLAIJON, HEAI KEFEAI	IKANSPOKI FROIEIN SEKRISTIKEI RNA POLYMERASE I SUPPRESSOR	PROTEIN; ARM REPEAT	TRANSPORT PROTEIN SERINE-RICH	RNA POLYMERASE I SUFFRESSON PROTEIN: ARM REPEAT		NUCLEAR IMPORT RECEPTOR	IMPORT RECEPTOR, NUCLEAR	LOCALIZATION SIGNAL, 2	ARMADILLO REPEATS,	AUTOINHIBITION, INTRASTERIC REGULATION	NUCLEAR IMPORT RECEPTOR	KARYOPHERIN ALPHA; NUCLEAR	IMPORT RECEPTOR, NOCLEAN 1 OCAT 12 A TION SIGNAL. 2	ARMADII I.O REPEATS.	AUTOINHIBITION, INTRASTERIC	REGULATION	SMALL GTPASE KARYOPHEKIN  BETA DOS SMAII GTPASE	NUCLEAR TRANSPORT RECEPTOR	STRUCTURAL PROTEIN	ARMADILLO REPEAT, BETA-
Coumpound		PROTEIN PHOSPHATASE PP2A;	CHAIN: A, B;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;		KARYOPHERIN ALPHA;	ONCOGENE PROTEIN; CHAIN:	KARYOPHERIN ALPHA;	CHAIN: A, B; MYC PROTO-	C. D. E. F.	IMPORTIN ALPHA; CHAIN: A;					IMPORTIN ALPHA; CHAIN: A;						RAN, CHAIN: A, C, IMPORTIN	BEIA SUBUNII; CHAIN: B, D,	BETA-CATENIN; CHAIN: NULL;	
SEQFOL D score											118.96														
PIMF		0.23		-0.07		1.00		0.86								0.53	}					-0.15		90.0	-
Verify		0.07		0.04		0.36		0.57								0.50						0.01		0.51	
Psi Blast		1.6e-09		1.6e-45		1.7e-10		1 46-44		•	1.3e-43					1 30-43	1.50-45					4.8e-15		1.1e-39	
END	8	643		625		473		643	!		628					643	<u>}</u>					633		643	
STAR	1 33	320		71		211		270	<u> </u>		179					020	7/7					318		239	
CHAI	a z	4	ı	A		Ą			ς .		4						∢			_		В			
PDB	3	1130		1b3u		lee4			1991		lial						lial					libr		2hot	1 7
SEQ	ΒÖ	1219		1219		1219		0.0.	1219		1219						1219					1219		1210	1617

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PD'B annotation	CATENIN STRIICTIRAL PROTEIN	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON		OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMODOCTENI PASO DENANY	OXIDOREDUCTASE (OXYGENASE)		OXIDOREDUC.IASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE,	HEMOPROTEIN, P450 REMARK	OXIDOREDUCTASE FATTY ACID	MONOOXYGENASE,	HEMOPROTEIN, P450 REMARK	OXIDOREDUCTASE PROGESTERONE 21-	HYDROXYLASE, CYPIICS P450 1,	MEMBRANE PROTEIN,	FROGESTERONE 21-	HYDROXYLASI; BENZO(A) 2	FINENE HIDROATLASE,	ESTRADIOL 2-EMDROXYLASE,	OXIDOREDUCT ASE NITRIC OXIDE	REDUCTASE, CYTOCHROME	OXIDOREDUCTASE (OXYGENASE)
Coumpound		BETA-CATENIN; CHAIN: NULL;		CYTOCHROME P450; CHAIN: A, B;	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6		CYTOCHROME P450; CHAIN: A, B;		CYTOCHROME P450; CHAIN: A, B:	î		CYTOCHROME P450 2C5; CHAIN: A;							IDE REDUCTASE;		CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NIJI. 10XA 6
SEQFOL D score				174.17	94.76									•							
PMF score		0.24					0.04	000	67.0			0.99							0.05		0.28
Verify score		0.46					-0.20		-0.23		8	-0.02							-0.08		-0.40
Psi Blast		3.2e-35		9.6e-53	3.2e-24	1	1.3e-18	†	0.46-30		1	3.26-92							1.7e-21		6.8e-33
END		643		486	486	1	324	310	210		306	676			_				318		318
STAR T AA		277		19	27		ç.	17			3.1	10							48		61
CHAI N ID				V .			∢	4	:			ς .							∢		
PDB ID		3bct		lbu7	loxa	,	/nor	141,7			1446								9711		loxa
SEQ D NO:	,	1219		1221	1221	5	7777	1222			1222	7777	-						1222		1222

TOXIN BINDING PROTEIN TWO	DOMAINS: BETA FROFELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA!, TRANSDUCIN BETA SUBUNIT:	GAMMAI, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2	SIGNAL TRANSDUCTION	COMPLEX (G1F- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA	SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-
TOLB PROTEIN; CHAIN: A;		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A,	THANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A,	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B. C:	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;	CHAIN: G;		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G:		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;
					119.11					
0.04		1.00	0.29	1.00				0.53		1.00
-0.06		0.57	0.40	0.38				0.14		0.64
0.00032		4.8e-73	1.3e-58	1.6e-66	1.3e-77			1.3e-77		4.8e-54
11		431	285	373	370			328		431
130	}	116	4	65	12			14		166
	τ	¥	A	A	В		···	æ		В
1	707	lerj	1erj	1erj	Igot		•	1got		1got
NO:	1771	1227	1227	1227	1227			1227		1227
	130 352 0.00032 -0.06 0.04 TOLB PROTEIN; CHAIN: A;	1crz         A         130         352         0.00032         -0.06         0.04         TOLB PROTEIN; CHAIN: A;	1crz         A         130         352         0.00032         -0.06         0.04         TOLB PROTEIN; CHAIN: A;           1erj         A         116         431         4.8e-73         0.57         1.00         TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C.	1crz         A         130         352         0.00032         -0.06         0.04         TOLB PROTEIN; CHAIN: A;           1erj         A         116         431         4.8e-73         0.57         1.00         TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;           1erj         A         4         285         1.3e-58         0.40         0.29         TRANSCRIPTIONAL TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	1crz A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A; Tolar of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	1crz   A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A;   1.00   TRANSCRIPTIONAL   1.01   TRANSCRIPTIONAL   1.02   TRANSCRIPTIONAL   1.03   1.04   0.29   TRANSCRIPTIONAL   1.04   1.05   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPTIONAL   1.00   TRANSCRIPT	1crz   A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A;   1	16rz   A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A;   1	Iuz   A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A;   1   1   4.8e-73   0.57   1.00   REPRESSOR TUP1; CHAIN: A, B, C;   1.3e-58   0.40   0.29   REPRESSOR TUP1; CHAIN: A, B, C;   1.5e-66   0.38   1.00   REPRESSOR TUP1; CHAIN: A, B, C;   1.5e-66   0.38   1.00   REPRESSOR TUP1; CHAIN: A, B, C;   1.5e-77   119.11   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA   GT-ALPHA/GI-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALPHA   GT-ALP	Icrz   A   130   352   0.00032   -0.06   0.04   TOLB PROTEIN; CHAIN: A;   1

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PDB annotation	BINDING/TRA'NSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDIJCTION		IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN	DONOR STRAND COMPLEMENTATION, 2	CHAPERONE/STRUCTURAL PROTEIN	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN	DONOR STRAND	COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN		LIGASE CYCLIN A/CDK2. ASSOCIATED P45; CYCLIN A/CDK2.	ASSOCIATED P19; SKP1, SKP2, F.	REPEATS, SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN LIGASE	HELICASE DNA REPAIR, DNA REPLICATION SOS RESPONSE	HELICASE, 2 A1P-BINDING, DNA-	BINDING	COMPLEX (HELICASE/DNA)	HELICASE, DNA INWINDING	HYDROLASE/DIVA ATP-DEPENDENT
Coumpound			ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O;	MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, B.	F.	PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O;	MANNOSE-SPECIFIC ADHESIN	P;		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;			PCP A: CHAMI: MIN I.	CIVA, CITAIN: NOLL;		ATD DEBENDENE DAY			4; CHAIN: A, F;
SEQFOL D score																		-		90.62
PMF score			0.35	-0.18			-0.19				0.13			0.58		-	900			
Verify			-0.14	-0.00			11.0				-0.25			-0.22		<u> </u>	-0.55			
Psi Blast		0,000	0.0068	1.2e-15			6.8e-16			1	0.00034			3.2c-68			1.6e-47	<u> </u>		1.3e-62
END		0,3	218	· 089			10/				293			960		_	872			166
STAR T AA		412	413	321	· <u>-</u> -	,	408	-			214			430		_	441			430
CHAI N ID		ב	<b>c</b>	m			9		1		<del></del>						¥			₹ I
PDB ID		1016		Iqun		+				t	7811			Ipjr			luaa /		$\top$	4pjr /
SEQ ID NO:		1235	(621	1235		1225				1000	957			1236			1236		1226	┪

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PDB annotation	HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION,	EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE),	COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,
Coumpound	HELICASE PCRA; CHAIN: B, G; DNA (5'-D(*TP*TP*TP*TP*T)-3'); CHAIN: C, D; DNA (5'-D(*GP*C)- 3'); CHAIN: H; DNA (5'- D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A. D. ANGIOGENIN;	CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score								
PMF		0.89	0.09		0.35	0.51	0.71	0.04
Verify score		-0.01	0.04	~	0.04	0.28	0.36	0.04
Psi Blast		3.4e-22	6.4e-07		3.4e-13	3.2e-07	8.5e-24	3.46-20
END		213	299		151	101	187	196
STAR T AA		10	126		12	70	51	72
CHAI N ID		A	Ą		4	A	<	4
PDB ID		1a4y	1a4y		1a9n	1a9n	1a9n	1a9n
SEQ ID	ÖN	1237	1237		1237	1237	1237	1237

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PDE annotation	SNRNP RIBONI ICI EOPROTEINI	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA	SNRNP RIBONI ICI FOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	OFIT A PITTOLINA	REPEAT, CALCIUM BINDING, CELL	TD ANICHER AGE CHARGE	STRIICTIBE BAB	GER ANYI GED ANYI TE ANGEED AGE	2.0 A 2 RESOLUTION N.	FORMYLMETHIONINE ALPHA	SUBUNIT, BETA SUBUNIT		TRANSFERASE (TRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE	2.0 A 2 RESOLUTION, N.	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL STRUCTURE, RAB
Coumpound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;	INTERNALIN B. CUARI. A.	Comments of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of the Property of th	RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBLIMIT:	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	B, D;	RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	В, Џ;	RAB GERANYLGERANYLTRANSFE
SEQFOL D score																			•	•		<del></del>			
PMF score		0.35		99.0		0.71	100	0.07	-0.02		0.96				-			0.94				_		,	-0.03
Verify score		0.49		0.05	710	-0.14	000	-0.20	0.15		0.35						,	0.47							0.20
Psi Blast		3.2e-07		5.1e-24	30,00	3.25-27	00,00	67-98.0	6.4e-21		1.6e-11						1	3.2e-13	-		_	<del>-</del>		Ť	4.06-10
END AA		101		192	107	707	22.1	177	268		100						;;	527	•					270	0/7
STAR T AA		70		51	7	)	Ę	<b>.</b>	52		11						130	000						160	
CHAI N ID		ပ		ပ	A	1	4		A		Ą							τ.						4	
PDB ID		1a9n	,	la9n	140h		1904		1d0b		1dce						1976							1909	
SEQ ID NO:	100	1237		1237	1237		1237		1237		1237						1237			_	_			1237	

PDB annotation	TO A CHARACTER ATTENTION AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND THE COMPANY AND T	GERANYLGEKANYLIKANSFEKASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN 14F (NFA1), RIBONUCLEOPROTEIN (RNP.RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING FROTEIN 174 (WEAT), RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	ASSOCIATED P45; CYCLIN A/CDK2-
Coumpound		RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B D.	GRAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: R D:	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;
SEOFOL	D score								
PMF	score		0.33	0.09	0.22	0.45	0.65	0.60	0.46
Verify	score		0.21	-0.31	-0.20	-0.54	-0.03	0.25	0.15
Dei Rlact			3.2e-11	4.8e-12	3.2e-14	1.6e-11	1.1e-06	1.1e-06	1.2e-25
UNG	AA		169	146	252	169	192	192	206
0.4.00	TAA		44	=	130	37	132	132	10
	N ID		4	∢	Ą	V V	<	æ	4
-  - 	2 A		1dce	1489	1489	1ds9	1fo1	1f01	1fs2
	SEQ	NO:	1237	1237	1237	1237	1237	1237	1237

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PDIS annotation	ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEN 1 1GA SF	LIGASE CYCLIN A/CDK2- ASSOCIATED F45; CYCLIN A/CDK2- ASSOCIATED F19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3,	ACETYLATION ENGASE ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACITYLATION, LEUCINE-RICH REPEATS		HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TITRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRICTURE	HYDROLASE TITRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY	HYDROLASE HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTISIN INTERACTIONS, TPR, 2 SUPER-HELLX, X-RAY
Coumpound		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 3; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;
SEQFOL D score								
PMF score		0.22	0.82		0.80	0.51	0.76	0.23
Verify score		0.34	-0.03		0.10	0.27	0:30	0.01
Psi Blast		1.1e-06	1.5e-28			6.4e-14	4.8e-13	8e-13
END		294	223		279	250	296	153
STAR T AA		130	19		119	133	153	20
CHAI N ID		∢						
PDB ID		1fs2	2bnh	,	1ai7	Ial7	1a17	1a17
SEQ ID NO:		1237	1237	,	1238	1238	1238	1238

						<del></del> -		
PDB annotation	STRUCTURE	HYDROLASE LEIKAIN OF ELICA, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPERTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS,
Coumpound	T COMP	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;
SEQFOL D score							,	
PMF .		66.0	0.94	0.80	0.52	0.11	0.74	0.37
Verify		0.31	0.56	0.22	0.22	0.18	-0.14	0.41
Psi Blast		5.1e-19	9.6e-13	9.6e-13	3.2e-14	1.7e-15	1.7e-18	4.8e-13
END		368	348	392	416	142	414	421
STAR T AA		221	232	263	290	29	300	338
CHAI								
PDB ID	+	1a17	1a1 <i>7</i>	1a17	la17	1a17	1a17	1817
SEQ ID	Ö	1238	1238	1238	1238	1238	1238	1238

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PDl3 annotation	TPR, 2 SUPER-HELIX, X-RAY	HYDROLASE TETRATRICOPEPTIDE.	TRP; HYDROLASE, PHOSPHATASE,	TPR, 2 SUPER-HELIX, X-RAY	STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE,	PROTEIN-PROJEIN INTERACTIONS,	STRUCTURE	TRP. HYDROLASE TETRATRICOPEPTIDE,	PROTEIN-PROTEIN INTERACTIONS,	TPR, 2 SUPER-HELIX, X-RAY STRICTURE	HYDROLASE TETRATRICOPEPTIDE,	PROTEIN PROTEIN PROTEIN PROTEIN	TPR, 2 SUPER-HELIX, X-RAY	STRUCTURE	TRANSFERASE FTASE; FTASE;	FARENT TRANS.	FAMILIA MAINSFEKASE,	FARNESYL 2 IRANSFERASE, CAAX,	ices, craces.	TRANSFERASE FTASE: FTASE:	FTASE, PFT, PFTASE,	FARNESYLTRANSFERASE,	FARNESYL 2 TRANSFERASE, CAAX,	KAS, CANCER
Coumpound		SERINE/THREONINE PROTEIN	PHOSPHATASE 5; CHAIN: NULL:		SERVICE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR	PHOSPHATASE 5; CHAIN:	NOLL;		SERINE/THREONINE PROTEIN PHOSPHATASE 5: CHAIN:	NULL;		SERINE/THREONINE PROTEIN PHOSPHATASE 5. CHAIN.	NULL:		DA DAITCONE OF TAXONIA LOS	(A) PHA SIBIRITY CITABLE	FARNESYLTRANSEEPASE	(BETA STIBLINITY: CHAIN: B. V	RAS4B PEPTIDE SUBSTRATE:	CHAIN: P;	FARNESYLTRANSFERASE	(ALPHA SUBUNIT); CHAIN: A;	FAKNESYLTRANSFERASE	(BEIA SUBUNII); CHAIN: B; K-RASAR PEPTIDE SUBSTRA	CHAIN: P;
SEQFOL D score						,										•		•							
PMF		0.70			0.41				0.58			0.65			0.90	3					0.18				
Verify score		0.18			0 34	;			0.12			0.12			-0.23	}					-0.04				
Psi Blast		1.7e-15			8e-10	· · ·		11.07	4.86-11			3.4e-17		-	4.8e-07					1	3.46-15				
END AA		184			175			200	, , , , , , , , , , , , , , , , , , ,			212	-		410					1	007	_			
STAR T AA		99			63			20	3		-	68			217					90					
CHAI N ID															A							-			
PDB ID		1a17			1a17			1917				la!/			1d8d	_				1484					
SEQ NO:		1238			1238			1238			1220	1230			1238			_		1238	<u> </u>				

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PDB annotation		SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, 1PR-DUMAIN,
Coumpound		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEOFOL.	D score			·	·				
DME	score	0.48	0.76	0.98	0.86	0.21	0.47	1.00	0.96
17,000	score	0.15	0.40	0.14	0.05	0.12	0.38	0.24	0.02
	rsi Diast	1.4e-09	8e-10	4.8e-09	4.8e-09	0.00016	6.4e-15	6.4e-15	1.6e-10
	AA A	278	322	379	417	244	247	252	283
	STAK T AA	135	189	229	290	62	133	161	195
ŀ	CHAI	e e	æ	В	æ	В	V .	A	A
ŀ	PDB UI		1e96	1e96	1e96	1e96	leir	leir	lelr
	SEQ ID	NO: 1238	1238	1238	1238	1238	1238	1238	1238

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PDB annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN RINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP9), 2 PROTEIN	EINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMI'LEX, HELICAL REPECT, HSP90, 2 PROTEIN	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN	EINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT HSC70 2 HSP70 PROTEIN
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;
SEQFOL D score									
PMF score		0.99	0.74	0.29	0.55	0.33	0.99	0.96	1.00
Verify		0.47	0.27	0.13	0.54	0.31	0.46	0.47	0.63
Psi Blast		4.8e-12	3.2e-13	4.8e-11	4.8e-12	1.1e-11	1.1e-13	1.3e-12	3.2e-10
END		326	355	117	419	185	221	262	296
STAR T AA		228	262	28	334	93	135	153	196
CHAI N ID		∢	A	Ą	Ą	Ą	<b>V</b>	¥	4
PDB ID		lelr	lelr	1elr	1elr	lelr	lelw	lelw	lelw
SEQ ID NO:		1238	1238	1238	1238	1238	1238	1238	1238

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PDB annotation	BINDING TOP TOP DOMAIN	CHAFERONE HOF, ITEL COMPANY, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, IPK-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMALN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN-
Coumpound		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR I-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING
SEQFOL D score									
PMF score		1.00	0.57	0.03	0.98	0.21	0.82	1.00	0.96
Verify		0.76	0.32	0.25	0.23	0.29	0.32	0.32	0.07
Psi Blast		4.8e-13	4.8e-10	6.4e-14	3.2e-15	1.le-11	6.4e-10	9.6e-38	3.2e-09
END		332	122	66	408	419	155	413	420
STAR T AA		236	25	2	304	342	61	166	313
CHA1 N ID		A	4	A	4	Ą	<b>∀</b>	∢	A
PDB		Jelw	1elw	lelw	leiw	lelw	1clw	1fch	1fch
SEQ ID	ÖZ	1238	1238	1238	1238	1238	1238	1238	1238

T :	Т			<del></del>		<del></del>	
PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORI; RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,	2 HELICAL REPEAT SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,	Z HELICAL KEPEA I SIGNALING PROTEIN PEROXISMORE RECEPTOR I, PTSI- BP, PEROXIN-5, PTSI PROTEIN- PEPTIDE COMPLEX, TETRATRICOPIPTIDE REPEAT, TPR, 2 HELICAL REPEAT		CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12, CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN,	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM	EINDING PROTEIN CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1
PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;		E-CADHERIN; CHAIN: A, B;	E-CADHERIN; CHAIN: A, B;	E-CADHERIN; CHAIN: A, B;
	·						
	1.00	1.00	1.00		0.55	0.76	0.64
	0.48	0.38	0.46		01.0	-0.19	0.21
	6.4e-31	1.36-29	4.8e-29	000	3.26-20	6.8e-27	4.8e-17
	273	220	345	2	761	253	255
	34	7	86	7.7	<b>4</b>	22	83
	∢	₹	∢		- <del></del>	∢	4
	I toh	1fch	1fch	Jodh		ledh	ledh
	1238	1238	1238	1241		1241	1241
	PEPTIDE; CHAIN: C, D;	1.00 PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	Ifch         A         34         273         6.4e-31         0.48         1.00         PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: C, D;           1fch         A         7         220         1.3e-29         0.38         1.00         PEROXISOMAL TARGETING SIGNAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: C, D;           1fch         A         7         220         1.3e-29         0.38         1.00         PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: C, D;           1fch         A         7         220         1.3e-29         0.38         1.00         PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: C, D;	1fch   A   34   273   6.4e-31   0.48   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D; A   272   1.3e-29   0.38   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D; A   220   1.3e-29   0.38   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D; A   28   345   4.8e-29   0.46   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D; A   28   2751-CONTAINING SIGNAL I RECEPTOR; CHAIN: C, D; A   28   2751-CONTAINING SIGNAL I RECEPTOR; CHAIN: C, D; A   27   27   27   27   27   27   27	1feh A	1fch A   34   273   6.4c-31   0.48   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D;   1.6th A   7   220   1.3c-29   0.38   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   98   345   4.8c-29   0.46   1.00   PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: C, D;   1.5th A   34   152   3.2c-20   0.10   0.55   E-CADHERIN; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   34   152   3.2c-20   0.10   0.55   E-CADHERIN; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   34   1.5th A   34   1.5th A   35   3.2c-20   0.10   0.55   E-CADHERIN; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   34   1.5th A   35   3.2c-20   0.10   0.55   E-CADHERIN; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   35   3.2c-20   0.10   0.55   E-CADHERIN; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A   1.5th A	1feh

										 				$\neg$
PDB annotation		AND 2, ECAD12, CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN	CELL ADHESION PROTEIN CADHERIN INCI 13	CELL ADHESION PROTEIN CADHERIN INCI 13	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE,
Coumpound	•		N-CADHERIN; INCI 3	N-CADHERIN; 1NCI 3	N-CADHERIN; CHAIN: A;	N-CADHERIN; CHAIN: A;	N-CADHERIN; CHAIN: A;	LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	EPITHELIAL CADHERIN; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR
SEOFOL	D score													66.97
PME	score		0.04	0.31	0.28	9.65	0.35	0.40	0.04	1.00	1.00	1.00	0.93	
Vonifer	score		-0.07	0.15	-0.20	-0.03	-0.20	-0.08	-0.22	0.56	0.40	0.84	0.39	
10.00	FSI DIASI		5.1e-06	1.7e-05	1.4e-21	1.7e-21	6.4e-17	3.4e-20	1.7e-07	3.4e-30	3.4e-30	5.1e-29	1.5e-29	3.4e-30
H	AA AA		253	152	152	253	255	549	154	262	330	359	385	393
	STAR T AA		206	56	34	43	8	358	43	132	166	202	233	233
	CHAI		В	В	4	A	A	₹						
	PDB U		Inci	1nci	Incj	lncj	Incj	1qu0	1suh	1a5e	1a5e	1a5e	1a5e	1a5e
	SEQ E	NO:	1241	1241	1241	1241	1241	1241	1241	1246	1246	1246	1246	1246

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PDB annotation	ANTI-ONCOGENE, REPEAT, ANK	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	ACCULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	IKANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/JNA) GABPALPHA; GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATIONAI)NA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS.	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
Coumpound	P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	1	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B;	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	
SEQFOL D score				-					
PMF score		1.00	00	99:	-	1.00		1.00	
Verify		1.05	03			0.97		0.93	
Psi Blast		le-43	16-30			9.6e-41		1.6e-38	
END		298	165			298		165	
STAR T AA		145	14			051		17	
CHAI N ID		<b>n</b>	В			æ		В	
PDB ID		Iawc	lawc			lawc		lawc ]	
SEQ ID NO:	70.	1240	1246			1246		1246	

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PDB annotation		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABFALLIN, GABPBETAI; COMPLEX	(TRANSCRIPTION REGILLATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABFBE IAI; COM EST	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, E1S DOMESTY,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DIA) CADI ALLI ILL.	TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, E13 DOMALIN,	ANK I KLIN KEFEA 19, TRANSCRIPTION 3 FACTOR	-	(
Commonnd	•	GA BINDING PROTEIN ALPHA;	PROTEIN BETA 1; CHAIN: B;	DINA; CHAIN: D, E,		GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTFIN BETA 1: CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DIVA, CIESTIN: 25, 25			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BEIA I; CHAIN: B,	DIVA, CIMIN: D. 2;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING
IOAOao	D score																90.97							
a page	score	1.00				1 00	2				9	3:											0.23	
	verity score	0.84				0.55		, -				0.77											0.21	
	Psi Blast	3.4e-39				7	9.06-33					le-40					2, 4	<u> </u>			٠		3.2e-32	
ŀ	END AA	332					332					362					-	200		<del>-:-</del>		<u>.                                    </u>	395	
	STAR T AA	183					184					212						717			<del>.</del>		217	
	CHAI N ID	t c					ф					В						<u>m</u>					- la	
	PDB ID						lawc					lawc						1awc					1 Swel	
	SEQ	NO:	2				1246					1246						1246					1246	1240

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PDB annotation	GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PIOTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; (COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	IKANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION GABPETAL; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPI:ATS,	IKANSCKIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/INA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/INA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	TUMOR SUPPRESSOR TUMOR
Coumpound	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR;
SEQFOL D score					87.65	
PMF		1.00	1.00	1.00		1.00
Verify		0.88	0.55	0.68		0.38
Psi Blast		1.6e-33	8.5e-39	9.6e-37	8e-30	8e-30
END		132	199	199	301	301
STAR T AA		m	45	20	145	153
CHAI N ID		Д	В	В		
FDB TD		lawc	lawc	lawc	15d8	1bd8
SEQ NO:		1246	1246	1246	1246	1246

PDB annotation	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI- ONCOGENE) HEADER				COMPLEX (INHIBITOR PROTEIN/KINASB) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX
Coumpound	CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score					78.94	
PMF		1.00	0.10	1.00	·	1.00
Verify score		0.57	0.10	0.93		0.73
Psi Blast		1.7e-28	3.4e-38	1.7e-39	6.8e-40	3.4e-38
END		365	304	170	303	338
STAR T AA		244	114	13	147	183
CHAI		В	В	æ	В	В
PDB		1bi7	16lx	1blx	1blx	1blx
SEQ	Ö	1246	1246	1246	1246	1246

PDB annotation	(INTRIBUTED BE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE STEERING OF THE	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	ALPHA/BETA, COMPI EX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INITIBITOR	PROTEIN/KINASE) INHIBITOR	KINASE, CELI CYCLE 2 CONTROL	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INFIIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	PI8INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HURMONE/GROWTH FACTOR P18-	HINK4C; CELL CYCLE INHIBITOR,	PISINK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPIENDENT KINASE,	HORMONE/GROWTH FACTOR	HOKMUNE/GROWTH FACTOR P18-	PISINK4C, CELL CYCLE INHIBITOR, PISINK4C, TIIMOR, STIPPRESSOR	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR
Coumpound		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	á			CYCLIN-DEPENDENT KINASE	9, CHAIN: A; F19INK4D; CHAIN: B:				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B.	จ๋			CVOI IN PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON IN THE PERSON I	CICLIN-DEPENDENT KINASE	O INTERTION; CHAIN: A;			CYCLIN-DEPENDENT VINASE	6 INHIBITOR: CHAIN: A:	CHARLES CHARLES, A,			CYCI IN DEPENDENT KINAST	6 INHIBITOR CHAIN: A.	Carried City Charles A,		
SEQFOL D score																				-					•			_			
PMF		1.00				5	9				9	 }:					00	3				1.00					1.00				
Verify		0.89				0.20					1 03	5			-		0.78					0.97					0.87				
Psi Blast		1.7e-38				1 50.38					6 80-40			•			6.8e-37					1.6e-36 (					9.6e-37 0		···		
END		368				205	3			,	237	·			_		310					303					170			<del></del> ,	
STAR T AA		215				50	2				8						144					150					17				
CHAI N ID		<b>м</b>				В	)				В						~					¥					A				
PDB ID		Iblx				1blx				-	1blx	_		_		┪	Ibu9					Ibu9					1bu9 /				
SEQ ID NO:		1246				1246					1246					┪	1246				$\dashv$	1246				┪	1246				

PDB annotation		HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROW 1H FACTOR 118- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROW IN FACTOR TO INK 4C; CELL CYCLE INHIBITOR, P18INK 4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROW IN FACTOR TO INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	NK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HOYGINONE/GROWTH FACTOR HORMONE/GROWTH FACTOR P18.	HOKMONEJOKOW IN FACTORY IS INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,
Coumpound	•	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDEN I KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;
CEOFOL	D score							89.81
DAGE	score	1.00	0.99	1.00	1.00	0.51	1.00	
	score	0.61	0.25	0.63	0.79	0.47	0.94	
	Psi Blast	Ie-35	8e-33	3.4e-35	6.8e-33	3.4e-37	1.7e-39	1.7e-39
}	END AA	338	367	373	394	174	205	177
	STAR T AA	181	184	215	243	<b>е</b>	4	6
	CHAI	A	4	<b>∀</b>	4	∢	∢	A
	PDB ID	1bu9	1bu9	1bu9	1bu9	1bu9	1bu9	1bu9
	SEQ ID	NO:	1246	1246	1246	1246	1246	1246

	<del>i</del>							
PDB annotation	HORMONE/GROWTH FACTOR CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR CELL CYCLE INHIBITOR P18- INK4C(INK6); (JELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REP!AT, 2 CDK 4/6	INHIBITOR TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65:
Coumpound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-AI PHA: CHAIN: D.	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	D-ALFRA; CHAIN; D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B	NF-KAPPA-B P65 SUBUNIT;
SEQFOL D score				83.68				
PMF score	1.00	1.00	1.00		1.00	0.92	0.35	1.00
Verify score	0.88	0.78	0.28		0.47	0.20	0.22	0.18
Psi Blast	6.4e-36	3.2e-36	3.2e-32	3.2e-36	4.8e-35	1.6e-30	1.6e-34	8e-43
END	302	169	366	236	186	346	404	232
STAR T AA	150	17	184	81	12	179	212	45
CHAI N ID	<b>V</b>	∢	4	V V	Q	Q	Q	D
PDB ID	lihb	lihb	lihb	lihb		1ikn	lika	likn
SEQ NO:	1246	1246	1246	1246	1246	1246	1246	1246

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PDB annotation	PSOD; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	COMPLEX REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELLX	COMPLEX (IRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
Coumpound	CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- R-AI PHA: CHAIN: D:	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA: CHAIN: D;	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score		80.97	68.11					
PMF				1.00	1.00	1.00	1.00	1.00
Verify				0.69	0.81	0.55	0.62	0.65
Psi Blast		8e-43	9.6e-25	1.7e-48	1.4e-35	5.1e-47	1.7c-48	4.8e-30
END		253	130	311	186	338	367	346
STAR T AA		45	12	113	11	143	177	178
CHAI		Q		tŋ	Ħ	យ	ш	ы
PDB		likn	1myo	Infi	Infi	Infi	Infi	Infi
SEQ	NO.	1246	1246	1246	1246	1246	1246	1246

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PDB annotation	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX (TRANSCRIPTION	REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HEI IX	COMPLEX (TRANSCRIPTION REG/ANK REPIAT) COMPLEX	(TRANSCRIPTION REGULATION/ANK REPEAT),	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YKIN Z REPEAT HELIX	COMPLEX (TRANSCRIPTION	KEG/ANK REPEAT) COMPLEX	DEGIT ATTOMISME	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYKIN Z KEPEAT HELIX	COMPLEX (TRANSCRIPTION	AEGMEN KEPEAL) COMPLEX	TICH TICH	KEGULATION/ANK REPEAT),	ANN I KIN Z KEFEAT HELLX	COMPLEX (IRANSCRIPTION	AEG/AINE REFEAT) COMPLEX	REGULATION/ANK REPEAT)
Coumpound	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E,		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN; E, F;	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ů.	ME VARBA P. P.C. CUTARIA	NF-KAFFA-B F65; CHAIN: A, C;	I-KAPPA-B-ALPHA: CHAIN: E	F:	•	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	· ·	+	NF-KAPPA-B P65; CHAIN: A, C;		T.		NE-K APPA B P65. CHAIN: A C.		_	
SEQFOL D score			-							•			-	89.07	-											
PMF score	1.00		0.21		1.00				1 00	20.1		••						2	3	•			8			
Verify score	0.85		0.26		0.53	_	-		0.53									77.0	<u>.</u>				0.66			
Psi Blast	3.4e-38		9.6e-35		1.5e-44				1.70-51					1.7e-51		_		1 6e-42					5.1e-50		•	
END AA	170		404		394				238	}				242			··· <del>-</del>	232	-				278			
STAR T AA	17		210		215				43	}			,	54	•			44					82			
CHAI	Ħ		បា		ய				Э	. ,		_	ŗ	ı)				E					3			
PDB ID	Infi	,	ta Ta		Infi				Infi									lofi				7	1nfi			
SEQ NO:	1246	,	1246		1246				1246				1046	0471				1246					1246			

					·			<del></del>
PDB annotation	ANKYRIN 2 REPEAT HELIX	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	CARDO A SEC.	STRUCTURAL PROTEIN 1 WO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR	
Coumpound		REGULATORY PROTEIN SWI6; CHAIN: A, B;	P53; CHAIN: A; 53BP2; CHAIN: B;		ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4
SEQFOL D score		60.99	69.71					
PMF					0.29	0.03	0.11	0.25
Verify score					-0.03	0.02	0.07	0.13
Psi Blast		1.3e-21	3.26-18		5.1e-12	5.1e-07	0.0051	0.0051
END		320	398		591	159	150	150
STAR T AA		9/	214		375	436	120	120
CHAI		A	B		∢	4		
PDB		1sw6	1 ycs		lcun	1cun	1hae	Thre
SEQ	Ö	1246	1246		1250	1250	1250	1250

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PD B annotation			APOPTOSIS TIVAIL; DRS; LIGAND- RECEPTOR COMPLEX, TRIMERIC	JELLY-ROLL, TNF-R 2	SUPERFAMILY, APOPTOSIS	BLOOD COAGULATION, SERINE PROTFASE COMPLEY OF EACTOR	2 RECEPTOR ENZYME INHIBITOR	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)	SERINE PROTEINIA SE	COAGHI ATTOM FACTOR II.	COAGIL ATTON FACTOR II.	FETOMODIE IN TW CD141	ANTIGEN: EGR.CMK SERINE	PROTEINASE EGF-LIKE DOMAINS	ANTICOAGULANT COMPLEX 2	ANTIFIBRINOL YTIC COMPLEX	SERINE PROTEINASE	COAGULATION FACTOR II:	COAGULATION FACTOR II:	FETOMODULIN, TM, CD141	ANTIGEN, EGR-CMK SERINE	PROTEINASE, I:GF-LIKE DOMAINS.	ANTICOAGULANT COMPLEX, 2	ANTIFIBRINOL YTIC COMPLEX	SERINE PROTEINASE	COAGULATION FACTOR II;	COAGULATION FACTOR II;	FETOMODULIN, TM, CD141	ANTIGEN; EGR.CMK SERINE	PROTEINASE, EGF-LIKE DOMAINS.	ANTICOAGULANT COMPLEX >
Coumpound			TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B;	DEATH RECEPTOR 5; CHAIN:	P1 000 00 100 1	FACTOR VIIA; CHAIN; L. H.	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C.	THROMBIN LIGHT CHAIN:	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M. N.	O, P; THROMBOMODULIN	CHAIN: 1, J, K, L; THROMBIN	INHIBITOR L-GLU-L-GLY-L-	ARM; CHAIN: E, F, G, H;		THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M, N,	O, P; THROMBOMODULIN;	CHAIN: I, J, K, L; THROMBIN	INHIBITOR L-GLU-L-GLY-L-	AKM; CHAIN: E, F, G, H;		THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M, N,	O, P. THROMBOMODULIN;	CHAIN: I, J, K, L; THROMBIN	INTIBITOR L-GLU-L-GLY-L-	AKM; CHAIN: E, F, G, H;
SEQFOL D score											_			_		`			_								; 			<u>۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ ۔ </u>	= :	4
PMF score			-0.14		-013	0.15				-0.20								-0.20		•			<u>.                                      </u>		9,0	ر د ا		_				
Verify score		0.0	0.1.0	-	0.06					0.02				•			†	6.03	-						010							
Psi Blast		\$ 10.10			8e-09					3.2e-12							T	0.46-13			<u></u>			,	1 16-12						-	
END		476			449					346							707			-					436							
STAR T AA		326			351					233			-				348	-		-					308	_						
CHAI N ID		A			1					_																						
80g C1		1d4v			1dan				;	S S							1dx5	-				_			1dx5 1							
SEQ NO.		1252			1252				10,00	7671						_	1252								1252							

PDB annotation		ANTIFIBRINOLYTIC COMPLEX	MATRIX PROTEIN	EXTRACELLULAR MAIRIX, CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENI, MAIRIX PROTEIN	MATRIX PROTEIN EVTB A CET I III AR MATRIX	CAI CHIM-BINDING	GI YCOPROTEIN, 2 REPEAT.	SIGNAL MILITIGENE FAMILY.	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEA,	INHIBITOR, REMOFRIENDEDI.	BLOOD COAGOLATION, 21 LASIMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CKYSTAL	STRUCTURE, FACTOR AND INHIBITOR, 2 SERINE PROTEASE
Coumpound			FIBRILLIN; CHAIN: NULL;							FIBRILLIN; CHAIN: NULL;				****			LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;							ANTISTASIN; CHAIN: NULL;			
SEQFOL	D score												na = -44					132.10														
PMF	score		0.04							-0.19							0.93		0.51	-0.03	-0.17								-0.14			
Verify	score		0.24							80.0				4			0.17		0.40	00.0	0.10	!						·	0.34			
Psi Blast			1.6e-13							3.2e-10							2 50-30	8.5e-39	1 60-20	3 26-18	3.2e-09								3.4e-17			
END	AA		305							431							410	411	153	404	144	:						<del></del>	414	:		
STAR	T AA		307	5						351							366	234	200	258	351	5							310	}		
CHAI	NID																					١										
PDR	A	1	100							1emn								1K10	JI-1	IKIO	1 kilo	Yndr —							10/2	2		
SEO	í A	S	1753	7671						1252								1252	777	1222	1952	7071							1253	7671	_	

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PDB annotation	INITION TO WOOD OF STREET	SERINE PROTISASE INHIBITOR SERINE PROTISASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, BPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN			LYASE 2-PHOSPHO-D-GLYCERATE	LYASE (CARBON-OXYGEN) 2- PHOSPHO-D-GLYCERATE DEHYDRATASE; 1PDZ 6		PROTEIN KINASE INHIBITOR PKCI- 1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKCI-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN	FAMILY, NUCLIFOTIDYL HYDROLASE, 3 NUCLEOTIDYL	I KANSFERASE PROTEIN KINASE INHIBITOD BEGI
Coumpound		ANTISTASIN; CHAIN: NULL;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	METALLOTHIONEIN METALLOTHIONEIN ISOFORM	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3		ENOLASE; CHAIN: A, B;	ENOLASE; 1PDZ 4 CHAIN: NULL; 1PDZ 5		PROTEIN KINASE C INTERACTING PROTEIN; CHAIN: NULL;		PROTEIN KINASE C
SEQFOL D score		·							-			144.01 F
PMF score		0.19	-0.18	0.00	-0.19		0.1	1.00		06: 1:00		
Verify		0.16	0.14	-0.05	0.04		0.25	0.15		0.90	·	
Psi Blast		5.1e-10	3.2e-09	1.3e-09	4.8e-15		9.6e-61	8e-63		9.06-41		9.6e-41
END		425	448	428	492		134	137	15	6		163
STAR T AA		355	355	368	298		1	=	63			53
CHAI N ID			L)		4		∢					
PDB ID		1skz	lxka	4mt2	9wga	$\dagger$	$\neg$	Ipdz	1knf			1kpf
SEQ NO:		1252	1252	1252	1252	1252	12.33	1253	1256	<del></del>		1256

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PDB annotation	1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKCI-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN	NUCLEO LIDE-BINDING TROTEIN HINT, NUCLEO TIDE-BINDING PROTEIN	ANTI ONCOGENE CELL CYCLE.	ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
Coumpound	INTERACTING PROTEIN; CHAIN: NULL;	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	4000	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16NK4A; CHAIN: NULL;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score		147.29							
PMF			1.00		0.48	1.00	1.00	0.40	00:1
Verify			0.86		0.27	0.80	0.65	0.16	0.61
Psi Blast		6.4e-41	6.4e-41		1.4e-21	8e-26	3.4e-25	4.8e-18	6.4e-37
END		163	163		151	154	162	121	164
STAR T AA	·	47	22		39	39	9	9	39
CHAI									ш
PDB		4rhn	4rhn		la5e	1a5e	1a5e	1a5e	lawc
SEQ	ON O	1256	1256		1257	1257	1257	1257	1257

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	COMPLEX (KINASE/ANTI- CONCOGENE) CDK6; PI6INK44, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-	ONCOGENE) HISADER COMPLEX (KINASE/ANTI- ONCOGENE) CINK6; PIGINK4A, MTSI; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRISSOR, 3 MTSI, COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX
Coumpound	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score					
PMF score	1.00	1.00	1.00	0.35	1.00
Verify score	0.40	0.48	0.62	0.22	0.82
Psi Blast	9.6e-40	1.3e-31	3.2e-26	8e-19	1.7c-32
END	154	157	154	121	164
STAR T AA	4	7	39	9	39
CHAI N ID	В		Δ	В	В
PDB ID	lawc	-	1517		1blx
SEQ ID NO:	1257	1257	1257	1257	1257

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PDB annotation	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX	(INHIBITOR PROTEINMINASE) HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-1 UKN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING PROTEIN	METAL BINDING PROTEIN ZINC-	BINDING MODULE, ANKYKIN REPEATS, METAL BINDING	PROTEIN DESTRUCTION P18.	INK4C(INK6); CELL CYCLE	ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;	STOREST PERENTRAL KINASE	CYCLIN-Derendent August 6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA: CHAIN: A;		PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;		CYCLIN-DEPENDENT KINASE   6 INHIBITOR; CHAIN: A, B;		STOREST TO THE PROPERTY OF THE ACT	6 INHIBITOR; CHAIN: A, B;	
SEQFOL D score				-														-	
PMF		1.00			0.88		1.00	20.0	رد. در	0.80		000	66:0		1.00			1.00	
Verify		0.38			0.34		0.70	5	0.47	0.41		900	co		0.52			0.47	
Psi Blast		1.6e-30			8e-37		1.6e-26		3.2e-20	6.4e-15		,	1.16-17		4.8e-36			8e-18	
END		157			159		154		127	91			157		158			163	
STAR		7			9		39		9	2			17	<u></u>	9			73	
CHAI		В			∢		<		Ą	4			٧		₹.			A .	
PDB		1blx			1bu9		1498		1d9s	1dcq			1dcq		1ibb			lihb	
SEO	- 3	1257			1257		1257		1257	1257			1257		1257			1257	

PDB annotation	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPHIN,	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	REGULATION/ANK REPEAT),	ANK YKIN Z KEPEAT HELIX	COMPLEX (AN.TI- ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULIIGENE 2 FAMILY, NUCLEAR	DISEASE MITATION 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANT).	ONCOGENE/ANK YRIN REPEATS) P53BP2: ANK YRIN REPEATS SH3	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION, DISEASE MUTATION 3	POLYMORPHISM, COMPLEX (ANTI-
Coumpound	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-R-AI PHA: CHAIN: F	F;	DS3. CUARI. 4. 62002. CITARI	B;						D62. CITABL 4. Conno. Civ. n.	F33; CHAIN: A; S3BPZ; CHAIN:	a a		***************************************		
SEQFOL D score		52.27														1						
PMF	0.84		96.0	86.0	1.00	1.00	_		0.86	}						8	3					
Verify score	0.08		0.32	0.22	0.04	0.39	· ·	•	0.04							0.24						
Psi Blast	8e-38	3.2e-26	3.2e-26	6.4e-24	1.1e-23	1.6e-38			1.4e-19							1.6e-25				<del></del>		
END	162	152	156	106	164	162			95							154						
STAR T AA	4	35	40	S	74	4			12				<del>-</del>		<del></del> -	39	_					
CHAI N ID	Q					<b>3</b>			В							В						
PDB ID	likn	1туо	1myo	lmyo	1myo	Infi			lycs							lycs ]				_		
SEQ ID NO:	1257	1257	1257	1257	1257	1257			1257							1257						

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PDB annotation		ONCOGENE/ANK YRIN REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANK YRIN REPEATS)	LECTIN CL-QPDWG; 1AFB 7 C-TYPE	LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22	COLLAGEN BINDING PROTEIN IX-	BP; IX-BP; COAGULATION FACTOR IX-RINDING HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE	LECTIN SUPERFAMILY, COLLAGEN RINDING PROTEIN	COLLAGEN BINDING PROTEIN IX-	BP; IX-BP; COAGULATION FACTOR	VENOW HARIT SNAKE, C-TYPE	LECTIN SUPERFAMILY, COLLAGEN	BINDING PROTEIN	MEMBRANE PROTEIN C-1 YFE		HAVE O MEMORE SHAPE	MEMBRANE PROTEIN C-1 I'FE LECTIN-LIKE DOMAINS	
Coumpound			DE22. CHAIN: A: 53BP2: CHAIN:						MANNOSE-BINDING PROTEIN-	A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB	COAGIII ATION FACTOR IX-	BINDING PROTEIN A; CHAIN:	A; COAGOLATION FACTOR IX BINDING PROTEIN B; CHAIN:	B;	COAGIT ATION FACTOR IX-	BINDING PROTEIN A; CHAIN:	A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAILY:   B.	î	FLAVOCETIN-A: ALPHA	SUBUNIT; CHAIN: A;	SUBUNIT; CHAIN: B	FLAVOCETIN-A: ALPHA	FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B
SEQFOL	D score								00 63	32.00					,	61.48								
PMF	score			00.1							:	 								0.89			10.0	
Verify	score			0.44								0.42								0.20			0.03	
Pei Rlast			7	1.6e-22		<del></del>				3.4e-20		8e-34				8e-34				6.4e-28	2		1.4e-30	
GND	¥ ¥			161						183		180				181				185	}		183	
CTAD	TAA			73			,			3		31				34				31	<u> </u>		31	
-	Z E Z			m						-		¥				A					₹		В	
H	PDB TD		-	lycs	<del></del>					1afb		16j3				1bj3					1634		1c3a	
	SEQ	Ş		1257						1258		1258				1258				9	1258		1258	

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PDB annotation	SIGNALING PROTEIN HEPATIC	INTIMIN INTIGO INTIMIN, ESCHERICHIA COLI, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL, CELL,	SUGAR BINDING PROTEIN C-TYPE I FOTH MANNOSE BECEPTOR	ELECTIFY, MANANOSE RECEFTIOR				CELL ADHESION IMMINOGI OBITINI IKE BOLD C	TYPE LECTIN-LIKE FOLD	LECTIN TETRANECTIN, PI A SMANOGEN BRIDGIC VARIOUS	4, ALPHA-HELICAL 2 COILED COIL,	C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN	C-TYPE LECTIN ALPHA-HELICAL	COLLED-COIL 1HUP 12	COAGULATION FACTOR BINDING IXX-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	COAGULATION FACTOR BINDING
Coumpound	ASIALOGLYCOPROTEIN RECEPTOR 1. CHAIN: 4.	INTIMIN; CHAIN: I;	MACROPHAGE MANNOSE RECEPTOR: CHAIN: A R.	CELL ADHESION PROTEIN E- SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESI 3 (FORMER! Y KNOWN	AS ELAM-1) 1ESL 4	CELL ADHESION PROTEIN E- SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157)	1ESL 3 (FORMERLY KNOWN AS ELAM-1) 1ESL 4	INTIMIN; CHAIN: I;		TETRANECTIN; CHAIN: NULL;			MANNOSE-BINDING PROTEIN;	1HUP 4 CHAIN: NULL; 1HUP 5	COAGULATION FACTORS IXX-BINDING PROTEIN:	CHAIN: A, B, C, D, E, F;		COAGULATION FACTORS
SEQFOL D score						60.26				68.61			50.48					58.55
PMF score	99.0	0.57	0.36	0.89				0.40							0.21			
Verify	0.72	-0.69	0.41	0.45				-0.19						1	0.21			
Psi Blast	6.4e-28	0.0093	1.6e-29	4.8e-30		4.8e-30		0.0093		1.3e-23			6.4e-21	1	4.8e-32		<del>-</del>	4.8e-32
END	180	08	187	213		220		08	į	 54			183	9	 08 180			181
STAR T AA	31	52	29	44		45		52		7.			<b>∞</b>	;	15			34
CHAI	A	<b>⊢</b>	В					<b>—</b>			. —				<			¥
PDB UI	ldv8	leSu	legg	lesi		8		1 <del>1</del> 00					lhup	1				lixx
SEQ ED GN	1258	1258	1258	1258		8621		1258	1360	0071			1258	1250	867			1258

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ion	IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING IXX-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE		7.
PDB annotation	FULATIO YPE LEC JDING, C	N FACT FULATIO YPE LEC FOING, C	N FACT FULATION YPE LEC FULL CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONT	STONE I STONE I	STONE I	NG PRO STONE I STONE I	NG PRO STONE STONE		ANECTI
O.A.	BP COACING, C-T AIN 2 BIN F, LOOP	SULATIO BP COAC ING, C-T AIN 2 BI E, LOOP	SULATIO BP COAC ING, C-T AIN 2 BII F, LOOP	REATIC REATIC IN	REATIC REATIC IN	METAL BINDING PROTEIN PANCREATIC STONE PROT PANCREATIC STONE INHII LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROT PANCREATIC STONE INHII LITHOSTATHINE		LECTIN TETRANECTIN,
	ENX. BIND DOM.	COAC IXX- BIND DOM MOTI	COAC IXXX- BIND DOM MOT	PANCRE PANCRE LECTIN	PANCRE PANCRE LECTIN	MET PAN( PAN( LITH	MET PAN( PAN( LITH		LEC
Coumpound	PROTEIN; D, E, F;	v FACTORS PROTEIN; , D, E, F;	v FACTORS PROTEIN; , D, E, F;	VE; CHAIN:	NE; CHAIN:	NE; CHÁIN: A;	NE; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	TETRANECTIN; CHAIN: NULL;
Coun	IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	LECTIN MANNOSE-BINDIN PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 13	TETRANECTIN
SEQFOL D score			53.06		71.84	72.35		50.72	59.80
PMF score		0.45		0.30			0.52		
Verify score		0.24		0.51			0.65		
Psi Blast		1.3e-29	1.3e-29	1.6e-31	1.6e-31	1.6e-31	1.6e-31	5.1e-19	1.2e-24
END		183	183	182	183	183	182	183	184
STAR T AA		31	34	31	31	18	31	m	28
CHAI N ID		m	æ			¥	∢		
809 U		1ixx	1ixx	11it	11it	1qdd	1qdd	1.rtm	1tm3
SEQ NO:		1258	1258	1258	1258	1258	1258	1258	1258

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PDB annotation	4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN		OXIDOREDUCTASE DAPDH; NADP, DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2 BIOSYNTHESIS, ASYMMETRIC	DIMER, OXIDOREDUCIASE				COMPLEX (PROTEASE INHIBITOR/PEP TIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRA TE INHIBITOR?	COMPLEX, PEP/IIDE	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOD
Coumpound		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;		DIAMINOPIMELIC ACID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE (/NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE	DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	OXIDOREDUCTASE (NAD\$(A)- ALDEHYDE(D)) D- GLYCERALDEHYDE-3- PHOSPHATE DEHYDROGENASE (F.C. 1.2.1.12) 3GPD 4	- G 100 (G1111111111111111111111111111111	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C		ANTICHYMOTRYPSIN; CHAIN: A, B;
SEQFOL D score					491.59				115.78		
PMF score		0.54		0.13			1.00				0.96
Verify score		-0.06		-0.51			0.93				0.25
Psi Blast		1.6e-27		4.8e-05	0		0		4.8e-91		
END		179		33	336		336		463	430	430
STAR T AA		29			2		ဇ		83	°	e l
CHAI N ID		∢		<	R		<b>~</b>		∢		
PDB ID		2atp	1902	Idap	3gpd	_	3gpd		1a7c	1964	$\neg$
SEQ ID NO:	9	1258	1260	1239	1259		1259		1263	1263	

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PDB annotation		ANTICHYMOTRYPSIN	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,	ANTICHYMOTRYPSIN			PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING	HYDROLASE INHIBITOR SERPIN	FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION	HYDROLASE INHIBITOR NATIVE	SERPIN, HYDROLASE INFIBITOR	NHIBITOR PROTEASE-INHIBITOR	COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN											
Coumpound	•		ANTICHYMOTRYPSIN; CHAIN: A B:	(7)	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	PLASMINOGEN ACTIVATOR INHIBITOR-2: CHAIN: A;	PLASMINOGEN ACTIVATOR	INHIBITOR-2; CHAIN: A;	PI-ARG ANTITR TP SIN, CITAIN. A; PI-ARG ANTITR YPSIN; CHAM: R:	PLASMINOGEN ACTIVATOR	INHIBITOR-1; CHAIN: A, B;	ALPHA-1-ANTITRYPSIN;   CHAIN: A; ALPHA-1-	ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE	INHIBITOR(SERINE   pp.OTETNASE) HORSE	FROI EINASE) HONSE   LEUKOCYTE ELASTASE	INHIBITOR (HLEI) 1HLE 3	HYDROLASE	NHIBITOR(SERINE	FROIEINASE) HONSE	LEUKOCY 1E ELASTASE   INHIRITOR (HLED 1HLE 3	SERPIN OVALBUMIN (EGG	ALBUMIN) 10VA 3	SERPIN OVALBUMIN (EGG
SEOROI.	D score		104.85		102.92			101.02			120.11								84.90				126.84		
DME	score					1.00	1.00			0.04			0.80		1.00										1.00
Vonifer	score					0.23	99.0			-0.75			0.23		0.38										0.62
1	rsi biasi		0		1.3e-96	1.3e-96	0	0		1.3e-09	3.26-94	2	0		3.2e-98	-			3.2e-98					> -	0
	AA A		438		464	464	463	463		463	163	}	432		426				432	2			463	403	463
	TAA		8		101	85	98	98		433	03	S	98		85				85	3			8	<u>~</u>	87
	CHAI		A		В	В	A	<b>A</b>	-	В		∢	⋖		<	!		·	4	٠ د				⋖	A
	PDB El		las4		lath	1ath	1by7	1hv7		1d5s	0.17	7gp7	lezx		Thle				1510					lova	lova
	SEQ ID	NO.	1263		1263	1263	1263	1263	3	1263	3	1263	1263		1963				1263	5071	_			1263	1263

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PDI annotation		SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR,	ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR,	SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION ACTITE	PHASE	SERINE PROTE ASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR.	ALPHA-1-ANTIPROTEINASE;	SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2	POLYMORPHISM, EMPHYSEMA, DISEASE MITTATION ACTITE	PHASE	SERINE PROTE/ASE INHIBITOR AL PHA-1-PROTE/NASE INHIBITOR	ALPHA-1-PI; SERPIN, ANTITRYPSIN,	POLYMER, CLEAVED	SERVIN AACT SERPIN, SERINE PROTEINASE INITIBITOD BADTIAL	LOOP 2 INSERTION, LOOP-SHEET	POLYMERIZATION, EMPHYSEMA,	DISEASE 3 MUTATION, ACUTE	PHASE PROTEIN,	CONFORMATIONAL DISEASE	SERINE PROTEASE INHIBITOR SPRINE PROTEASE INHIBITOR	SERPIN PROTEASE INTIBILIOR,	SERPIN SERPIN, HEPARIN,	INHIBITOR	SERPIN SERPIN, HEPARIN,
Coumpound	ALBUMIN) 10VA 3	ALPHA-1-ANTITRYPSIN; CHAIN: A;				ALPHA-1-ANTITRYPSIN; CHAIN: A;					ALPHA-1-ANTITRYPSIN; CHAIN: A, B;		AT DHA 1	ANTICHYMOTRYPSIN: CHAIN:	A;				SERVING OF A STATE S	SERVIN K; CHAIN: NULL;		ANTITHROMBIN; CHAIN: L, I;	ANITITUD OMBBI. CITABLE	ANTITUROWBIN; CHAIN: L, I;
SEQFOL D score						146.76						-						-	102.05	102.03		139.88		
PMF score		1.00									0.12		1 00	3									100	3
Verify score		0.49				_					-0.75		0.44	•				_					0.48	1
Psi Blast		0				•	-				4.8e-09		0						3 26-85	2			0	
END		463			777	400					403 ——		464						463	}		466	464	1
STAR T AA		%			00	× ×				.;;	+33		88						8			4/	49	
CHAI N ID		⋖			4	€				6	a		4							<del>, , , , , , , , , , , , , , , , , , , </del>		-	I	
PDB ID		dıbı			1212	dibi				1	Ombr		Iqmn						lsek			1117	2ant	
SEQ ID NO:		1263			1263	5077				1363	707		1263						1263		5,05	1203	1263	

PDB annotation	INHIBITOR	SERPIN SERPIN, HEPAKIN, INHIBITOR	SERPIN SERPIN, HEPARIN, INHIBITOR	See the Albumy (About Desperation Base)	MAJOR HISTOCOMPATIBILITY ANTIGEN MIC HIA H.A-B3501.	HIV, 2 NEF, COMPLEX (ANTIGENPEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35;	MAJOR HISTOCOMPATIBILITY	HIV, 2 NEF, COMPLEX	(ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEF LIDE) B33;	ANTIGEN, MHC, HLA, HLA-B3501,	HIV, 2 NEF, COMPLEX	(ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,	MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX	THETTOCONA ATTIBILITY COMPLEX	HIS IOCOMPATIBLE IT COM LESS BS, B2M; PEPTIDE HLA B8, HIV,	MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX	AND AND COURSE OF	HISTOCOMPATIBILITY COMPLEA B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,
Coumpound		ANTITHROMBIN; CHAIN: L, I;	ANTITHROMBIN; CHAIN: L, I;		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;		B*3501; CHAIN: A, B; PEPTIDE	VPLRPMTY; CHAIN: C;			B*3501; CHAIN: A, B; PEPTIDE	VELKEIMII; CREMIN: C,			B*0801; CHAIN: A; BETA-2	HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX	PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGI OBIII IN: CHAIN: B:	HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX	PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE
SEQFOL D score		125.53					237.20					·							239.77				
PMF			1.00		1.00						1.00				1.00								1.00
Verify			0.63		0.93						1.19				0.97								0.98
Psi Blast		0	0		6.4e-92		1 20-03				1.2e-93				3.2e-92				3.2e-92				8.5e-92
END		466	464		218		210	````			210				218				219				210
STAR T AA		59	81		25		36	3			26				25				25				26
CHAI		ı	1		A			ζ			4				A				A				A
PDB		2ant	2ant		lain			12111			lain				1agd			<u></u> .	1agd				1agd
SEQ ID	Ö	1263	1263		1264		1,765	1704		<del></del>	1264				1264				1264				1264

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PDB annotation	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM	IMIMONOGLOBULIN FOLD			IMMUNE SYSTEM MHC. HLA.	CLASS I, KIR, NK CFI.I, RECEPTOR	IMMUNOGLOBULIN 2 FOLD	RECEPTOR/MIIC COMPLEX			•	IMMUNE SYSTEM MHC, HLA.	CLASS I, KIR, NK CELL RECEPTOR	IMMUNOGLOEULIN 2 FOI D	RECEPTOR/MEIC COMPLEX																
Coumpound	אישש ואאאאאטט)	PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGI OBITI IN:	CHAIN: B, E; HTLV-1	OCTAMERIC TAX PEPTIDE;	CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	KIR2DL2; CHAIN: D, E;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	KIR2DL2; CHAIN: D, E;	HISTOCOMPATIBILITY	ANTIGEN MURINE CLASS I	MAJOR HISTOCOMPATIBILITY	COMPLEX CONSISTING 1HOC 3	OF H-2D===, B2-	MICROGLOBULIN, AND A 9-	RESIDUE PEPTIDE 1HOC 4	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3 /HLA-	B(AS1EKISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY
SEQFOL D score																				;	200.63	•						-		-		1	77.167
PMF			0.0				00.1							9.														00.1	•			1	
Verify			1.03			1.2								67.1						1	•	_					1	16.0				-	1
Psi Blast		1 62 00	1.0e-88			0 60.01	7.00-21				•	-	9 50 03	0.76-3.7						1 60.01	10-00-1		-				1	3.25-91				3 20-01	
END		210	718			218	917						210	017						218	3						210	_				219	1
STAR T AA		25	3			25	}						26	}						35	}						3,4	3	•			25	
CHAI N ID						A	1						\ \ \														4		•				
PDB ID		1duz	3			lefx						_	Iefx			-				Thoc					_		Thea					1hsa A	
SEQ ID	Ö	1264				1264							1264							1264							1264					1264	

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PDB annotation			-	VII HOTH A GA A COLORDAY SCOTT	MAJOK HISTOCOMPATIBLIA I I COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM	
Coumpound		ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: 4; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I
SEOFOL	D score			226.78	209.47		257.75
PMR	score		1.00			1.00	
Varify	score		1.15			1.17	
1010 to	rsi Diast		3.2e-89	3.26-89	4.8e-88	6.4e-89	9.6e-81
	AA		218	219	219	218	199
1	STAR T AA		25	25	26	56	25
	CHAI		A	∢	∢	∢	A
	PDB TD		1hsb	1hsb	Imhe	1qqd	1tmc
	SEQ ID	Ö	1264	1264	1264	1264	1264

	T	<del>                                      </del>					
PDB annotation		COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501,	HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE) COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501,	HIV, Z NEF, COMPLEX (ANTIGEN/PEPYIDE) HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBITIN 2 FOI D	RECEPTOR/MHC COMPLEX
Coumpound	HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAFFTIDE (GGKK KYNT I PRIDE)	PEPTIDE); CHAIN: C; B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX PEPTIDE); CHAIN: C; HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B;	PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIRZDL2; CHAIN: D, E; HISTOCOMPATIBILITY
SEQFOL D score			222.84		242.14		
PMF score		1.00		1.00		1.00	1.00
Verify score		0.82		0.93		96.0	1.04
Psi Blast		0	0	0	0	4.8e-100 (	1.6e-100 1
END		212	213	212	213	212	212
STAR T AA		25	25	25	25	25	25
CHAI N ID		A	<	<	A	4	4
PDB ID		lain	laIn	lagd	lagd	lefx ,	Ihsa A
SEQ ID NO:		1265	1265	1265	1265	1265	1265

PDB annotation		Manager and a second	IMMUNOGLOBULN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM			COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY
Coumpound	ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY 'ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;
SEQFOL D score		212.48			245.23	
PMF			1.00	1.00		1.00
Verify			0.83	1.00		0.88
Psi Blast		1.6e-100	1.3e-98	3.2e-93	3.2e-93	4.8e-97
END		213	212	199	199	210
STAR T AA		25	26	25	25	22
CHAI N ID		A	¥.	A	∢	A
PDB		Ihsa	Iqqd	Itmc	1tmc	lain
SEQ	NO:	1265	1265	1265	1265	1266

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PDE annotation	ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGENIDE)	COMPLEX (AN IIGENPEPTIDE) B35:	MAJOR HISTOCOMPATIBILITY	HIV, 2 NEF, COMPLEX	HISTOCOMPATIBILITY COMPLEX	B8; B2M; PEPTIDE HLA B8, HIV,	INSTOCOL AT THE TANK OF THE	FLS I OCOMPA LIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX	Bo; BZM; FEF IIDE HLA B8, HIV,	HISTOCOMPATIBILITY COMPLEX		IMMUNE SYSTEM	IMMUNOGLOBULIN FOLD			IMMUNE SYSTEM MHC, HLA,	CLASS I, KIR, NK CELL RECEPTOR,	IMMUNOGLOBULIN 2 FOLD,	ICCEL LONIMING COMPLEX						
Coumpound		B*3501; CHAIN: A, B; PEPTIDE	VPLRPMTY; CHAIN: C;		B*0801; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	GGKKKVKI INDEV	PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2	HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX	PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D;	BEIA-2 MICROGLOBULIN;	OCTAMERIC TAX PEPTIDE:	CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	MICKOGLOBOLIN; CHAIN: B;	ALPHA-2; CHAIN; C: NATURAL	KILLER CELL RECEPTOR	KIR2DL2; CHAIN: D, E;	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN THSA 3/HLA-
SEQFOL D score		202.13							212.14																	
PMF score					1.00								1.00				90.1						1.00			
Verify score					0.92								0.88				80.1				-		0.89		-	
Psi Blast		4.8e-97			1.1e-97		٠		1.1e-97				4.86-95				3.26-96					1	3.2e-96		<del>-, .,</del>	
END		210			210				210			8	\$07			0.5	017					1	017			
STAR T AA		22			22				22			,	77				77	•				5	77		-	1
CHAI N ID		∢			∢				<				ς				ς								_	
PDB ID		laln			lagd				lagd		<del></del>	1,411.2				1 a fe						1100				
SEQ NO:		1266			1266			2005	9071			1266	2071			1266	201					1266				

PDB annotation															IMMUNE SYSTEM	IMMUNOGLOBULIN (IG)-LIKE	DOMAIN, ALPHA HELIX, BEIA	SHEET, 2 IMMONE SYSTEM										
Coumpound		B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY	HISTOCOMPATIBILITY	ANTIGEN AW68.1	(LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY	ANTIGEN CLASS I	HISTOCOMPATIBILITY	ANTIGEN A W68.1	(LEUCOCY 1E 1HSB 3	HISTOCOMPATIBILITY	LEUKOCYTE ANTIGEN (HLA)-	CW4 CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	HLA-CW4 SPECIFIC PEPTIDE;	HISTOCOMPATIBILITY	ANTIGEN TRUNCATED	HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN HLA-AW68 LIMC 3	COMPLEXED WITH A	DECAMERIC PEPTIDE	HISTOCOMPATIBILITY	ANTIGEN TRUNCATED
SEOFOL	D score		195.27							189.34																	228.77	
PMF	score			-		1.00									9	2				1.00					_			
Verify	score					0.87									08.0	6.6				86:0								
Pei Rlact			3.2e-96			4.8e-96				4 80-96	2				20.00	2,25-74				4.8e-90							4.8e-90	
GNB	AA.		210			208				210	217				5	710				197							197	:
CTAD	TAA		22			22				5	77					3				22	l						22	3
1400	NB		A			Ą					∢					⋖				A	<u> </u>							¢
a da	a a		Ihsa			lhsb				11.	TUSD					] qqd				1tmc							$-\vdash$	) IIII
OH.	E C	ä	1266			1266				2200	0071					1266				1266	75.0						1266	1700

	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTINE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I. KIR. NK CELI. RECEPTOR
HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE): CHAIN: C.	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIFIS, CHAIN: CHAIN: B;	HLA-A*0201; CHAIN: C, HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAIN: C, E, C, C, C, C, C, C, C, C, C, C, C, C, C,	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-
		206.29		193.54		
	1.00		1.00		1.00	1.00
	1.01		0.95		0.96	0.91
	6.4e-100	6.4e-100	1.6e-100	1.6e-100	3.2e-97	1.6e-98
	214	214	214	214	214	214
	25	25	25	25	25	25
	₹	∢	A	A	4	A
	laIn	laln	lagd	lagd	I duz	lefx /
	1267	1267	1267	1267	1267	1267
	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	HUMAN CLASS I	HUMAN CLASS I	HUMAN CLASS   HUMAN CLASS	HUMAN CLASS I	HUMAN CLASS   HUMAN CLASS   HUMAN CLASS   HUMAN CLASS     Ialin   A   25   214   6.4e-100   1.01   1.00   B*3501; CHAIN: A, B; PEPTIDE     Ialin   A   25   214   6.4e-100   206.29   B*3501; CHAIN: A, B; PEPTIDE     Iagd   A   25   214   1.6e-100   0.95   1.00   B*0801; CHAIN: A, B; PEPTIDE     Iagd   A   25   214   1.6e-100   0.95   1.00   B*0801; CHAIN: A, B; BETA-2     Iduz   A   25   214   1.6e-100   0.95   1.00   B*0801; CHAIN: A; BETA-2     Iduz   A   25   214   1.6e-100   0.95   1.00   B*0801; CHAIN: B; BETA-2     Iduz   A   25   214   1.6e-100   0.95   1.00   B*0801; CHAIN: B; BETA-2     Iduz   A   25   214   3.2e-97   0.96   1.00   B*0801; CHAIN: A, D; D; D; D; D; D; D; D; D; D; D; D; D;

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PDB annotation	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX					IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM	
Coumpound	MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS 1 HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	HISTOCOMPATIBILITY
SEQFOL D score			198.64		190.28		
PMF		1.00		1.00		1.00	1.00
Verify score		1.02		86.0		0.95	0.91
Psi Blast		1.6e-99	1.6e-99	1.1e-98	1.1e-98	4.8e-97	6.4e-91
END		214	214	214	214	214	200
STAR		25	25	25	25	26	25
CHAI		∢	Ą	<b>4</b>	A	4	A
PDB	1	Ihsa	1hsa	1hsb	Ihsb	1qqd	1tmc
SEQ	NO:	1267	1267	1267	1267	1267	1267

PDi8 annotation			COMPLEY (ANTICEMENTALISM 1936	COMM LEA (ANTIGEN/FEF 11DE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX	COMPLEX (ANTIGENIPEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIL)E HLA B8, HIV,
Coumpound	ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) I TMC 4	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	B*3501: CHAIN: A B. PEPTIDE	VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE GIGKKKYKL INDEX PEPTIFE: CLAIN: CLAIN: C	B*0801; CHAIN: C; B*0801; CHAIN: A; BETA-2 MCROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE
SEQFOL D score		227.42			381.69		382.18
PMF score			1.00			1.00	
Verify score			0.83			0.79	
Psi Blast		6.46-91	0		0	0	0
END		200	301		301	301	301
STAR T AA		25	25	-	25	25	25
CHAI N ID		∢	₹	1	∢	¥	A
PDB ID		Itmc	lain		laln	lagd	lagd
SEQ ID NO:		1267	1268		1268	1268	1268

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PDB annotation		HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE	IMMUNG SYSTEM IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTORMHC COMPLEX	·		
Coumpound		(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E. F.	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4
SEQFOL	D score						381.68	
PMF	score		0.00	1.00	1.00	00.1		1.00
Verify	score		-0.28	0.83	0.83	0.80		0.82
Psi Blast	-		0.00034	0	0	0	0	0
END	AA		314	300	303	301	301	295
STAR	TAA		224	25	25	25	25	25
CHAI	NB		A	₹	Ą	∢	A	A
PAR	A		1dn2	Iduz	1efx	1hsa	Ihsa	1hsb
Ogo	a a	ÖZ	1268	1268	1268	1268	1268	1268

			<del></del>		<del></del>	
	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C	KEGION, IMMUNOGLOBULIN		IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPFIA HELIX, BETA SHEET, 2 IMMUNE SYSTEM	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC; HLA, HLA-B3501, HIV, 2 NEF. COMPLEX	(ANTIGEN/PEPTIDE) COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBLITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3	ANTIGEN) 1HSB 4 IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGG1) (MCG) WITH A HINGE	DELETION INCO 3 IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) OFFI FTION INCO 7	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C.	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;
416.11						279.39 I
	0.71	0.23	0.48	1.00	00.1	
	0.26	0.09	0.30	0.63	0.88	
0	1.6e-05	1.7e-05	6.8e-06	0	0	0
295	308	310	314	299	285	288
25	224	681	220	26	25	25
∢	В	H	Н	A	<	V V
Ihsb				pbbl	laln	lain
1268	1268			<del></del>	1269	1269
	A 25 295 0 416.11	1hsb   A   25   295   0   416.11   .HISTOCOMPATIBILITY   ANTIGEN CLASS I   HISTOCOMPATIBILITY   ANTIGEN CLASS I   HISTOCOMPATIBILITY   ANTIGEN AW68.1   (LEUCOCYTE 1HSB 3   ANTIGEN) IHSB 4   1igt   B   224   308   1.6e-05   0.26   0.71   IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	1hsb   A   25   295   0   416.11   .HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1   (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4 ANTIGEN) 1HSB 4 ANTIGEN JHSB 4 Inco H   189   310   1.7e-05   0.09   0.23   IMMUNOGLOBULIN GI (GG1) (MCG) WITH A HINGE HINGE	Ihish   A   25   295   0   416.11   HISTOCOMPATIBILITY	1hsb   A   25   295   0   416.11   HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN LIBB 3   Libe-05   0.26   0.71   Liga ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 3   ANTIGEN I HSB 4   Independent of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro	Ihsb   A   25   295   0   416.11   HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW681 I HISTOCOMPATIBILITY ANTIGEN AW681 I GCZA INTACT ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 4 ANTIGEN I HISB 5 ANTIGEN I HISB 6.8e-06 0.30 0.48 IMMUNOGLOBULIN GI (GGI) MANUNOGLOBULIN GI (GGI) ANTIGEN I HISG BELETION I MCO 3 IMMUNOGLOBULIN GI (GGI) ANTIGEN I HISG BELETION I MCO 3 IMMUNOGLOBULIN GI (GGI) ANTIGEN I HISG BELETION I MCO 3 IMMUNOGLOBULIN GI (GGI) ANTIGEN I HISG BELETION I MCO 3 IMMUNOGLOBULIN GI (GGI) ANTIGEN I HISG BETA-2 IMCROGLOBULIN; CHAIN: B. HIA-CW4 SPECIFIC PEPTIDE; CHAIN: B. HIA-CW4 SPECIFIC PEPTIDE; CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHAIN: C. CHA

PDB annotation	THE TOCOMBATIBILITY COMPLEX	B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNE SYSTEM	IMMUNOGLOBULIN FOLD		1 200	IMMUNE SYSTEM MHC, HLA,	CLASS I, KIK, NK CELL KECET I OK, IMMUNOGLOBULIN 2 FOLD,	RECEPTOR/MHC COMPLEX				-								
Coumpound	C THE	B*0801; CHAIN: A; BE1A-2 MICROGLOBULIN; CHAIN: B;	(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX	TEP IIDE); CHAIN: C,	BETA-2 MICROGLOBULIN;	CHAIN: B, E; HTLV-1	CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN);	CHAIN: A; BETA-2-	PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR	KIKZDLZ; CHAIN: D, E,	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3/HLA-	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3 /HLA- P(A) STEPISK)2705\$ 1HSA 4	THETOCOMPATIBILITY	ANTIGEN CLASS I
SEQFOL	D score			278.31															284.65	20:107				
PMF	score	1.00				ļ	1.00			1.00					,	9. 1.6								1.0
Verify	score	0.87					0.93			0.94						0.93								0.83
Psi Blast		0		0			0			0	>					0			-	>				0
END	ΑA	285		288			285			285	67					285			0	288				285
STAR	T AA	25		25			25			30	3					25				25				25
CHAI	N IS	4		A			A				∢					A				∢				4
PDB	А	lagd		1agd			1duz			,	letx					1hsa		<del></del>		Ihsa				1hsb
SEO	e S	1269		1269			1269				1269					1269				1269				1269

			<del></del>		
PDE annotation			MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2	LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX,	MICKOGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC INMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOWAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
Coumpound	HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3	AN IGEN) IHSB 4 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (WAPPRTVI I): CHAIN: P. O.	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C.
SEQFOL D score		302.23		253.44	
PMF score			1.00		1.00
Verify score			0.70		0.86
Psi Blast		0	0	0	
END		288	285	288	285 0
STAR T AA		23	26	26	56
CHAI N ID		∢	4	4	
PDB ID		Insb	1mhe	1mhe	1qqd A
SEQ ID NO:	0)(1	1709		1269	1269

PDB annotation				100 (HUMBERT HOSE)	COMPLEX (AN 11GEN/FEF 11DE) D33, MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) 535; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV,
Coumpound		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;
SEQFOL	D score		257.46			239.16		
PMF	score	1.00			1.00		1.00	1.00
Verify	score	0.97			0.95		1.03	1.03
Psi Blast		88 89 98	8888		1.4e-94	5.1e-96	5.1e-96	3.2e-95
END	AA.	200	200		218	219	210	218
STAR	TAA	25	25		25	25	26	25
CHAI	NID	4	4		₹	A	∢	4
aua	<u> </u>	1tmc	1tmc		laln	laln	1aIn	1agd
Cap	E E	1269	1269		1271	1271	1271	1271

PDB annotation	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIUE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK. CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX		
Coumpound	HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE): CHAIN: C:	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX	HLA-A*0201; CHAIN; C; HLA-A*0201; CHAIN; A, D; BETA-2 MICROGLOBULIN; CHAIN; B, E; HTLV-1 OCTAMERIC TAX PEPTIDE;	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIRZDI 2: CHAIN: D F.	HLA-CW3, GHEAVY CHAIN); CHAIN: 4; BETA-2. MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KR2DI 2: CHAIN: D;	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHSA 3 /HLA-	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I
SEQFOL D score		243.91					235.85
PMF score			1.00	1.00	1.00	1.00	
Verify score			0.93	0.95	1.16	0.99	
Psi Blast		3.2e-95	3.2e-91	1.6e-93	1e-95	4.8e-94	4.8e-94
END		219	218	218	210	218	219
STAR T AA		25	25	25	26	25	25
CHAI N ID		∢	∢	A	Ą	₹	Ą
PDB ID		lagd	Iduz	lefx	lefx	Ihsa	lhsa
SEQ NO:		1271	1271	1271	1271	1271	1271

PDB annotation				MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HSTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC	IMMUNE SYSTEM
Coumpound	HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HLA CLASS I HISTOCOMPATBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HISTOCOMPATIBILITY
SEQFOL D score			238.52		218.16	
PMF score		1.00		1.00		1.00
Verify score		11.1		0.94		0.95
Psi Blast		4.8e-92	4.8e-92	1.6e-92	1.6e-92	1.6e-92
END AA		218	219	218	219	218
STAR T AA		25	25	26	%	26
CHAI N ID		A	<b>4</b>	<b>V</b>	∢	A
PDB		1hsb	Ihsb	Imhe	Imhe	Iqqd
SEQ ID		1271	1271	1271	1271	1271

	·										
PDB annotation	IMMUNOGLOBIJLIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM			COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY	ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35, MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I.	HISTOCOMPATHIBLITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8: B2M: PEPTIDE HI A B8. HIV	MHC CLASS I,	HISTOCOMPATIBILITY COMPLEX
Coumpound	LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C.	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN H.A-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE EVAPPEYHRK) ITMC 4		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	(GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HIV-1 GAG PEPTIDE	PEPTIDE); CHAIN: C:
SEQFOL D score		267.94				150.68			152.02		
PMF score			,	1.00			1.00				
Verify				0.92			0.79			•	
Psi Blast		1.46-83		8e-91		8e-91	3.2e-91		3.2e-91		
END		199		213		213	213		213		
STAR T AA		25		25		25	25		53		
CHAI N ID		∢		<b>V</b>		∢	V		<del></del>		
PDB ID		ltmc		lain		laIn	lagd		lagd		
SEQ ID NO:		1271		1272	CE C	7/71	1272	1939	7/71		

		·			<del></del> 1	<del></del> 7
PDB annotation	IMMUNG SYSTEM IMMUNGGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX				
Coumpound	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	H.A-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIRZDL2; CHAIN: D, E;	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3/HLA- B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY ANTIGEN CLASS:1 HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4
SEQFOL D score				151.46		178.43
PMF score	1.00	1.00	1.00		1.00	
Verify score	0.75	0.89	0.92		0.87	
Psi Blast	6.4e-90	6.4e-91	1.6e-90	1.6e-90	3.2e-91	3.2e-91
END AA	213	213	213	213	213	213
STAR T AA	25	25	25	25	25	25
CHAI N ID	A	⋖	<b>V</b>	<b>V</b>	⋖	A
PDB	1duz	lefx	Ihsa	Ihsa	1hsb	1hsb
SEQ ID	1272	1272	1272	1272	1272	1272

ion	IBILITY ASSICAL MHC CLASS COMPLEX, IIDE,	SS IB MHC IBILITY ASSICAL MHC CLASS COMPLEX, TDE,	S IB MHC		
PDI3 annotation	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-	CLASSICAL MHC, CLASS IB MHC MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BITTA 2 MHC, HLA, 2 BITTA 2 HARROGLOBULIN, PEPTIDE, HARROGLOBULIN, PEPTIDE,	CLASSICAL MIC, CLASS IB MHC IMMUNE SYSTEM IMMUNOGLOBULN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM		
Coumpound	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE;	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE	HISTOCOMPATIBILITY ANTIGEN TRUNCATED
SEQFOL D score		144.34			215.19
PMF score	1.00		1.00	1.00	
Verify score	0.92		0.67	0.83	
Psi Blast	4.8e-87	4.8e-87	8e-89	9.6e-87	9.6e-87
END	213	213	213	201	205
STAR T AA	26	26	26	25	25
CHAI N ID	∢	∢	A	<b>∀</b>	4
PDB ID	Imhe	Imhe	Iqqd	Itmc	1tmc
SEQ ID	1272 1272	1272	1272	1272	1272

PDB annotation		COMPLEX (ANTIGENPEPTIDE) B35; MAJOR HISTOCOMPATBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGENPEPTIDE)	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX	IMMUNG SYSTEM IMMUNOGLOBULIN FOLD	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,
Coumpound	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-
SEQFOL D score			221.84		223.96		1
PMF score		1.00		1.00		1.00	1.00
Verify score		0.98		1.14		1.27	1.17
Psi Blast		6.4e-97	6.4e-97	3.2e-97	3.2e-97	1.1e-95	4.8e-97
END		205	219	205	219	205	205
STAR T AA		25	25	25	25	25	25
CHAI N ID		A	4	A	4	A	A
PDB ID		laln	lain	lagd	lagd	1duz	1efx
SEQ ID	Ž	1273	1273	1273	1273	1273	1273

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PDB annotation		IMMUNOGLOBULIN 2 FOLD, RECEPTORMHC COMPLEX																									IMMUNE SYSTEM	IMMUNOGLOBULIN (IG)-LIKE	DOMAIN, ALPHA HELIX, BETA	SHEET, 2 IMMUNE SYSTEM			
Coumpound		MICROGLOBULIN; CHAIN; B; PEPTIDE FROM IMPORTIN	ALPHA-2; CHAIN: C; NATURAL	KILLER CELL RECEPTOR KIR2DL2: CHAIN: D. F:	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3 /HLA-	B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY	ANTIGEN HUMAN CLASS I	HISTOCOMPATIBILITY	ANTIGEN 1HSA 3 /HLA-	B(ASTERISK)2705\$ 1HSA 4	HISTOCOMPATIBILITY	ANTIGEN CLASS I	HISTOCOMPATIBILITY	ANTIGEN AW68.1	(LEUCOCYTE 1HSB 3	ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY	ANTIGEN CLASS I	HISTOCOMPATIBILITY	ANTIGEN AW68.1	(LEUCOCYTE 1HSB 3	ANTIGEN) 1HSB 4	HISTOCOMPATIBILITY	LEUKOCYTE ANTIGEN (HLA)-	CW4 CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B;	HLA-CW4 SPECIFIC PEPTIDE;	CHAIN: C;	HIS I OCOMPATIBILITY
SEQFOL	D score									222.04											245.70												
PMF	score				1.00										0.1												1.00				<del></del>	9	20.1
Verify	score				1.12										1.03				-						-		1.07				<del></del> ,	1 25	1
Psi Blast					1.6e-96			•		1.6e-96		<del></del>			1.6e-97						1.6e-97					1	1.1e-95					1 66.03	1
END	AA				205				3.0	219				1	507			-			218					,	205		_			190	
STAR	1 AA				25				20	3				,	3					,	52						97				- ,	25	1
CHAI					∢					₹					←						—			-						_			
PDB					1hsa				1100	11134	_			1,01						+	osut	_				+	7 dda		-			1tmc A	i
SEQ	NO.				1273				1272	(/71				1273	2/71					1077	12/2					1273	12/2					1273	1

PDB annotation						GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	
Coumpound		ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HI A-AW68 1TMC 3	COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE	(EVAPPEYHRK) 1TMC 4	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;		OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE
SEQFOL	D score			273.81						
PMF	score					1.00		0.99		0.17
Verify	score					0:30		0.41		0.05
Psi Blast				1.6e-93		1.6e-22		3.4e-28		1.1e-11
END	AA			199		126		128	····	458
STAR	T AA			25		-		8		291
CHAI	NID			¥		A		A		
PDB	a			1tmc		Ibuo		1buo		lgof
SEO	í a ġ			1273		1274		1274		1274

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PDI: annotation					STRUCTURAL PROTEIN TWO REPEATS OF SPECTEIN AT BUA	HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE. HELIX COILED COIL,	CONTRACTILE PROTEIN	TRANSCRIPTION REGULATION SIGMA70: RNA POLYMERASE	SIGMA FACTOR, TRANSCRIPTION REGII ATTON						RIBOSOME RIBOSOME	INACTIVATING PROTEIN TYPE 11			RIBOSOME RIBOSOME-	INACTIVATING PROTEIN TYPE II			TRANSFERASE	GLYCOSYLTRANSFERASE
Coumpound	(F C 113 8) (BH 4 5) 100 m	(E.C.1.1.3.9) (F.f. 4.3) IGOF 3	OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (F.C.1.13.9) (PH.4.5), 1505.2	(2) (C.1.1.1) (C.C.1.1.2)	ALPHA SPECTRIN; CHAIN: A, B, C;		HIMAN SVEI ETAI MAISCHE	ALPHA-ACTININ 2; CHAIN: A;		KNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;			COMPLEX	(GLYCOSIDASE/CARBOHYDRA	TE) ABRIN-A COMPLEXED	WITH I WO SUGAR CHAINS	RIBOSOME-INACTIVATING	PROTEIN TYPE II; CHAIN: A;	RIBOSOME-INACTIVATING	PROTEIN TYPE II; CHAIN: B	RIBOSOME-INACTIVATING	PROTEIN TYPE II; CHAIN: A;	KIBUSUME-INACTIVATING	PROTEIN TYPE II; CHAIN: B		POLYSACCHARIDE BIOSYNTHESIS PROTEIN
SEQFOL D score					65.74		59 43	?	7. 7.	/0.10																
PMF score		5	0.13										0.40				0.21			:	0.13				0.28	
Verify score		200	77:0							<u>-</u>			0.45				0.16			†	-0.23			$\dagger$	60.0	
Psi Blast		1 60 00	0000		6.8e-09		3.4e-12		5 10-05				1.4e-09 (		··-		1.2e-15 (			0 00011				0 00 00		
END		405			385		415		416	2			552	-			552			543				345	_	
STAR T AA		383			170		180		130	· · · · · · · · · · · · · · · · · · ·			413				441		-	450	2			123		
CHAI N ID					Ą	***************************************	A						<b></b>				<u>—</u>			B				A		
PDB ID		1gof	)		1cun		Idun		Isig	)		+	labr			+	lce7			Ice7				laga /	_	
SEQ ID NO:		1274			1275		1275		1275			750.	17/0				9/71			1276				1276		1
																						_				

PDB annotation		THE TOTAL A GET WAT AN	HYDROLASE A LLAN DEGRADATION					IMMUNOGLOBULIN	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIRODY 8F5:	IMMUNOGLOBULIN, ANTIBODY,	RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPITOPE, COMPLEX	(IMMUNOGLOBULIN/VIRAL PEPTIDE)	IMMUNOGLOBULIN, ANTIBODY,	CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN
Coumpound		CHAIN: A;	ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	GLYCOSIDASE RICIN (E.C.3.2.2.2) 2AAI 3	CO - Grande	TRANSFERASE (PHOSPHOTRANSFERASE) ADENYLATE KINASE	ISOENZYME-3 (GLP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E C 2 7 4 10) 24K3 4	2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	29G11 FAB; CHAIN: L, H;	29G11 FAB; CHAIN: L, H;	IGG2A; CHAM: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN	VP2; CHAIN: F;			IMMUNOGLOBULIN, DIELS ALDER CATALYTIC	ANTIBODY; CHAIN: L, H, A, B;	MONOCLONAL ANTI-E- SELECTIN 7A9 ANTIBODY; CHAIN: L, H;
SEQFOL	D score								61.67		60.58						61.06
PMF	score		99.0	0.03		0.98		0.21		0.27					0.17		
Verify	score		-0.02	-0.31		-0.87		0.01		-0.31					-0.11		
Psi Blast			1.6e-16	1.3e-07		1.3e-16	-	1.3e-38	6.4e-37	6.4e-37	1.3e-36				9.6e-37		3.2e-35
END	AA		543	543		38		253	254	253	256				252		256
STAR	TAA		441	441		1		59	50	59	50				51		48
CHAI	OI N		A	В		A		H	Н	H	н				L		H
PDB	A		lxyf	2aai		2ak3		12e8	1a0q	1а0q	la3r				1a4j		la5f
SEO	î A Ş	5	1276	1276		1279		1280	1280	1280	1280				1280		1280

PDB annotation	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGE N) COMPLEX (IMMINOGLOBII N/AITCOANTIGE	(IMMONOCIODE DE LINA DE LA COMPTIGE N), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX	COMPLEX (VIIVAL CAPSID/IMMUNOGLOBULIN) HIV-1	CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV,	IMMUNOGLOBULIN	IMMUNOGLOBULIN, ANTIBODY	REACTION	IMMUNE SYSTEM	IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY	ENGINEERING, HUMANIZED AND	CHIMERIC ANTIBODY, FAB, 2 X-	RAY STRUCTURE, THREE-	GAMMA- 3 INTERFERON. IMMUNE	SYSTEM	ANTIBODY ENGINEERING	ANTIBODY ENGINEERING,	ANTIRODIES 2 FAR X-RAV	STRUCTURES GAMMA-	INTERFERON	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-
Coumpound	IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;		HUMAN IMMUNODEFICIENCY VIRUS TYPE I CAPSID CHAIN:	A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;		IMMUNOGLOBULIN IGG2A:	CHAIN: L, H;		ANTIBODY (LIGHT CHAIN);	CHAIN); CHAIN: H;						ANTIBODY; CHAIN: L, H;					IMMUNOGLOBULIN; CHAIN: A, B;
SEQFOL D score		·				56.82													_		
PMF score	0.00		0.58		•				-0.07							60.0					0.13
Verify	-0.04	ļ	0.08						0.04							0.00					-0.12
Psi Blast	1.1e-37		4.8e-37			4.8e-33			8e-39						1	1.4e-37					4.8e-37
END	255	,	253			256			258						9,0	807					252
STAR T AA	20		75			51			15						15	ī				;	51
CHAI N ID	1	ļ	Ľ.			H			<b>.</b>							د.					4
PDB ID	ladq		larv			laxt			wZq1						15.41	104î					poq
SEQ ID NO:	1280	C C	1280			1280		000.	1280						1300	1400				000.	1280

PDB annotation	CHAIN DIMER HEADER	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM	IMMUNG SYSTEM IMMUNGGLOBULIN		IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM	ANTIBODY THERAPEUTIC, ANTIBODY, CD52	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI- PRION ANTIBODY, FAB 3F4	
Coumpound		FAB FRAGMENT; CHAIN: L, H, I, K; VASCULAR ENDOTHELIAL GROWTH FACTOR: CHAIN: V. W:	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNOGLOBULIN OPG2 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB, VARIABLE DOMAIN; CHAIN: H;	COMPLEX (ANTIBODY/ANTIGEN) HYHEL- 5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME 1BOL 3 1BQL 95	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B:	CAMPATH-IH:LIGHT CHAIN; CHAIN: L; CAMPATH- IH:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE
SEQFOL D score			57.09	57.73	59.53	57.49			56.80
PMF score		-0.09					-0.03	09.0	
Verify score		0.09					0.11	-0.12	
Psi Blast		8e-38	4.8e-35	1.6e-34	3.2e-36	1.6e-26	9.6e-37	8e-39	1.6e-36
END		252	252	258	255	250	252	255	255
STAR T AA		51	47	51	20	51	51	89	48
CHAI N ID		H	A	н	Ħ	B	1	H	Н
PDB ID		16,1	1bln	15m3	lbq!	1bz7	lce1	1cr9	1fbi
SEQ ID	NO:	1280	1280	1280	1280	1280	1280	1280	1280

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PDB annotation		IMMUNOGLOBULIN			CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB,	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)		
Coumpound	MONOCLONAL ANTIBODY F9.13.7 (IGG1) IFBI 3 COMPLEXED WITH	4-4-20 (IG*GZA=KAPPA=) FAB FRAGMENT; IFLR 5 CHAIN: L, H: IFLR 6	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD. 3	IMMUNOGLOBULIN 6D9; CHAIN: L, H;	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 11A1 5 CHAIN: L, H; IIA1 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); IIAI 9 CHAIN:	COMPLEX COMPLEX COMPLEX CANTIBODY/BINDING PROTEIN) IGGI FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III)	STREPTOCOCCUS HGC 15 IMMUNOGLOBULIN IGGI FAB' FRAGMENT (B1312) HGF 3
SEQFOL D score		56.39		57.20	57.33	60.65	57.26	58.26
PMF score			-0.12					
Verify score			0.11					
Psi Blast		3.2e-33	1.4e-37	6.4e-32	1.3e-34	4.8e-33	1.6e-32	8e-35
END		256	258	258	255	254	258	258
STAR T AA		51	51	51	47	48	51	47
CHAI N ID		Н	Ą	В	Ţ	H	н	L
PDB ID		1fir	1fvd	1fvd	Ihyx	liai	ligc	ligf
SEQ NO:	_	1280	1280	1280	1280	1280	1280	1280

PDB annotation	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY		MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	IMMUNOGLOBULIN,	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,
Coumpound	IGGI INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	28B4 FAB; CHAIN: L, H;	IMMUNOGLOBULIN FAB D44.1 (IGG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) IMLB 5	TITIN; CHAIN: NULL;	NIG9 (IGGI=LAMBDA=); CHAIN: L, H;	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;
SEQFOL D score		57.31	56.48			58.83		56.66
PMF score	0.37			0.35	0.22	·	0.41	
Verify	0.02			0.08	-0.09		-0.09	
Psi Blast	1.6e-36	6.4e-34	8e-36	0.0015	6.4e-37	1.6e-36	1.6e-36	3.2e-30
END	253	255	258	254	253	256	253	252
STAR T AA	59	51	48	178	51	51	59	50
CHAI N ID	B	н	В		Н	Н	н	ы
PDB	ligy	1kel	lmlb	Inct	Ingp	1sm3	1sm3	1sm3
SEQ B	1280	1280	1280	1280	1280	1280	1280	1280

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PDB annotation	2 COMPLEX (ANTIBODY/PEPTIDE REPTORE)	eriore)		COMPLEX (ANTIBODY/ELECTRON	ANTIGEN; IMMUNOGLOBULIN, IGGI KAPPA, FAB FRAGMENT.	HORSE 2 CYTOCHROME C, COMPLEX (AN TIBODY/ELECTRON	TRANSPORT) TRANSFERA & SE TREE DE CERTECON	RECEPTOR TYROSINE KINASE, 3D. DOMAIN SWAPPING, 2	TRANSFERASE CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB. RING	CLOSURE REACTION	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING	CECCOME MEAN TION		
Coumpound		IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA I TET 3 TOXIN	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) TINM 3 (NMR, MINIMIZED	ES ANTIBODY; CHAIN: L, H;			NT-3 GROWTH FACTOR	RECEPTOR TRKC; CHAIN: A;	IGG 5C8; CHAIN: L, H;	100 509. CHARLT 11.	IOG JCo; CHAIN: L, H;	IMMUNOGLOBULIN IGG2B	COMPLEXED WITH ANTIGEN	2CGR 3 N-(P-CYANOPHENYL)- N'-(DIPHENYLEMETHYL)
SEQFOL D score		57.32							57.06			57.12		
PMF score			0.05	0.70			0.01			0.53	}			
Verify			-0.05	0.55			-0.18			0.11				
Psi Blast		6.4e-36	0.0051	3.2e-37			0.0051		1.1e-37	1.1e-37		1.6e-31		
END AA		256	254	253		· · · · · ·	254		254	253		254		
STAR T AA		48	178	59			164		48	59		51		
CHAI N ID		Ħ		Н			A		Н	н		=		
PDB ID		Itet	ltnm	Iwej			lwwc		25c8	25c8		2cgr		1
SEQ ID NO:		1280	1280	1280			1280		1280	1280		1280		

PDB annotation				COMPLEX (KI/DNA/FAB) HIV-1 K1; FAB 28; AIDS, HIV-1, RT, POLYMERASE			TRANSFERASE TRANSFERASE, CREATINE KINASE	TRANSFERASE BB-CK, BRAIN-TYPE CREATINE KINASE, BRAIN-TYPE CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DISORDERS	TRANSFERASE (CREATINE KINASE) UMTCK, MIA-CK; MITOCHONDRIAL CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY	TRANSFERASE CREATINE KINASE,
Coumpound		GUANIDINEACETIC ACID 2CGR 4	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	HIV-I REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	:	CREATINE KINASE; CHAIN: A, B, C, D;	CREATINE KINASE, B CHAIN; CHAIN: A, B, C, D;	CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL; CHAIN: A, B, C, D, E, F, G, H;	CREATINE KINASE; CHAIN: A;
SEQFOL	D score			56.78	57.01					
PMF	score		-0.08				0.27	0.30	0.33	0.19
Verify	score		0.00	:			-0.83	-0.83	-0.83	-0.83
Psi Blast			1.6e-38	4.8e-33	3.2e-31		3.2e-19	4.8e-19	6.4e-19	1.4e-19
END	AA		258	258	255		46	46	46	46
STAR	TAA		51	47	49		-	-	_	
CHAI	O N		i i	၁	H		A	⋖	4	Ą
PUR	A		2fgw	2hmi	7fab		lcrk	1qh4	IqkI	2crk
CEO	A S	2	1280	1280	1280		1284	1284	1284	1284

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PDE annotation	TRANSFERASE	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	MOLECULAR CHAPERONE HDJ-1;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE		PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSI HOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRAN SFERASE RHOGAP DOMAIN; PHOSPHOTRAN SFERASE, TPASE ACTIVA: ITING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL	G-PROTEIN CDC.42 GTPASE-ACTROATING PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN, G-PROTEIN,	COMPLEX(GTPASE ACTIVATIVPROTO-ONCOGENE)
Coumpound		DNAJ; CHAIN: NULL;	DNAJ; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;		PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	RHOGAP; CHAIN: NULL;	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN
SEQFOL D score			68.92		83.03			93.22	94.15	109.76	114.46
PMF score		1.00		1.00		1.00					
Verify score		0.89	·	0.77		1.26					
Psi Blast		1.1e-27	1.1e-27	3.4e-30	3.4e-30	1.6e-27		6.4e-08	8e-09	4.8e-17	1.1e-17
END		69	78	77	08	69		300	314	288	302
STAR T AA		2	5	01	5	7		112	112	66	105
CHAI N ID								4	Д		A
PDB ID		1590	1bq0	1hdj	1hdj	1hdj		Ipbw	1pbw	lrgp	1tx4
SEQ ID NO:		1287	1287	1287	1287	1287		1292	1292	1292	1292

PDB annotation	GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	COMPLEX (METALLOPROTEINASE/RECEPTOR ) CDMT1-MMP; TIMP-2 MATRIX METALLOPROTEINASE, TISSUE INHIBITOR OF 2 METALLOPROTEINASES, PROTEINASE COMPLEX, PROGELATINASE A 3 ACTIVATOR, CRYSTAL STRUCTURE, COMPLEX 4 (METALLOPROTEINASE/RECEPTOR )		METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR	HYDROLASE MMP-2,72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL- LENGTH, METALLOPROTEINASE, 2 GELATINASE A	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE	METALLOPROTEASE
Coumpound	RHOA; CHAIN: B;	MEMBRANE-TYPE MATRIX METALLOPROTEINASE; CHAIN: M; METALLOPROTEINASE INHIBITOR; CHAIN: T;	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	STROMELYSIN-1; CHAIN: A;	GELATINASE A; CHAIN: A;	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	FIBROBLAST (INTERSTITIAL)
SEQFOL D score		103.34	120.96	132.96	647.13	90.80	151.00
PMF score							
Verify score							
Psi Blast		9.6e-54	8e-60	4.8e-63	0	9.6e-14	3.2e-70
END		281	254	272	669	333	449
STAR T AA		112	110	107	25	274	107
CHAI		×		<b>∀</b>	4	⋖	
PDB		1bqq	1cge	lciz	1ck7	Icxw	Itbl
SEQ ID	NO:	1293	1293	1293	1293	1293	1293

PDI: annotation		HYDROLASE (METALLOPROTEASE) MMP-2, 72KD TYPE IV COLLAGENASI; HYDROLASE, HEMOPEXIN DOMAIN, HYDROLASE, METALLOPROTEASE	ı	METALLOPROTEASE MMP-9, PUMP-1, MATRIN: 1MMO 7	METALLOPROTEASE MMP-13; C- TERMINAL HEMOPEXIN-LIKE DOMAIN OF MATRIX- METALLOPROTEINA SF	HYDROLASE MATRIX METALLOPROTEINASE-2; INHIBITOR, MATRIXIN, MATRIX METALLOPROTEINASE-2 (MMF-2), 2 GELATINASE A, METZINCIN, HYDROLASE	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION	MATRIX METALLOPROTEASE MMP-13; MATRIX METALLOPROTEASE		HYDROLASE MMP-2,72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-
Coumpound	COLLAGENASE (MMP-1); 1FBL 4 CHAIN: NULL; 1FBL 5	GELATINASE A; CHAIN: NULL;	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) 1HFC 3	MATRILYSIN; IMMQ 5 CHAIN: NULL; IMMQ 6	COLLAGENASE-3; CHAIN: NULL;	GELATINASE A; CHAIN: A;	STROMELYSIN-1; CHAIN: NULL;	MMP-13; CHAIN: A, B;	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	GELATINASE A; CHAIN: A;
SEQFOL D score		99.59	117.07	119.28	84.70	144.06	187.06	138.28	0000	419.38
PMF										
Verify score										
Psi Blast		9.6e-50	8e-60	8e-56	4.8e-63	1.6e-57	1.6e-82	1.6e-59		0
END		669	265	279	669	272	272	267	557	427
STAR T AA		474	115	107	477	112	44	107	30	67
CHAI N ID		·				A		4	<	£
PDB ID		lgen	1hfc	mml 9	1pex	Iqib	1slm	830c	10101	7
SEQ ID NO:		1293	1293	1293	1293	1293	1293	1293	1207	1671

PDB annotation	LENGTH, METALLOPROTEINASE, 2 GELATINASE A	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR) GI- ALPHA-1; REGULATOR OF G- PROTEIN SIGNALLING 4; GI-ALPHA- 1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN	COMPLEX (SIGNAL
Coumpound		HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	HEMOLIN; CHAIN: A, B;	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	GUANINE NUCLEOTIDE- BINDING PROTEIN G(I); CHAIN: A, D; RGS4; CHAIN: E, H;	GUANINE NUCLEOTIDE-
SEQFOL D score		90.47	80.92	176.45	104.50	104.57	146.45	133.76
PMF score								
Verify score								
Psi Blast		3.2e-21	3.2e-44	8e-44	8e-18	3.2e-18	4.8e-48	6.4e-43
END		333	562	1834	2042	1645	172	169
STAR T AA		274	400	1462	1660	1370	45	54
CHAI N ID		A		A		В	ப	H
PDB		lcxw	2ucz	1bih	1fnf	litb	lagr	lagr
SEQ	Ö	1294	1297	1298	1298	1298	1301	1301

PDE annotation TRANSDUCTION/REGULATOR) GI-	PROTEIN SIGNALLING 4; GI-ALPHA- 1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE	SIGNATION PROTEIN REGULATION SIGNALING PROTEIN REGULATION; GAIP, RGS, REGULATOR OF GPROTEIN, SIGNALING PROTEIN 2 REGULATION	OXIDOREDUCTASE METHYLENETHF DEHYDROGENASE/ METHENYLTHF THF, METHENYLTHF THF, DEHYDROGENASE, CYCLOHYDROLASE, FOLATE, 2 OXIDOREDIICTASE HEADED	OXIDOREDUCTASE, HYDROLASE FOLATE, DEHYINGGENASE, CYCLCOHYDROLASE, BIFUNCTIONAL, 2 CHANNELING, OXIDOREDUCTASE, HYDROLASE	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION FEGULATION/DNA) DNA-BINDING
TRAN			OXIDOREDUCT AN METHYLENETHF DEHYDROGENAS METHENYLTHF 1 BIFUNCTIONAL, DEHYDROGENAS CYCLOHYDROLA SOXIDOR FIDILITA S	OXIDORED FOLATE, D CYCLCOHY BIFUNCTIC	COMPLEX (TRANSCRIP REGULATIONDNA) GAI GABPBETA1; COMPLEX (TRANSCRIPTION REGII ATTONDNA) DN
Coumpound BINDING PROTEIN G(I); CHAIN: A. D. RGS4. CHAIN: F	H;	GAP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	METHYLENETETRAHYDROFO LATE DEHYDROGENASE / CHAIN: A, B;	FOLD BIFUNCTIONAL PROTEIN; CHAIN: A;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score	·	121.40	94.97	106.54	
PMF					0.52
Verify					-0.23
Psi Blast		3.2e-46	4.8e-74	8e-77	8e-34
END		172	235	235	157
STAR T AA		46	'n	_	18
CHAI N ID		A	∢	4	В
PDB ID		lcmz	] a4i	1b0a	lawc
SEQ ID NO:		1301	1302	1302	1307

PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK44, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE FINACH STERMS	COMPLEX (KINASE/ANTI- COMPLEX (KINASE/ANTI- ONCOGENE) HEADER COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN/CIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score							
PMF score		0.29		0.19	0.04	0.00	0.37
Verify score		-0.09		-0.01	0.14	-0.17	0.01
Psi Blast		4.8e-29		8e-27	6.4e-17	6.4e-26	1.3e-23
END AA		125		160	260	160	183
STAR T AA		ю		21	443	21	50
CHAI N ID		В			Д	В	В
PDB		lawc		1bd8	16i7	16lx	1blx
SEQ ID	SO.	1307		1307	1307	1307	1307

PDIs annotation	(INHIBITOR PROTEIN/KINASE) HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-HELIX ANKYRIN REPRAT	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPISAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPI!AT, 2 CDK 4/6 NJHBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RICEPTOR, TUMOUR- ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN
Coumpound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	MAC-2 BINDING PROTEIN; CHAIN: NULL;	TROPINONE REDUCTASE-I; CHAIN: A, B;
SEQFOL D score						112.99	73.73
PMF score	0.15	0.06	0.10	0.37	0.01		
Verify score	-0.12	0.14	-0.12	0.01	0.14		
Psi Blast	6.4e-25	1.6e-17	1.3e-25	3.2e-24	1.6e-20	1.1e-44	1.6e-66
END AA	130	267	161	129	127	138	304
STAR T AA	-	443	18	-	61	26	34
CHAI N ID	A	Ą	Ą	∢			A
PDB ID	1bu9	149s	lihb	lihb	lmyo	16y2	lael
SEQ ID NO:	1307	1307	1307	1307	1307	1314	1315

PDB annotation	DEHYDROGENASE	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS,	REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE	OXIDOREDUCTASE NAD- DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE	DEHYDROGENASE DEHYDROGENASE, 17-BETA- HYDROXYSTEROID	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASEREDUCTASE, BILE ACID CATABOLISM		OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRAHYDROBIOPTERIN, OXIDOREDUCTASE	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE	OXIDOREDUCTASE
Coumpound		TROPINONE REDUCTASE-1; CHAIN: A, B;	,	CIS-BIPHENYL-2,3- DIHYDRODIOL-2,3- DEHYDROGENASE; CHAIN: NULL;	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	17-BETA-HYDROXYSTEROID- DEHYDROGENASE; CHAIN: NULL:	7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B:	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) 1HDC 3 COMPLEXED WITH CARBENOXOLONE 1HDC 4	SEPIAPTERIN REDUCTASE; CHAIN: NULL;	TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	TROPINONE REDUCTASE-II;
SEQFOL D score		76.92		65.57	69.13	79.80	82.26	74.82	65.22	82.44	76.67
PMF score											
Verify score											
Psi Blast		9.6e-68		1.6e-47	3.2e-54	4.8e-32	6.4e-66	4.8e-67	3.2e-21	3.2e-61	9.6e-65
END		304		314	297	319	298	306	297	308	291
STAR T AA		34		35	35	38	30	35	35	24	32
CHAI N ID		В			A		4	4		4	A
PDB		1ae1		1bdb	lcyd	1 fds	1fmc	1hdc	loaa	lybv	2ae2
SEQ ID	ÖN	1315		1315	1315	1315	1315	1315	1315	1315	1315

PDIs annotation	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKB112 HOMOLOGOUS DOMAIN OF HITKBP25, ISOMERASE	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING),	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT,	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TPANSPORT TPANSPORT,	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFISCTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYPALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX,	SMALL GTPASE KARYOPHERIN
Coumpound	CHAIN: A, B;	FKBP25; CHAIN: NULL;	P50-RHOGAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B.	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A DKN: CHAIN: B.	RAN; CHAIN: A, C; IMPORTIN
SEQFOL D score		194.11	50.20	61.74	64.26	79.57	93.92	52.92	60.48
PMF score									
Verify score									
Psi Blast		1.3e-24	3.2e-43	3.2e-32	4.8e-33	4.8e-64	1.3e-64	1.6e-50	1.1e-31
END		339	218	244	245	203	204	204	209
STAR T AA		224	31	29	27	31	33	28	34
CHAI N ID			Q	<b>∀</b>	e B	¥	A	¥	Ą
PDB ID		1pbk	lam4	1byu	1byu	1c1y	lctq	lcxz	1ibr
SEQ ID NO:		1321	1323	1323	1323	1323	1323	1323	1323

PDB annotation	BETA, P95 SMALL GTPASE, NUCLBAR TRANSPORT RECEPTOR	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2
Coumpound	BETA SUBUNIT; CHAIN: B, D;	RAP2A; CHAIN: NULL;	RAC1; CHAIN: NULL;	RAN; CHAIN; A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	RAB3A; CHAIN: A;	PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;
SEQFOL D score		91.54	62.77	59.75	63.61	57.05	67.16	107.93
PMF score								
Verify								
Psi Blast		6.4e-61	1.6e-51	1.1e-31	9.6e-58	1.6e-46	1.6e-58	1.6e-80
END		204	222	227	209	230	204	536
STAR T AA		31	30	31	29	33	30	167
CHAI				O	A	A	∢	
PDB		1kao	1mh1	1лтр	Izbd	2ngr	3rab	1a60
SEQ	NO:	1323	1323	1323	1323	1323	1323	1324

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PDB annotation	SER/THR KINASE	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION,	MITOSIS, INFIBITION COMPLEX (KINASE/INFIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INFIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE,	HEADER HELLY	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)			PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORY A TON
Соитроинд		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3	CATALITIC SUBONII) ICIP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;
SEQFOL D score		129.21	122.05		133.50	2000	102.25	102.19	141.09
PMF score									
Verify									
Psi Blast		0	1.6e-81		3.2e-91	80.49	0	3.2e-47	0
END		503	493		499	503	3	503	503
STAR T AA	,	196	197		761	160		165	196
CHAI N ID			⋖		∢	E		ı)	
PDB ID		Iaqı	1bi8	1	IOIX	1cmk		ıctp	Ihcl
SEQ ID NO:	7007	1324	1324	1224	+7c1	1324			1324

		m,				IAP		z Ö,
PDB annotation	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE	KINASE KINASE, I WII CHIN, INTRASTERIC REGULATION	ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
Coumpound	P38 MAP KINASE; CHAIN: NULL;	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	ERK2; CHAIN: NULL;	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;
SEQFOL D score	117.40	136.35	105.97	150.88	128.64	140.27	108.11	129.37
PMF score								
Verify score								
Psi Blast	1.6e-97	9.6e-100	1.6e-51	0	0	0	6.4e-80	0
END	292	563	522	570	568	509	496	503
STAR T AA	180	180	170	179	190	181	167	196
CHAI			A					
PDB	1ian	1jnk	1kob	1p38	lpme	3erk	1a60	laq1
SEQ	NO: 1324	1324	1324	1324	1324	1324	1325	1325

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COMPLEX (KINASE/INHIBITOR) CDK6; P19TRAD; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HFADER HELIX	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX ANHIBITOR PROTEIN/KINASE)			PROTEIN KINASI! CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORY ATTOM	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38, PROTEIN SER/THR-KINASI;, SER/THR-THREONINE-PROTEIN KINASE	TRANSFERASE JINK3;
CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	P38 MAP KINASE; CHAIN: NULL;	C-JUN N-TERMINAL KINASE;
122.26	133.76	102.41	102.34	141.19	118.03	136.46
8e-86	1.3e-94	3.2e-49	3.2e-49	0	0	4.8e-100
493	499	503	503	503	267	563
197	192	091	165	196	180	180
¥	A	щ	<b>ച</b>			
15i8	1blx	lcmk	lctp	Ihcl	lian	Ijnk
1325	1325	1325	1325	1325	1325	1325
	1bi8 A 197 493 8e-86 122.26 CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	1bi8   A   197   493   86-86   122.26   CYCLIN-DEPENDENT KINASE   6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPENDENT KINASE   CYCLIN-DEPEN	1bi8   A   197   493   86-86   122.26   CYCLIN-DEPENDENT KINASE   6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE   102.41   102.41   102.41   102.41   102.41   102.41   102.41   102.41   102.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   103.41   1	1bi8   A   197   493   86-86   122.26   CYCLIN-DEPENDENT KINASE   6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE   156-94   1.36-94   1.33.76   CYCLIN-DEPENDENT KINASE   6; CHAIN: B, D;   156-94   1.36-94   1.33.76   CYCLIN-DEPENDENT KINASE   6; CHAIN: B, D;   156-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1.36-94   1	1bis   A   197   493   86-86   122.26   CYCLIN-DEPENDENT KINASE   6; CHAIN: A, G; CYCLIN-DEPENDENT KINASE   6; CHAIN: B, D;   CYCLIN-DEPENDENT KINASE   6; CHAIN: B, D;   CYCLIN-DEPENDENT KINASE   6; CHAIN: A; P19INK4D; CHAIN: B   CAMP-DEPENDENT KINASE   CAMP-DEPENDENT KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN KINASE   CAMP-DEPENDENT ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTEIN ROTE	1bis   A   197   493   8e-86   122.26   CYCLIN-DEPENDENT KINASE

PDB annotation	TRANSFERASE, JMK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	L; HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE	L; HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE	B; CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
Coumpound	CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	ERK2; CHAIN: NULL;	TITIN; CHAIN: A, B;	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	HUMAN PROCATHEPSIN L; CHAIN: A;	HUMAN PROCATHEPSIN L; CHAIN: A;	E-CADHERIN; CHAIN: A, B;
SEQFOL D score		106.60	151.09	128.85	99.53	140.42	368.72	412.39	124.30
PMF									
Verify score									
Psi Blast		9.6e-53	0	0	1.1e-44	0	0	0	8e-50
END		522	570	568	519	809	350	391	269
STAR T AA		170	179	190	194	181	1	19	65
CHAI N ID		Ą			¥		V	4	⋖
PDB ID	,	1kob	1p38	1pme	1tki	3erk	1cs8	1cs8	ledh
SEQ ID		1325	1325	1325	1325	1325	1327	1328	1333

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PDB annotation	CELL ADHESION PROTEIN CELL ADHESION PROTEIN						GUANINE NUCLEOTIDE EXCHANGE FACTOR RCCI; GUANINE NUCLEOTIDE IXCHANGE FACTOR, GEE, RAM, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER		EYE LENS PROTEIN EYE LENS PROTEIN	EYE LENS PROTEIN EYE LENS	CRYSTALLIN GAMMA II. CRYSTALLIN EYE LENS PROTEIN,	EXE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN R
Coumpound	N-CADHERIN; CHAIN: A;		LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING PROTEIN COMPLEXED WITH ARACHIDONIC IADL 3 ACID	LPID-BINDING PROTEIN FATTY ACID BINDING PROTEIN (HUMAN MUSCLE, M-FABP) COMPLEXED 1HMR 3 WITH ONE MOLECULE OF FILENDIC ACID 11MR 4	CELLULAR LIPOPHILIC TRANSPORT PROTEIN P2 MYELIN PROTEIN (P2) IPMP 3		REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;		GAMMAF CRYSTALLIN; CHAIN: NULL	GAMMAE CRYSTALLIN; CHAIN: A B	GAMMA B-CRYSTALLIN; CHAIN: NULL;	CIRCULARLY PERMUTED BB2- CRYSTALLIN; CHAIN: A, B;
SEQFOL D score	129.50		158.94	146.24	161.49		141.30		122.87	121.88	125.68	96.08
PMF score												
Verify score												
Psi Blast	8e-52		9.6e-56	6.4e-58	3.2e-55		1.6e-78		1.4e-61	4.8e-63	3.2e-65	1.6e-39
END	268		133	133	133		409		148	148	148	147
STAR T AA	64		ო	E	3		1		-	-	-	-
CHAI N ID	Ą				A		∢			¥		4
PDB LD	Incj		ladi	Ihmi:	Ipmp		lai2		la45	Ia5d	lam m	1bd7
SEQ ID NO:	1333	100.	1335	1335	1335		1340		1345	1345	1345	1345

PDB annotation	EYE-LENS PROTEIN, 2 MULTIGENE FAMILY	EYE LENS PROTEIN EYE LENS PROTEIN	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION		IRON STORAGE IRON STORAGE	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION	COMPLEX (TRANSCRPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
Coumpound		GAMMA-D CRYSTALLIN; CHAIN: A, B	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	EYE LENS PROTEIN BETA-B2- CRYSTALLIN 2BB2 3	FERRITIN; CHAIN: NULL;	HUMAN BETA2- GLYCOPROTEIN I; CHAIN: A;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
SEQFOL D score		122.84	60.77	99.58	273.99	84.05	64.05	54.79
PMF score						·		
Verify score								
Psi Blast		1.3e-62	9.6e-31	1.6e-47	8e-73	1.6e-11	1.66-39	8e-30
END		148	388	148	177	484	192	161
STAR T AA		1	48	1	9	184	38	2
CHAI N ID		Ą	м			А	Д	
PDB ID		1elp	lgot	2bb2	2fha	1qub	lawc	1bd8
SEQ	Ö	1345	1345	1345	1352	1353	1363	1363

PDI annotation		HORMONE/GROWTH FACTOR P18- HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN 2 DEPENDENT KINASE,	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPI!AT, 2 CDK 4/6	INHIBITOR TRANSCRIPTION FACTOR P65; P50D; TRANSCRUPTION FACTOR, IKB/NFKB COMPLEX	ANK-REPEAT MYOTROPHIN,	COMPLEX (TRANSCRIPTION COMPLEX (TRANSCRIPTION (TRANSCRIPTION REGULANK REPEAT) REGULANK REPEAT), ANKYRN 2 REPEAT HER IX	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2	DOMAIN ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2
Coumpound	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-AI PHA: CHAIN: C	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	SYNAPTOTAGMIN III; CHAIN: A;	SYNAPTOTAGMIN III; CHAIN: A;
SEQFOL D score	55.34	54.53	54.88	67.03	53.66	64.27		
PMF score							1.00	1.00
Verify score							0.64	0.49
Psi Blast	8e-29	1.6e-34	8e-34	4.8e-38	3.2e-25	1.6e-38	8.5e-91 (	3.2e-46 C
END	165	212	162	307	156	243	415	415
STAR T AA		31	5	73	39	31	143	144
CHAI N ID	B	V	∢	Q		ш	A	
PDB ID	1blx		lihb	likn ]	Q	Infi	1dqv /	1dqv A
SEQ ID NO:	1363	1363	1363	1363		1363	1366	1366

PDB annotation			OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK	OXIDOREDUCTASE (OXYGENASE)	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
Coumpound	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CYTOCHROME P450; CHAIN: A, B;	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	KINESIN; CHAIN: NULL;	KINESIN; CHAIN: NULL;	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;
SEQFOL D score		122.64	197.06	67.59	210.20		·	
PMF score	1.00					1.00	1.00	1.00
Verify score	0.40					.0.54	0.65	0.46
Psi Blast	3.4e-40	3.4e-40	1.6e-92	3.2e-31	8e-89	8e-89	6.8e-79	3.2e-72
END	270	270	505	504	340	340	340	341
STAR T AA	134	134	42	23	2	4	_	-
CHAI N ID			¥				4	A
PDB	lrsy	lrsy	1bu7	10ха	1bg2	1bg2	1cz7	1cz7
SEQ ID	1366	1366	1368	1368	1372	1372	1372	1372

PDI annotation	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMII V	CONTRACTILE PROTEIN MOTOR PROTEIN	CYTOSKELETON MOTOR PROTEIN MOTOR PROTEIN.	CYTOSKELETON MOTOR PROTEIN MOTOR PROTEIN,	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR	NCD, CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN,	NCD, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTIIN, ATPASE, P.	PROTEIN CONTRACTILE PROTEIN CONTRACTILE PROTEIN KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBULE BINDING
Coumpound	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, CD;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN MOTOR NCD; CHAIN: CA;	KINESIN MOTOR NCD; CHAIN: C		KINESIN-LIKE PROTEIN KAR3; CCHAIN: NULL; CHAIN: NULL; K	KINESIN-LIKE PROTEIN KAR3; COCHAIN: NULL; COCHAIN: NULL; KI
SEQFOL D score	156.19	139.58						152.53		185.05	
PMF score			1.00	1.00	0.98	0.99	1.00				1.00
Verify			0.25	0.29	-0.01	-0.02	0.46				0.31
Psi Blast	6.8e-79	1.2e-58	3.2e-57	1.2e-58	3.4e-28	8e-27	1.6e-72	1.6e-72	\$ 10.74		6.4e-72
END	342	252	252	252	352	358	339	340	338		339
STAR T AA	1	2	4	9	265	265			5	3	9
CHAI N ID	∢	4	A		В	В	A	∢ .			
PDB ID	1cz7	2kin	2kin			2kin	Zncd	2ncd .	3kar		3kar
SEQ NO:	1372	1372	1372	1372	1372	1372	1372	1372	1372		1372

SDG         TAB         ATA         PAIR BIAST         Verify Voltage         PAIR SERVED         Commpound         PDB amount thou           1372         38a         7         338         5.1e-74         0.50         1.00         KINBSIN-LIKE PROTEIN KAR3, CONTRACTILE PROTEIN, KAR3, CARATILE PROTEIN, ATTARS, P. LOOP, MICKOTIBD ROTEIN, MOTOR 2 PROTEIN, ATTARS, P. LOOP, MICKOTIBD LE BINDING           1372         3kin         B         269         332         1.4e-26         0.19         0.98         KINBSIN-HEAVY CHAIN; MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, ATTARS, P. LOOP, MICKOTIBD LE BINDING           1372         3kin         B         269         KINBSIN-HEAVY CHAIN; MOTOR PROTEIN, MOTOR PROTEIN, CHAINS, A.B. C.D.         CYTOSKELETON           1373         1i44         A         1.8e-12         0.19         0.98         KINBSIN-HEAVY CHAIN; MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, CHAINS, B.C.D.           1373         1i44         A         1.8e-12         0.19         0.98         KINBSIN-HEAVY CHAIN; MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEIN, MOTOR PROTEI					<del></del>		T		<del></del>
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation		CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P- LOOP, MICROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   Score   Score   Score   Score   Skir   A   A   338   5.1e-74   0.50   1.00	Coumpound		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
PDB   CHAI   STAR   END   Psi Blast   Verify	SEQFOL	D score							
PDB         CHAI         STAR         END         Psi Blast           3kar         7         338         5.1e-74         (           3kin         B         269         352         1.4e-26         6           3kin         B         269         384         3.2e-26         6           1a4y         A         123         448         4.8e-12           1a4y         A         134         545         4.8e-09           1a4y         A         45         361         9.6e-14           1a4y         A         63         230         1e-19	PMF	score	1.00	0.99	86.0	0.04	-0.05	0.00	0.37
PDB         CHAI         STAR         END           3kar         7         338           3kin         B         269         352           3kin         B         269         384           1a4y         A         123         448           1a4y         A         134         545           1a4y         A         134         545           1a4y         A         45         361           1a4y         A         63         230           1a4y         A         63         230	Verify	score	0.50	0.19	-0.10	0.19	0.26	0.10	0.29
PDB         CHAI         STAR           3kar         7           3kin         B         269           3kin         B         269           1a4y         A         123           1a4y         A         134           1a4y         A         45           1a4y         A         45           1a4y         A         63           1a4y         A         63	Psi Blast		5.16-74	1.4e-26	3.2e-26	4.8e-12	4.8e-09	9.6e-14	16-19
3kin B 3kin B 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a4y A 1a	END	¥¥	338	352	384	448	545	361	230
3kin 3kin 1a4y 1a4y 1a4y 1a4y	STAR	TAA	7	569	269	123	134	45	63
	CHAI	NID		æ	В	⋖	A	A	A
SEQ NO: 1372 1372 1373 1373 1373 1373	PDB	A	3kar	3kin	3kin	la4y	la4y	la4y	1a4y
	SEO	ΑŞ	1372	1372	1372	1373	1373	1373	1373

	$\neg$	Т		т	_	<del></del>																		
PDB annotation	3 REPEATS	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX	SNRNP.RIBONICI.FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONIJCL EOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONI (CI BORD OTER)	COMPLEY OF THE BAD	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONU/CLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONIICI EODBOTEINI	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING	HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN
Coumpound		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B. D:		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B";	Cream: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A; CHAIN: A, C; U2 B";	CHAIN: B, D;	U2 RNA HAIRPIN IV: CHAIN: O	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	110 BMA HAIRING CHI	D. 172 A': CHAIN: Q, I'S TIS A':	CHAIN: P. D.	C. C. C. C. C. C. C. C. C. C. C. C. C. C	HEMOLIN; CHAIN: A, B;	-		HEMOLIN; CHAIN: A, B;			IIIIN; CHAIN: NOLL;
SEQFOL D score																								
PMF score		0.42		0.17	27.0	0.00		0.53			0.04			0.55	}			0.77			C7:0		0.07	
Verify score		0.66		0.43	0.55	66.0		0.48			0.24			0.66	)			0.33		120			-0.04	
Psi Blast	0.	5.1e-19		3.46-22	3 de-10	0.101.0		3.4e-18			1.4e-22			3.4e-19	_			6.8e-14		1 70 10			3.4e-07	
END	170	70 <del>7</del>	3	077	23.1			264			220			231				387		427	ì		506	
STAR T AA	114	<del>+</del>	77	8	6	) )		114			ჯ -			8				<b>567</b>	-	205	}		421	
CHAI N ID	<b>A</b>	¢		¢	A			ر			۔۔۔			၁				₹	···	\  _				
PDB	1900		1001	14211	la9n		_	layn 		十	ומאו -			1a9n			11:11			1bih	_		Ibpv	
SEQ NO:	1373		1373		1373		1273	5/51		1277	C/CT			1373			1372			1373			1373	

PDB annotation	TIO IT MINISTERNATION TO THE	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMENTATION, GROWTH	FACTOR RECEPTOR	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL A DIRECTON I ELICINE PICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL	ADRESION ETICINE DICE	REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,
Coumpound		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;		FIBROBLAST GROWTH FACTOR 2: CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	i j	INTERNALIN B; CHAIN: A;	THE STATE OF THE STATE OF	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;		NTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT;
SEQFOL	D score								•									
PMF	score	-0.05	0.19	1.00		0.57				0.05		-0.15	0.57		-0.19		0.30	0.23
Verify	score	0.01	0.31	0.65		0.29				0.02		0.09	0.13		0.05		0.31	-0.43
Psi Blast		8.5e-15	3.4e-12	8.5e-14		1.2e-14				6.4e-26		8e-24	1.4e-22		1.6e-14		8e-22	60-e9.6
END	AA	388	409	389		383				310		332	211		547		265	95
STAR	TAA	286	295	306		296		.,		152		176	37		423		79	32
CHAI	N II	A	A	ပ		D				A		Ą	A		A		⋖	∢
PDB	A	1cs6	1cs6	lcvs		1cvs				1d0b		140b	1d0b	•	140b		1d0b	Idce
SEO	A Ö	1373	1373	1373		1373				1373		1373	1373		1373		1373	1373

	<del></del>		<del></del>			
2.0 A 2 RESOLUTION, N. FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, IBTA-BETA-ALPHA CYLINDER, DYNEIN, 2	GROWTH FACTOR/GROWTH GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELCNGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B TREEST	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I. SET 2 SUBGROUP WITHIN IG-LIKE	LIGASE CYCLIN ACDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BUX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2	LIGASE CYCLIN A/CDK2-
CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B. D:	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B. D:	OUTER ARM DYNEIN; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: A, C; SKP1;
		·				
	0.15	0.28	-0.08	0.13	0.54	0.31
	-0.03	-0.41	0.13	0.22	0.26	0.03
	8e-08	1.6e-10	5.1e-14	6.8e-16	1.7e-13	3.4e-18
,	171	186	383	387	231	231
	37	95	292	296	64	53
	Ą	¥	ក	Ů	A	A
	Idce	1ds9		lev2	1fqv	1fs2
	1373	1373	1373	1373	1373	1373
	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D.	1dce   A   37   171   8e-08   -0.03   0.15   RAB   GERANYLGERANYLTRANSFE   RASE BETA SUBUNIT; CHAIN: B, D; RAB   GERANYLGERANYLTRANSFE   RASE BETA SUBUNIT; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	1 dce         A         37         171         8e-08         -0.03         0.15         RAB GERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;           1 dce         A         37         171         8e-08         -0.03         0.15         RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: CHAIN: CHAIN: B, D;           1 dcs         A         56         186         1.6e-10         -0.41         0.28         OUTER ARM DYNEIN; CHAIN: A;	1dce	1dee   A   37   171   8e-08   -0.03   0.15   GERANYLGERANYLTRANSFE	1dee   A   37   171   8e-08   -0.03   0.15   RAB   GRANYLGERANYLTRANSFE

PDB annotation	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE		MUSCLE PROTEIN CONNECTIN, NEXTMS; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN			CELL ADHESION PROTEIN VCAM- D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN
Coumpound	CHAIN: B, D;	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) IHNF 3	TITIN; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1 SCHPO;
SEQFOL D score						,		
PMF		0.27	0.31	0.76	0.40	0.16	0.00	-0.14
Verify		0.39	0.56	0.60	-0.29	0.46	0.37	0.04
Psi Blast		1.7e-08	6.8e-19	1.7e-16	3.4e-07	1.7e-11	3.4e-12	1.1e-09
END		405	383	383	502	394	411	362
STAR T AA		303	292	305	424	297	280	132
CHAI						A	₹.	A
PDB ID		1hnf	Inct	1thm	1ttf	1vca	1wio	lyrg
SEQ ID	NO:	1373	1373	1373	1373	1373	1373	1373

Secret   Description   Secret   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Descriptio							
2 PDB CHAI STAR END Fi Blast Verify FWF SEQFOL Score B N ID T AA AA SCORE SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCORE B SCOR	PDF annotation	FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	MERCHEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACITYLATION, I FIICNE-BICH PEDEATE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, I FIICHE PICH PEDEATE	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, MATINGORY RECEPTOR,	CELL ADHESION PROTEIN NCAM MODULE 2: CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 ISINDING, CELL	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL BLOTTEN
2 PDB CHAI STAR END Psi Blast Verify PMF score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score s	Coumpound	CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	ALPHA SPECTRIN; CHAIN: A, B, C;
2 PDB CHAI STAR END Psi Blast Verify score  1 LAA AA AA Score  2 bnh 45 359 1.4e-18 0.04 0  2 bnh 47 231 1.7e-23 0.13 0  2 dli A 294 396 3.4e-11 0.20 -6  3 ncm A 296 383 3.4e-17 0.92 0  1 cun A 65 293 0.0017	SEQFOL D score						61.31
2 PDB CHAI STAR END Psi Blast ID NID TAA AA AA AA AA AA AA AA AA AA AA AA AA	PMF score		0.03	0.06	-0.05	0.35	
2 PDB CHAI STAR END Psi Blast 1 ID NID TAA AA 3 25bnh 45 359 1.4e-18 2 2bnh 47 231 1.7e-23 3 3 3 3 3 4e-11 3 3 ncm A 296 383 3.4e-17 1 cun A 65 293 0.0017	Verify		0.04	0.13	0.20	0.92	
2 PDB CHAI STAR  1 DB N ID TAA  2 2bnh 45  2 2dli A 294  3 3ncm A 296  3 1cun A 65  2 1cun A 65  2 2 2	Psi Blast		1.4e-18	1.7e-23			0.0017
PDB CHAI  ID NID  S 2bnh  2dli A 2  3ncm A 2	END		359	231	396	383	293
PDB  LDB  LDB  LDB  Sancm  A  Coun A	STAR T AA		45	47	294	296	65
PDB  LD  LD  LD  S  Sbnh  S  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  Sold  S	CHAI N ID				∢	4	4
SEQ ID NO: 1373 1373 1373 1374	PDB ID		2bnh	2bnh	2dli	Зпсш	lcun
	SEQ ID NO:		1373	1373	1373	1373	1374

PDB annotation	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIFLE- HELIX COILED COIL, CONTRACTILE PROTEIN	IKANSCKIP IION KEGOLA IION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P. LOOP, MICROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR
Coumpound	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MEROZOITE SURFACE PROTEIN 1; CHAIN: A;
SEQFOL D score		66.44	65.31			65.43			68.48	
PMF score	0.66			0.12	0.81		0.60	0.86		0.03
Verify	-0.46			-0.55	-0.41		-0.52	-0.15		-0.02
Psi Blast	5.1e-34	3.4e-05	0.0017	5.1e-15	1.7e-27	1.7e-27	1e-30	6.8e-25	6.8e-25	5.1e-19
END	131	295	318	42	141	154	127	142	176	405
STAR T AA	1	53	36	1	55	55	-	59	59	323
CHAI	∢	A		A	В	В		В	В	A
PDB	1cz7	lquu	lsig	2kin	2kin	2kin	3kar	3kin	3kin	Icej
SEQ	NO: 1374	1374	1374	1374	1374	1374	1374	1374	1374	1376

	1.																					
PD/8 annotation	PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR	BLOOD-STAGIS EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN.	MALARIA VACCINE COMPONENT, SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE	BLOOD-STAGE EGF-LIKE DOMAIN	EXTRACELLULAR, MODULAR	PROTEIN, SURFACE 2 ANTIGEN,	SURFACE PROJEIN	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1. MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR	MAI ABIA WACCINE COMESSIES	SURFACE PROTEIN	APOPTOSIS TRAIL; DR5; LIGAND.	RECEPTOR COMPLEX, TRIMERIC	SI DEPERANTI V ADOPTOSIS	MEMBRANE PROTEIN NMR	THROMBIN, EGF MODULE,	ANTICOAGULANT,	GLYCOSYLATION	MEMBRANE PROTEIN NMR, THROMBIN EGE MODILLE
Coumpound		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;			MEROZOITE SURFACE	TO THE THE PARTY OF		٠		MEROZOITE SURFACE PROTEIN I; CHAIN: A;					TNF-RELATED APOPTOSIS	INDOCING LIGAND; CHAIN; B; DEATH RECEPTOR 5: CHAIN:	A:	THROMBOMODULIN; CHAIN:	A;			1 HKOMBOMODULIN; CHAIN: A;
SEQFOL D score																						
PMF score		0.41			-0.14					0.53					-0.13			0.78	<del>-</del>		31.0	0.13
Verify score		-0.11			80.0	•				0.09					0.30			0.76			030	
Psi Blast		6.8e-17			5.1e-09					5.1e-21				1	1.46-08			5.1e-14			5 18-18	
END		435			481	_				871				5	- 55/			252			406	3
STAR T AA		364			403					<del>.</del> C				100	100			181			321	
CHAI N ID		∢			∢					<								Α			A	
PDB ID		Jej							1	<u> </u>				194:			+	1dqb			1dqb	$\dashv$
SEQ ID NO:		1376		1276	0/51				1376	0/01				1376	2		, i	13/6			1376	

PDB annotation	ANTICOAGULANT, GLYCOSYLATION	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX,	ECOAGULATION FACTOR BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN NHIBITOR COMPLEX,
Coumpound		THROMBOMODULIN; CHAIN: A;	THROMBOMODULIN; CHAIN: A;	FACTOR IX; CHAIN: B, C;	BLOOD COAGULATION FACTOR VII; CHAIN: A;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION
SEQFOL D score									
PMF score		0.00	0.21	0.23	0.04	0.23	0.42	0.25	0.94
Verify score		-0.07	0.25	-0.14	60.0	99:0	0.27	-0.13	0.08
Psi Blast		5.1e-10	5.1e-18	3.4e-07	5.1e-07	1.2e-12	3.46-20	1.7e-17	1.4e-15
END		485	131	433	433	254	335	374	445
STAR T AA		400	44	403	403	216	284	327	407
CHAI N ID		A	A	<b>B</b>	A	ı	H	H	L
PDB ID		ldqb	1dqb	1edm	1f7e	1fjs	1fjs	1fjs	1fjs
SEQ ID	SOS.	1376	1376	1376	1376	1376	1376	1376	1376

PDI annotation	COAGULATION COFACTOR, PROTEASE	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE					COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX COAGULATION, 2 COMPLEX	COMPLEX (PROTEASE/INHIBITOR)  RTAP; GLYCOPROTEN, SERINE  PROTEASE, PLASMA, BLOOD  COAGULATION, 2 COMPLEX  COAGULATION, 2 COMPLEX	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX	GLYCOPROTEIN GLYCOPROTEIN
Coumpound	FACTOR XA; CHAIN: L;	COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	COAGULATION FACTOR BLOOD COAGULATION FACTOR XA 1HCG 3	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	LAMINI; CHAIN: NULL:
SEQFOL D score										
PMF score		0.59	0.46	0.33	0.89	0.95	0.31	0.82	0.34	-0.11
Verify score		0.83	0.50	0.34	0.45	0.45	0.01	-0.06	99.0	0.47
Psi Blast		1.7e-12	3.4e-12	1.2e-18	8.5e-15	5.1e-12	3.4e-18	6.8e-15	5.1e-12	6.8e-14 (
END		06	254	334	445	06	374	445	06	322
STAR T AA		49	217	286	407	49	327	407	49	135
CHAI N ID		Ţ	В	B	В	В	T	L	н —————	
PDB ID		lfjs	Ihcg	lhcg	lhcg		1kig	lkig	1kig	1klo
SEQ ID NO:		1376	1376	1376	1376	1376	1376	1376	1376	1376

PDB annotation	Mato adopt to Interograph	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-	GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE
Coumpound	A 22 22 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;		FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;
SEQFOL	D score								
PMF	score	-0.18	0.00	0.01	0.23		0.89	0.37	0.72
Verify	score	0.16	0.38	0.04	0.02		0.21	0.28	0.18
Psi Blast		1.7e-20	8.5e-10	1.7e-14	3.4e-27		8.5e-26	1.4e-22	8.5e-16
END	AA	433	787	254	427		152	226	252
STAR	T AA	286	626	121	289		41	131	177
CHAI	N ID			Н	i i		ы	٦	l l
PDB	<u> </u>	1klo	1Klo	1pfx	1pfx		1pfx	1qfk	1qfk
SEQ	A Š	1376	1376	1376	1376		1376	1376	1376

PDI3 annotation	PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGILATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE			
Coumpound	COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;
SEQFOL D score						
PMF score		0.22	0.29	0.99	0.92	0.52
Verify score		-0.11	-0.01	0.22	0.12	-0.29
Psi Blast		3.4e-26	1.5e-21	le-18	1.7e-24	6.8e-23
END		389	419	445	141	189
STAR T AA		286	326	367	48	68
CHAI N ID		ı	J	J	$\Gamma$	ı
PDB ID		1qfk	1qfk	1qfk	lqfk	1qfk
SEQ B B S		1376	1376	1376	1376	1376

PDB annotation	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION	COAGULATION FACTOR SEKINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERVINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
Coumpound	HUMAN BETA2. GLYCOPROTEIN I; CHAIN: A;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	ASFP; CHAIN: NULL;	MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B
SEQFOL D score							
PMF	-0.18	0.35	-0.01	0.94	-0.15	0.48	0.65
Verify score	0.02	0.24	0.29	0.13	0.67	0.64	0.37
Psi Blast	1.7e-46	1e-13	3.4e-19	3.4e-11	8.5e-12	3.4e-21	3.4e-22
END	444	228	339	445	102	918	922
STAR T AA	41	175	285	407	49	805	608
CHAI N ID	∢	В	æ	В	В		Ф
PDB	1qub	lrfh	1rfn	1rfn	Irfn	lsfp	1spp
SEQ D	1376	1376	1376	1376	1376	1376	1376

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PDI: annotation	PLASMINOGEN ACTIVATION	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, HPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, FPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERNE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	KINASE KINASE, SIGNAL TRANSDICTION	CALCIUM/CALMODULIN KINASE KINASE, SIGNAL TRANSDICTION
Coumpound	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	MODULIN- ROTEIN KINASE:	
SEQFOL D score								109.19
PMF score	0.04	0.59	0.43	0.69	0.40	0.55	0.71	
Verify score	0.05	0.09 ,	-0.01	0.25	0.28	0.01	-0.04	
Psi Blast	1.5e-21	1.7e-15	1.7e-15	5.1e-20	3.4e-19	3.4e-22	5.1e-62	5.1e-62
END	158	230	254	380	444	145	530	534
STAR T AA	89	131	182	286	367	48	205	236
CHAI N ID		니	1	J	1	1		
PDB	Itpg	Ixka	1xka	lxka	Ixka	1xka	1a06	1a06
SEQ ES	1376	1376	1376	1376	1376	1376	1381	1381

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PDB annotation	CALCIUM/CALMODULIN	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	PHOSPHOTRANSFERASE		
Coumpound	CHAIN: NULL;	PROTEIN KINASE CK2/ALPHA- SUBUNIT; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CASEIN KINASE-1; 1CSN 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3
SEQFOL D score		84.57		92.79			154.37	
PMF score		,	1.00		1.00	0.74		1.00
Verify score			0.21		0.40	90.0		0.41
Psi Blast		6.8e-40	5.1e-41	1.2e-46	1.2e-46	6.8e-48	3.4e-71	3.4e-71
END		550	485	495	485	469	524	498
STAR T AA		194	204	198	199	203	169	196
CHAI N ID			∢	Α .	A		m m	ъ
PDB		1a60	1bi8	1blx	16k	1csn	1ctp	1ctp
SEQ ID	ÖZ	1381	1381	1381	1381	1381	1381	1381

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PDB annotation		PROTEIN KINASE CDK2; TRANSFERASE,	SERINE/THREONINE PROTEIN	KINASE, ATP-BINDING, 2 CELL	CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	PROTEIN KINASSE CDK2;	TRANSFERASE,	SERINE/THREONINE PROTEIN	MINASE, AIF-BINDING, 2 CELL	CICLE, CELL DIVISION, MILIOSIS, PHOSPHORYLATION	SERINE/THREONINE-PROTEIN	KINASE CSBP, RK, P38; PROTEIN	SER/THR-KINASE,	SERINE/THREONINE-PROTEIN	KINASE	SERINE/THREONINE-PROTEIN	KINASE CSBP, RK, P38; PROTEIN	SER/THR-KINASE,	SERINE/THREONINE-PROTEIN	MINASE TRANSFER ASE MINS	TRANSFERANCE JINKS;	I KANSFEKASE, JNK3 MAP KINASE,	SEKINE/I HKEOMINE PROTEIN 2 KINASE	TRANSFERASE JNK3:	TRANSFERASE, INK3 MAP KINASE.	SERINE/THREONINE PROTEIN 2	KINASE	KINASE KINASE, TWITCHIN,	INTRASTERIC RIGULATION	KINASE KINASE, TWITCHIN,
Coumpound	(CATALYTIC SUBUNIT) 1CTP 4	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;				HUMAN CYCLIN-DEPENDENT	KINASE 2; CHAIN: NULL;				P38 MAP KINASE; CHAIN:	NULL;				P38 MAP KINASE; CHAIN:	NOLL;			C.II IN N. TERMINAL VINASE.	CHAIN: MI I .	Citativi Mobe,		C-JUN N-TERMINAL KINASE;	CHAIN: NULL;			TWITCHIN; CHAIN: A, B;		TWITCHIN; CHAIN: A, B;
SEQFOL D score		-				115.78					92.87									112 39	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\							127.80		
PMF		1.00													000	0.88								1.00						1.00
Verify score		0.39														10.0								0.21					25 0	U.32
Psi Blast		1.7e-53				1.7e-53		•	•		3.4e-40				7 77	3.46-40				1.7e-46				1.7e-46				1.7e-68	T	1./5-00
END		495				499					555				175	<del>,</del>				577				512				0/0	402	122
STAR T AA		202				202					183				202	507				185	*****			203			00.	2	205	777 1
CHAI N ID																			-									<		1
PDB ID		Ihcl				1hcl					lian				lian	1				1jnk				ljnk —			1604	T YOU	1koh	7
SEQ ID NO:		1381				1381					1381				1381					1381				1381	-		1201	1001	1381	

PDB annotation	INTRASTERIC REGULATION	IKANSFEKASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T- CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL	PEPTIDE/RECEPTOR	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-	CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2	HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
Coumpound	1	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D: T CF11 RECEPTOR	BETA; CHAIN: E;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE: CHAIN: C; T	CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR PETA: CHAIN: E.	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA:
SEQFOL D score			98.67			128.38				143.49
PMF score		1.00		1.00				1.00		
Verify score		0.54		0.39				0.48		
Psi Blast		8.5e-53	8.5e-53	9.6e-54		9.6e-54		3.2e-66		3.2e-66
END		498	562	210		210		210		210
STAR T AA		198	213	52		52		52		52
CHAI N ID				ធ		<u>ш</u>	·	ш		ជា
PDB		3erk	3erk	lao7		lao7		1bd2		1bd2
SEQ	S.	1381	1381	1384		1384		1384		1384

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PDB annotation		RECEPTOR T CELL RECEPTOR IBEC	RECEPTOR T CHILL RECEPTOR 1BEC	IMMUNE SYSTEM HLA-DRI, DRA; HLA-DRI, DRBI 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, BETTOPE MAPPING, LEUCINE-RICH	S KEFEA IS COMPLEX (NUCL)EAR
Coumpound	CHAIN: D; T CELL RECEPTOR BETA: CHAIN: E:	14.3.D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN:	NOLL, IBEC 6 14.3.D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NIII 1 IBEC 6	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T- CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q,
SEQFOL D score		130.56				131.76		
PMF score			1.00	1.00	1.00		-0.11	-0.01
Verify score			0.49	0.25	0.43		0.04	0.43
Psi Blast		6.4e-66	6.4e-66		9.6e-64	9.6e-64	3.2e-17	3.4e-21
END		210	210	210	210	210	309	156
STAR T AA		52	53	33	ر م	51	21	26
CHAI N ID				ш	g	д	4	A
PDB ID		1bec	1 pec			1tcr	la4y	la9n /
SEQ ID NO:		1384	1384	1384	1384	1384	1388	1388

PDB annotation	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	SNRNP.RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION NEURAL CELL	ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Coumpound	D. 112 A. CHAIN: A C. 112 B".	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B";	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	112 RNA HAIRPIN IV: CHAIN: O.	R: U2 A': CHAIN: A. C: U2 B";	CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q,	R: U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q,	R: U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;		AXONIN-1: CHAIN: A:		INTERNALIN B; CHAIN: A;			INTERNALIN B; CHAIN: A;
SEQFOL D score	21025															_												-		
PMF	a loas		010	}		0.65	}		0 51	5			800-	}			0.06	}			0.89				0.07	<u>.</u>	0.77			0.89
Verify	score		0.28	27:0		0.48	2		0.51	17.0			0.41	:			0.42	1			19.0	;			0.15	2:5	0.50			0.27
Psi Blast			4 00 06	4:00-00-		1 50-20	27-20-1		17.05	1.35-03			1 20-21	17_07.1			4 80.06	20-20:+			6 86-20				0.00034	+50007	6 48-27	i !		1.4e-12
END	AA		166	C		121	171		,3,	991			156	2			155	5			121	1			000	700	104	<u> </u>		128
STAR	TAA		ļ	40		,	t			7.4			70	97			7/2	<del></del>				<b>-</b>			1	`_	10	2		4
CHAI	A IS		-	∢		-	∢ .		_	ပ_				ر				ر			ر	رر				∢	<	ζ		A
PDB	A			layn	•		layn			la9n			,	Iayn				layn			1001	14211			,	1080	1901	100		1406
SEQ	ΑÖ		0.00	1388		900,	1388			1388			900,	1388				1388			1200	1300				1388	1700	1300		1388

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
										ADHESION
1388	1405	⋖		216	1.4e-25	0.28	0.43		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
1200			-							ADHESION
1388	1906	<b>K</b>	87	236	3.2e-25	-0.05	0.04		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH
										REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1dce	۷_	21	127	3.2e-11	0.27	0.00		RAB	TRANSFERASE CRYSTAL
						,			GERANYLGERANYLTRANSFE	STRUCTURE, RAB
									RASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFERASE.
									CHAIN: A, C; RAB	2.0 A 2 RESOLUTION, N.
									GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA
									KASE BETA SUBUNIT; CHAIN: R D:	SUBUNIT, BETA SUBUNIT
1388	1dce	A	46	170	1 6-12	0.50	900		DAB	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
				)	2	<u> </u>	2		GERANYLGERANYLTRANSFE	IKANSFERASE CRYSTAL STRUCTURE, RAB
									RASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFERASE
									CHAIN: A, C; RAB	2.0 A 2 RESOLUTION, N-
								•	GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA
									RASE BETA SUBUNIT; CHAIN:	SUBUNIT, BETA SUBUNIT
1388	1ds9	4	103	236	6.4e-13	80.0	-0.02		OUTER ARM DYNEIN: CHAIN:	CONTRACTILE PROTEIN I ETICINE
									A;	RICH REPEAT BETA-BETA-AI PHA
								-		CYLINDER, DYNEIN, 2
1200	1.51		,							CHLAMYDOMONAS, FLAGELLA
1388	1101	∢	4]	103	3.2e-06	-0.05	0.40		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);
									FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP, RBD
										OR RRM) AND LEUCINE-RICH-
1388	1601	4	08	171	4 80 07	200	,		1 10 11 11 11 11 11 11 11 11 11 11 11 11	KEPEA1 2 (LKK)
		:	3	:	4.05-07	00.0-	0.10	<u> </u>	NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);
									FACTOR I; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP, RBD
										OK KKM) AND LEUCINE-RICH- REPEAT 2 (1 RR)
1388	Itol	В	41	103	3.2e-06	0.26	0.04		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1):

PDB annotation	PERSONAL CORPORATION (BND PRD	RIBONOCLEOTRO LEIN (ANY PAGE) OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2-	ASSOCIATED PROTEIN P45; CYCLIN	A/CDK2-ASSOCIATED PROTEIN P19;	SKP1, SKP2, F-BOX, LKK, LEUCINE-	KICH KEFEA1, SCF, OBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED PROTEIN P45; CYCLIN	A/CDK2-ASSOCIATED PROTEIN P19;	SKP1, SKP2, F-BOX, LRR, LEUCINE-	RICH REPEAT, SCF, UBIQUITIN, 2	E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED PROTEIN P45; CYCLIN	A/CDK2-ASSOCIATED PROTEIN P19;	SKP1, SKP2, F-BOX, LRR, LEUCINE-	RICH REPEAT, SCF, UBIQUITIN, 2	E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN A/CDK2-	ASSOCIATED P19; SKP1, SKP2, F-	BOX, LRRS, LEUCINE-RICH	REPEATS, SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN A/CDK2-	ASSOCIATED P19; SKP1, SKP2, F-	BOX, LRRS, LEUCINE-RICH	REPEATS, SCF, 2 UBIQUITIN, E3,	UBIQUITIN PROTEIN LIGASE	ACEL TEATION KNASE INTIBILOR,
Coumpound		FACTOR I; CHAIN: A, B;	SKP2: CHAIN: A. C. E. G. I. K. M.	O; SKP1; CHAIN: B, D, F, H, J, L,	N, P;			SKP2: CHAIN: A. C. E. G. I. K. M.	O; SKP1; CHAIN: B, D, F, H, J, L,	ijŽ				SKP2; CHAIN: A, C, E, G, I, K, M,	O; SKP1; CHAIN: B, D, F, H, J, L,	Z, P;				SKP2: CHAIN: A. C; SKP1;	CHAIN: B, D;					SKP2: CHAIN; A. C; SKP1;	CHAIN: B, D;				4 (14)	RIBONUCLEASE INHIBITOR;
SEQFOL	D score																					المنسوب ف										
PMF	score		800					0 10	2					-0.15						000	3					0 03	3					-0.12
Verify	score		000	67.0				21.0	71.0					0.08						0.01	17.0					700	5					0.07
Psi Blast	•		1 42 00	1.46-03				16.14	1.00.1					4 8e-11	20:1					2 40.12	21-04-0					1 60-14	1.00.1					1.7e-19
END	¥¥		;	2/1				;;	617					208	2					120	170					213	C17					131
STAR	TAA			<b>-</b>				8	2					3	1					=	<u>-</u>					5	9				•	5
CHAI	e E			∢				,	\ لا					<	ζ						∢.						≮					
PDB	A		1	Itqv				,	Ifgv					1 6000	Ahrr l					0,	1182					,	1137					2bnh
SEQ	ВŞ			1388					1388					1700	1366						1388					000	1388					1388

PDB annotation	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, I ELICINE-RICH REPEATS	ACETYLATION RIASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		GLYCOPROTEIN GLYCOPROTEIN	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCHIM BENERIC	CALMODULING PROTEIN CALMODULING CALMODULING CALMODULING CERUM TRIC- DOMAIN, RESIDUES 1 - 75; CERUM- LOADED, CALCIUM-BINDING				STRUCTURAL PROTEIN HELIX-	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
Coumpound	CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;		LAMININ; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT BECTERN VILLS	CALCUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICIL 3	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICIL 3	CARDIAC TROPONIN C; CHAIN: A:	CALMODULIN; CHAIN: A;
SEQFOL D score								53.74			
PMF score		-0.15		-0.20	0.01	0.48	0.16		0.11	0.12	0.23
Verify score		0.06		0.05	-0.36	0.21	-0.32		-0.37	-0.54	-0.22
Psi Blast		3.2e-20	,	1.6e-13	3.2e-23	3.2e-22	4.8e-33	3.2e-38	3.2e-38	1.6e-21	1.6e-35
END		439	,	643	114	61	117	132	117	117	117
STAR T AA		74	į	476	10	2	2	1	2	10	2
CHAI N ID							A			A	A
PDB ID		2bnh		IKIO	laj4	1ak8	lcdm	Icil	lcll	1dtl	lexr
SEQ NO:		1388	2000	1369	1392	1392	1392	1392	1392	1392	1392

				- 1		l l	ı	1
CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)		TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2
TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;
56.30			51.47		51.68			
	0.11	0.33		0.36		0.27		1.00
	-0.35	-0.32		-0.03		-0.42		1.07
3.26-28	3.26-28	8e-24	4.8e-28	4.8e-28	1.46-37	1.4e-37		1.7e-24
139	=======================================	Ξ	141	111	135	117		1000
_	2	2	-	2		2		934
	í				A	∢		∢
Itef	ltof	1tnx	Itop	Itop	lvrk	1vrk		1b0x
1392	1392	1392	1392	1392	1392	1392		1396
	1tcf 1 139 3.2e-28 56.30 TROPONIN C; CHAIN: NULL;	Itef         1         139         3.2e-28         56.30         TROPONIN C; CHAIN: NULL;           Itef         2         111         3.2e-28         -0.35         0.11         TROPONIN C; CHAIN: NULL;	ltcf         1         139         3.2e-28         56.30         TROPONIN C; CHAIN! NULL;           ltcf         2         111         3.2e-28         -0.35         0.11         TROPONIN C; CHAIN! NULL;           ltmx         2         111         8e-24         -0.32         0.33         TROPONIN C; ITMX 4 CHAIN!           ltmx         2         111         8e-24         -0.32         0.33         TROPONIN C; ITMX 5	Itef         1         139         3.2e-28         56.30         TROPONIN C; CHAIN: NULL;           Itef         2         111         3.2e-28         -0.35         0.11         TROPONIN C; CHAIN: NULL;           Itmx         2         111         8e-24         -0.32         0.33         TROPONIN C; ITNX 4 CHAIN: NULL;           Itmx         2         111         8e-24         -0.32         0.33         NULL; ITNX 5           Itop         1         141         4.8e-28         51.47         PROTEIN TROPONIN C; ITOP 3	Itef   1   139   3.2e-28   56.30   TROPONIN C; CHAIN: NULL;   C   C   C   C   C   C   C   C   C	Hef   1   139   3.2e-28   56.30   TROPOMIN C; CHAIN: NULL;   C   C   C   C   C   C   C   C   C	Ticf   1   139   3.2e-28   56.30   TROPONIN C; CHAIN: NULL;   C   C   C   C   C   C   C   C   C	Tief   1   139   3.2e-28   56.30   Troponin C; CHAIN: NULL; C   C   C   C   C   C   C   C   C   C

	Τ	<del></del>			<del></del>			<del></del>		
PDB annotation	DIMERIZATION DOMAIN, TRANSFERASE	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TO ANSINICATION OF LEGATED	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER (OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE, RECEPTOR,	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAIR OSPORINE TRANSEER ASE	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLA: ITON STATISTICS STATISTICS TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA TO A MICHIGANIA	TRANSFERASE (SK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMANI	CYTOKINE GCSF; G-CSF-R; CLASS1 CYTOKINE HEMATOPOIETIC RECEPTOR, SIGNAL
Coumpound		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	GP130; CHAIN: NULL;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: R.	TITIN; CHAIN: NULL;	C-TERMINAL SRC KINASE; CHAIN: A;	C-TERMINAL SRC KINASE; CHAIN: A;	C-TERMINAL SRC KINASE; CHAIN: A;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A:	GRANULOCYTE COLONY- STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR;
SEQFOL D score						169.44				,
PMF score		1.00	0.46	0.01	0.60		1.00	1.00	1.00	0.07
Verify score		0.92	0.26	-0.06	0.20		0.83	0.64	0.46	0.40
Psi Blast		8.5e-27	7.5e-22	1.5e-25	4.5e-18	3e-93	1.4e-90	3e-93	6e-19	4.5e-35
END		666	537	531	536	668	897	868	531	524
STAR T AA		934	431	328	438	627	628	629	437	328
CHAI N ID		⋖		В		٧	<b>A</b>	ď	Ą	В
PDB ID		164f	15j8	1bp3	1bpv	1byg	1byg	1byg	1c8p	1cd9
SEQ ID NO:		1396	1396	1396	1396	1396	1396	1396	1396	1396

PDB annotation		TRANSDUCTION	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR	CYTOKINE EBP; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA	HELICAL BUNDLE, IENNARY I COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPRINDING, 2 PHOSPHORYLATION.	RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHORYLATION, RECEPTOR, ANSFER A SEPHOSPHOTRA	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION,
Coumpound		CHAIN: B, D;	GRANULOCYTE COLONY. STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	ERYTHROPOIETIN RECEPTOR; CHAIN: A, B;	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;		FGF RECEPTOR 1; CHAIN: A, B;		FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;
SEQFOL	D score						179.56			182.22
PMF	score		0.63	0.28	0.15	-			1.00	
Verify	score		0.32	-0.12	-0.05				0.91	
Psi Blast			6e-19	4.5e-22	4.5e-13		0		0	0
END	ΨΨ		531	531	531		006		895	899
STAR	TAA		454	338	408		219		621	614
CHAI	N II			A	S		4		<b>4</b>	В
PDB	A		1cto	1ern	1f6f		1fgk		1fgk	1fgk
SEO	A Ş	2	1396	1396	1396		1396		1396	1396

PDIs annotation	RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAŞT (ROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO- ONCOGENE, PHOSPHOTYROSINE, PROTO- PHOSPHOTYROSINE, PROTO-		CELL ADHESION PROTEIN RGD, EXTRACELLIL AR MATRIX IENE 18	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571 ACTIVATION I OOP	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX TO ANSTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTER A CENTE	COMPLEX
Coumpound		FGF RECEPTOR 1; CHAIN: A, B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	CELL ADHESION PROTEIN FIBRONECTIN CELL- ADHESION MODULE TYPE III- 10 IFNA 3	FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL: CHAIN: A. B.	NSÚLN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	INSULIN RECEPTOR; CHAIN: A;
SEQFOL D score							188.00	
PMF score		1.00	1.00	0.63	-0.05	1.00		1.00
Verify score		0.87	0.88	0.39	0.08	0.71		0.81
Psi Blast	•	0	0	1.2e-13	3e-26	0	0	0
END AA		<i>\$68</i>	. 606	524	531	897	910	910
STAR T AA		620	615	454	322	623	623	979
CHAI N ID		В				A	¥	Ą
PDB ID		Ifgk	1fmk	lfha	1fnf	1fpu	lir3	lir3
SEQ D NO:		1396	1396	1396	1396	1396	1396	1396

PDB onnotation		(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL	IKANSDUCIION, PHOSPHOTRANSFERASE, 2	COMPLEX (KINASE/PEPTIDE	SUBSTRATE/ATP ANALOG),	ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	CELL ADHESION PROTEIN CELL	EXTRACELLULAR MATRIX, 2	HEPARIN-BINDING,	GLYCOPROTEIN	TRANSFERASE NUK;	TYROSINE KINASE,	TRANSFERASE NUK;	TYROSINE KINASE.	TYROSINE KINASE TYROSINE	KINASE-INHIBITOR COMPLEX,	DOWN-REGULATED KINASE, 2	STRUCTURAL PROTEIN INTEGRIN,	HEMIDESMOSOME, FIBRONECTIN,	CARCINOMA, STRUCTURAL 2	PROTEIN	STRUCTURAL PROTEIN INTEGRIN,	HEMIDESMOSOME, FIBRONECTIN,	CARCINOMA, STRUCTURAL 2	TRANSFERASE ALPHA BETA FOLD	STRUCTURAL PROTEIN TENASCIN,	FIBRONECTIN TYPE-III, HEPARIN,
	Соимроини	PEPTIDE SUBSTRATE; CHAIN: B;	•				FIBRONECTIN; CHAIN: NULL;				TYROSINE-PROTEIN KINASE	NECEL TON EATH, CLEARY, FA,	TYROSINE-PROTEIN KINASE	RECEPTOR EPH; CHAIN: A;	HAEMATOPOETIC CELL	KINASE (HCK); CHAIN: A;		INTEGRIN BETA-4 SUBLINIT:	CHAIN: A. B:			INTEGRIN BETA-4 SUBUNIT;	CHAIN: A, B;		LCK KINASE; CHAIN: A;	TENASCIN; CHAIN: A, B;	
, 040	SEQFOL D score											-112	182.17														
	PMF						0.53				1.00				1	3		0.23	77.0			0.18			1.00	-0.03	
	Verify						80.0				0.58				600	06:0		0 10	V.17			0.03			10.07	0.27	
	Psi Blast						1.3e-25				1.5e-83		1.5e-83		-	>		16.01	1.35-30			6.8e-11	;		c	1.5e-30	
	END						533				202		202		200	706		7.53	134 1			522	!		000	529	
	STAR T AA						331				31		31		610	010		000	676			331	·		691	331	
	CHAI N ID				_						A		A			₹			∢			A	:	, .	<	€ <	:
	PDB CI						1mfn				Inuk		Inuk		3	Idei		,	1985			1003	<u>}</u>		1 gap	14P2	
	SEQ U			_			1396				1396		1396		700,	1396			1396			1306	2		1206	1396	;

		1									,	<del></del>				Ţ
PDE annotation	EXTRACELLUI AR 2 MATRIX, ADHESION, FUSION PROTEIN,	TYROSINE-PROTEIN TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPHOSPHORY ATTOM STEAMAL	TRANSDUCTION, TYROSINE- PROTEIN 3 KINASE		TRANSFERASE KDR; TYROSINE KINASE	on Campaign	FROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2	BINDING PROTEIN BINDING ED-B,	FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	COAGULATION FACTOR		COMPLEX (TWO DNA-BINDING PROTEINS DNA MAT AT BITA	COMPLEX (TWO DNA-BINDING	PROTEINS/DNA), COMPLEX, 2 DNA-	BINDING PROTEIN, DNA, TRANSCRIPTION REGILLATION	COMPLEX (DNA-BINDING PROTEIN/DNA) (3HE 1: COMPLEY
Соптроина		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR 36 STPIICTIBES) 17775	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR	PIRPONECTRI: CHARI: 4	(U.M.) CHORNER,	FIBRONECTIN; CHAIN: A;		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5		MATING-TYPE PROTEIN A-1; CHAIN: A: MATING-TYPE	PROTEIN ALPHA-2; CHAIN: B;	DNA; CHAIN: C;		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;
SEQFOL D score																
PMF		1.00	100	0.25	1.00	-0.14		0.17		-0.18		66.0				0.94
Verify score		1.03	:	61.0	0.88	0.07		0.36		0.22		17:1				0.82
Psi Blast		1.7e-25	10.17	16-17	5.1e-98	3e-09		96-19	-	6e-34	1	co-ao				0.00015
END		995	703	<b>†</b> 70	897	423		529		524	121	121			,	52
STAR T AA		934	440		622	326		439		324	81					§
CHAI N ID				·	₹	A		¥			<b>▼</b>	4				•
EDB ID		lsgg	1110		lvr2	2fnb		2fnb	d c	11U7	1akh				_	Jan',
SEQ ID NO:		1396	1396		1396	1396		1396	1306	0661	1401				1401	-

PDB annotation	MNA-BINDING PROTEIN/DNA).	PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN	GENE REGULATION PBX1; HOMEODOMAIN	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION		COMPLEX (TRANSCRIPTION/HOMEOBOX/DNA ) PHEROMONE RECEPTOR TRANSCRIPTION FACTOR; MATTING-TYPE PROTEIN ALPHA-2; TRANSCRIPTION REGULATION, TRANSCRIPTIONAL REPRESSION, 2 DNA-BINDING PROTEIN, COMPLEX (TRANSCRIPTION/HOMEOBOX/DNA	DNA-BINDING PROTEIN	
Coumpound			HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B;	DNA CHAIN: D', DNA CHAIN: E, INSUL'IN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	HOMEOBOX PROTEIN PBX1; CHAIN: A;	PARED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP 3	MCMI TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F;	OCT-3; 10CP 5 CHAIN: NULL; 10CP 6	DNA BINDING PROTEIN OCT-1 POU HOMEODOMAIN DNA- BINDING PROTEIN MUTANT
SEQFOL D score										
PMF			0.43	0.93	0.03	0.99	0.80	1.00	0.84	0.96
Verify			0.27	0.73	-0.11	0.82	0.50	0.63	0.28	0.41
Psi Blast			0.0006	9-05	0.0003	0.0003	0.00015	0.00015	9e-06	0.0001
END	8		125	125	127	125	125	125	125	125
STAR	- W		83	83	83	83	83	82	83	83
CHAI	A N		В		A	В		. [.] U		
PDB	3		1672	1bw5	1du6	161	1hdp	Imn B	10cp	1 pog
SEQ	a ë		1401	1401	1401	1401	1401	1401	1401	1401

PDB annotation		COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA,	IOTOSOMEKASE 1 ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPI PX MII TI-STIRI PINT	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN- BINDING, PLASMA PROTEIN, HDL, VI DI	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BI:TA, SERUM PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BIJTA, SERUM PROTEIN	SERUM PROTEIN ACRP30 CIQ TNF TRIMER ALL-BITA, SERUM PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2
Coumpound	WITH 1POG 3 ARG GLY SER HIS MET INSERTED AT THE N- TERMINUS AND ASP ILE 1POG 4 INSERTED AT THE C- TERMINUS (INS(RGSHM- R6),INS(166-D1) 1POG 5 (NMR, 13 STRUCTURES) 1POG 6	TOPOISOMERASE I; CHAIN: A; DNA; CHAIN: B, C;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN IA; CHAIN: B:	APOLIPOPROTEIN E; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A. B. C:	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A. B. C.	30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A. B. C.	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score									
PMF		-0.09	0.00	0.19	0.04	0.39	-0.13	0.43	0.29
Verify score		0.03	-0.16	-0.13	-0.12	1.14	0.71	0.84	-0.03
Psi Blast		5.1e-08	0.00017	0.00017	6e-15	le-27	6e-22	4.5e-18	6e-12
END		772	556	634	551	947	947	947	591
STAR T AA		644	389	527	367	826	827	826	375
CHAI N ID		A	В	¥	4	A	м	ن ن	A
PDB ID		1a36	1dn1	1or3	Idun	1c28	1c28	1c28	Icun
SEQ ID NO:		1403	1403	1403	1403	1404	1404	1404	1404

PDB annotation	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR		COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHOR YLATION, RECEPTOR, PHOSPHOTRANSFERASE
Coumpound		ALPHA SPECTRIN; CHAIN: A, B, C;	SSO1 PROTEIN; CHAIN: A;	HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) IHRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IHRE 4	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	FGF RECEPTOR 1; CHAIN: A, B;
SEQFOL D score							
PMF score		0.03	0.19	0.11	0.25	0.12	0.04
Verify score		0.02	-0.08	0.07	0.13	-0.26	-0.02
Psi Blast		4.5e-07	6e-07	0.0045	0.0045	1.4e-09	1.7e-05
END		651	467	150	150	129	126
STAR T AA		436	292	120	120	25	22
CHAI N ID		A	A			æ .	4
PDB ID		Teun	1fio	lhae	lhre	1660	1fgk
SEQ ID	NO:	1404	1404	1404	1404	1407	1407

PDI: annotation	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PROFESSIONE, PRO	TRANSFERASE PISO. C-ABL; KINASE, KINASE INHIBITOR, STI.	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE TO ANGEED A SE	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2	TRANSFERASE AT BHA BETA EOI D	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	LPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING	LIPID-BINDING LIPID-BINDING, SIGNALLING	LIPID-BINDING J.IPID-BINDING, SIGNALLING
Coumpound	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL: CHAIN: A B:	ERKŽ; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	LCK KINASE: CHAIN: A:	EXTRACELLÚLAR REGULATED KINASE 2; CHAIN: NULL;	PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN:	NULL; PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN:	PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN: A B.	PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN:
SEQFOL D score								267.15		271.38
PMF	0.36	0.18	0.37	0.11	0.23	0.09	1.00		1.00	
Verify	0.17	-0.09	-0.12	-0.56	-0.75	-0.35	0.60		0.89	
Psi Blast	3e-05	1.5e-05	7.5e-06	9e-05		1.5e-05	4.5e-70	4.5e-70	3e-68	3e-68
END	127	130	131	129	61	126	168	168	168	168
STAR T AA	77	22	21	22	22	21	2	2	3	3
CHAI N ID		Ą		<b>V</b>	Ą				A	A
PDB ID	lfmk	Ifpu	Ipme	Iqef	1qpc	3erk	1a44	1a44		1beh
SEQ ID NO:	1407	1407	1407	1407	1407	1407	1408	1408	1408	1408

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PDB annotation		HALOPEROXIDASE	BROMOPEROXIDASE L,	HALOPEROXIDASE L; HALOPEROXIDASE.	OXIDOREDUCTASE	HALOPEROXIDASE	HALOPEROXIDASE F; HALOPEROXIDASE,	OXIDOREDUCTASE, PROPIONATE COMPLEX	AMINOPEPTIDASE	AMINOPEPTIDASE, PROLINE	DE OTE A SE 2 X ANTHOMONAS	CAMPESTRIS	AMINOPEPTIDASE	AMINOPEPTIDASE, PROLINE	DOUTE OF 1 X ANTHOMONAS	CAMPESTRIS	HYDROLASE HYDROLASE,	HALOALKANE DEHALOGENASE,	ALPHA/BEIA-HIDROLASE	HYDROLASE HYDROLASE,	HALOALKANE DEHALOGENASE, A1 PHA/BETA-HYDROLASE	HYDROLASE A/B HYDROLASE	FOLD, DEHALOGENASE I-S BOND		HYDROLASE LINB, 1,3,4,6-	CYCLOHEXADIENE :
Coumpound	A, B;	CHLOROPEROXIDASE L;	CHAIN: A, B, C;	•		CHLOROPEROXIDASE F;	CHAIN: NULL;		PROLINE IMINOPEPTIDASE;	CHAIN: A, B;		,	PROLINE IMINOPEPTIDASE;	CHAIN: A, B;			HALOALKANE	DEHALOGENASE; CHAIN:	NULL;	HALOALKANE	DEHALOGENASE; CHAIN:	HAI DAI KANE	DEHALOGENASE; 1-	CHLOROHEXANE CHAIN: A;	HALOALKANE	DEHALOGENASE; CHAIN: A;
SEQFOL D score									60.20								61.14									
PMF score		06.0				0.45							0.42							0.77		000	66.0		0.19	
Verify score		0.25	7.0			0.13							00.0							0.13		000	0.30		-0.16	
Psi Blast		0,00015	C1000.0			9e-08			4 50-05	20-20-			4.5e-05	}			1 50-08			1.5e-08		00	6e-03		3e-05	
END		210	616			319			310	217			319	}			325	77		318			319		154	
STAR T AA		F.	4			47	:		-	- -			47	È			12	<u> </u>		35		,	01		47	
CHAI N ID			<b>4</b>		,				\ \	₹.		_	4	ζ									∢		A	
PDB		8	1288			1988				lazw			10711	Iacw			1160	Bool		166	0		Icqw		lcv2	
SEQ	S.		1410			1410				1410			1710	01+1			17.10	1410		1410	-		1410		1410	i

				***																		•			
PDB annotation	DEHALOGENAISE, LINDANE, BIODEGRADATION, ALPHA/BETA- HYDROI ASF	HYDROLASE HOMODIMER, ALPHA/BETA HYDRO! ASE FOLD	DISUBSTITUTED UREA 2 INHIBITOR	AYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD,	HYPRO! AGE 115 GE	HYDROLASE LIPASE	PSEUDOMONADACEAE, CIS-	PEPTIDE, CLOSED	CONFORMATION, 2 HYDROLASE,	LYASE OXVAITED TELVASE.	OXYNITEH ASE CVANOCEMEN	CYANHYDRIN FORMATION LYASE	HYDROLASE ALPHA BETA	HYDROLASE FOLD, PROLINE,	PROLYL AMINOPEPTIDASE, 2	HVDPOLASE ALBERT BETA	HYDROI ASE EGI D. DPO! DE	PROLYT, AMINOPEPTITA SE 2	SERRATIA, IMINOPEPTIDASE	LIPASE LIPASE; LIPASE,	HYDROLASE,	PSEUDOMONAD ACEAE, COVALENT	INTERMEDIATE, 2 TRIGLYCERIDE	AND THE PROPERTY OF THE AND AND AND AND AND AND AND AND AND AND	ENDOCYTOSIS/EXOCYTOSIS NSECI: PROTEIN-PROTEIN
Coumpound		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDDO! ASE. CITABL	A, B;	I.IPASE GASTRIC: CHAIN: A B.	TRIACYLGLYCEROL	HYDROLASE; CHAIN: D;	TRIACYLGLYCEROL	HYDROLASE; CHAIN: E;	HYDROXYNITRILE LYASE:	CHAIN: A:		PROLYL AMINOPEPTIDASE;	CHAIN: A;		PROLYL AMINOPEPTIDASE.	CHAIN: A:	•		TRIACYL-GLYCEROL-	HYDKOLASE; CHAIN: D, E;				SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A;
SEQFOL D score													57.92								<del>'</del>	<del>-</del>			S
PMF score		86.0	0.95	}	0.41	0.10				0.37			-			0.12				0.05					0.09
Verify		0.12	0.14		-0.15	-0.13				0.02						-0.51				0.06					-0.02
Psi Blast		1.1e-07	3e-07		0.003	90000				60-96		,	1.2e-05			1.2e-05				ye-05	_				0.00045
END AA		321	321		165	195				316		į	321			319			155	551					513
TAA		47	47		47	47				47		=	11			74			17	 ì					384
CHA!		<b>V</b>	В		A	<u> </u>				A			τ.			∀					-			1	<b>n</b>
FDB ID		leki	lek1		1hlg				7	Iqj4		194				loptr –	·		4lin			-		+	
NO B		1410	1410		1410	1410				1410		1410			$\dashv$	1410	-		1410					1415	$\dashv$

PDB annotation	COMPLEX, MULTI-SUBUNIT		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMMITTE (PRICED (DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTFIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGERODNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	ZINC FINGER TRANSCRIPTION	FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: B;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C F G:			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			SP1F3: CHAIN: NULL:		YY1; CHAIN: C; ADENO-
SEQFOL D score							76.20																					
PMF score			0.01		0.95						1.00					0.53					0.06	<u> </u>				0.25	}	0.07
Verify score			0.11		0.05						-0.09	<u>:</u>				-0.01	:				-0.31	· ·				-0 44		-0.01
Psi Blast			0.00015		3e-24		4.5e-25				4.5e-25					6e-23	}				1 2e-21	2				1 28-06	20-27:1	1.4e-24
END			426		485		486				485	3				543	3				575	3				517	<del>}</del>	543
STAR T AA			401		404		403				404	<u> </u>				432	ž		d 1 ;		461	Ē				603	776	408
CHAI N ID			A		Ą		O		-		ر	)			_	ر	)				c	)						C
PDB ID		1	lath		1a1h		1mey				1 mex	, micy				1mor	11115				Imost	liney					ıspı	1ubd
SEQ ID	SO.		1418		1418		1418				1/10	01410				1/10	1410				1410	0141				9,7,7	1418	1418

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PD13 annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELIMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGII ATTOMONA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGILI ATION/DNA	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR. ZINC FINGER NAR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR. 7 ZING FINGER NAME		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTIZIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGIS, COMPI FX (DNA-
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	ADR1; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score							
PMF score		0.03	0.17	0.03	90.0	0.47	0.25
Verify score		-0.42	0.04	-0.41	-0.69	-0.05	-0.16
Psi Blast		16-24	4.5e-14	1.4e-12	1.2e-14		4.5e-33
END AA		575	549	575	577	485	575
STAR T AA		432	461	522	522	369	404
CHAI N ID		၁			A	٧	∢
PDB ID		lubd	2adr	2adr	2drp		2gli
SEQ ID NO:		1418	1418	1418	1418	1418	1418

PDB annotation	BINDING PROTEIN/DNA)	TOO MY TEE SEE SEE	COMPLEX (BLOOD) COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA;	HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM	BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COAGULATION/INHIBITOR)	BLOOD COAGOLATION, SEALINE PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	rkolease/Coraci Grandonico)	SERINE PROTEINASE	COAGULATION FACTOR II;	RETOMODIE IN TM CD141	ANTIGEN; EGR-CMK SERINE	PROTEINASE, EGF-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2	ANTIFIBRINOL YTIC COMPLEX	SERINE PROTEINASE	COAGOLATION FACTOR II;	FETOMODULIN. TM. CD141	ANTIGEN, EGR-CMK SERINE	PROTEINASE, EGF-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2	ANTIFIBRINOLY IIC COMPLEA	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING
Coumpound			ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;				BLOOD COAGULATION FACTOR VIA: CHAIN: L. H:	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE OPFRCMK) WITH CHAIN: C;	THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; THROMBIN	HEAVY CHAIN; CHAIN: M, N,	CHAIN: I K I: THROMBIN	NHIBITOR L-GLY-L-	ARM; CHAIN: E, F, G, H;		THROMBIN LIGHT CHAIN;	CHAIN: A, B, C, D; I HKUMBIN	HEAVI CHAIN; CHAIN, IM, IN,	CHAIN: I. I. K. L. THROMBIN	NHIBITOR L-GLU-L-GLY-L-	ARM; CHAIN: E, F, G, H;		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;
SEQFOL D score							57.15																		
PMF score			0.17								0.24							0.55							-0.11
Verify			0.04								0.14							0.33							0.14
Psi Blast			3e-15				1.5e-15				1e-17							1.1e-13							3e-16
END			259				270				232							264							191
STAR T AA			118				136	···-			136							168							31
CHAI			ı				T					ı						-							A
PDB ID			laut				1dan				1dx5	}						1dx5							1ext
SEQ	Ö		1419				1419				1419	:						1419							1419

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PDE annotation	PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	GI YCOPROTEIN GI VCOPROTEIN	GLYCOPROTFIN GLYCOPROTFIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	SERINE PROTE/SE, CALCIUM-	BINDING, HYDROLASE, 3	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPI FX	INHIBITOR, HEMOPHILIA/EGF.	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR)
Coumpound		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	LAMININ: CHAIN: NIJI.I.:	LAMININ: CHAIN: NULL:	LAMININ; CHAIN; NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;					FACTOR IXA; CHAIN: C, L,; D.	PHE-PRO-ARG; CHAIN: 1;					FACTOR IXA; CHAIN: C, L.; D-	PHE-PRO-ARG; CHAIN: I;						FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score		59.06				78.19												67.49	-						
PMF score			-0.01	-0.01	0.23		-0.09					0.18													0.31
Verify score			0.05	0.54	0.51		0.07					-0.04					•							-	-0.30
Psi Blast		3e-16	9e-22	4.5e-26	4.5e-27	4.5e-27	1.1e-25					6e-21						6e-30				-			6e-30
END AA		243	298	185	247	234	128					298						165							223
STAR T AA		61	125	29	19	77	. 13					205						38							76
CHAI N ID		∢					٦ 					L						ᆸ							ı
PDB ID		lext	1klo	1klo	1klo	1klo	lpfx					1pfx						1pfx							žid.
SEQ ID NO:		1419	1419	1419	1419	1419	1419					1419						1419							1419

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CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	TO THE PROPERTY A CT. DIVITA . DIVITA .	SEKINE FROIDAND FOUR, FOUR, BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA, FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	PLASMINOGEN AC11VA11ON
	HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1PP2 4	COAGULATION FACTOR VILA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	T-PLASMINOGEN ACTIVATOR
					55.31	
	-0.18	0.30	-0.06	86.0		0.53
	0.24	0.11	0.09	-0.17		0.31
	1.5e-19	3e-15	7.5e-15	36-15	3e-15	4.5e-20
	691	216	247	271	179	237
	39	109	145	141	99	156
	R	1	ı			
	1pp2	1qfk	1qfk	1skz	1skz	Itpg
Ö	1419	1419	1419	1419	1419	1419
		Ipp2         R         39         169         1.5e-19         0.24         -0.18         HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2=           (E.C.3.1.1.4) IPP2 4	1pp2 R   39   169   1.5e-19   0.24   -0.18   HYDROLASE CALCIUM-FREE   PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1Pp2 4   COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	1pp2 R   39   169   1.5e-19   0.24   -0.18   HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4) 1Pp2 4   (E.C.3.1.4)	Ipp2   R   39   169   1.50-19   0.24   -0.18   HYDROLASE CALCTUM-PREE PHOSPHOLIP ASE A-2= (E.C.3.1.4) IPP2 4   COAGULATION PACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYI INHBITOR; CAAGULATION PACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYI INHBITOR; CHAIN: H; TRIPEPTIDYI INHBITOR; CHAIN: NULL; Iskz   141   271   30-15   -0.17   0.98   ANTISTASIN; CHAIN: NULL;	19p2 R   39   169   1.5e-19   0.24   -0.18   HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2=   169   1.5e-19   0.24   -0.18   HYDROLASE CALCIUM-FREE   19p2   216   3e-15   0.11   0.30   COAGULATION EACTOR VIIA   (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA   (HEAYY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; COAGULATION FACTOR VIIA   (HEAYY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; COAGULATION FACTOR VIIA   (HEAYY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: CHAIN: NULL;   18k2   66   179   3e-15   55.31   ANTISTASIN; CHAIN: NULL;

T-			T	<del></del>				T	
	PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LPID DEGRADATION PHOSPHOLIPASE A2, LIPID	LIPID DEGRADATION PHOSPHOLPASE A2, LIPID	DEGRADATION, HYDROLASE NEUROTOXIN PHOSPHOLIPASE AZ INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR	EVOLUTION, NEUROTOXIN BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN	OXIDOREDUCTASE CPR, P450R; X-RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE	SYNTHASE, 2 OKIDOREDUCTASE OXIDOREDUCTASE TWO DOMAIN MOTIF, ROSSMANN FOLD
F1-G; ITPG 7 CHAIN: NULL;	T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	T-PLASMINOGEN ACTIVATOR FI-C; ITPG 7 CHAIN: NULL; ITPG:8	PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	CHLOROPLAST FERREDOXIN- NADP+ OXIDOREDUCTASE; CHAIN: A. B:
	0.18	-0.01	-0.19	-0.19	-0.18	0.37	0.30	0.01	0.21
	-0.31	0.14	0.02	0.04	0.07	0.17	5.23	0.16	-0.13
	4.5e-15	7.5e-19	9e-16	7.5e-16	3e-19	9e-14	1.5e-24	6.8e-40	5.1e-57
	297	109	273	236	204	222	142	539	538
	220	29	145	81	81	145	13	272	252
			A	∢			A	A	4
	Itpg	Itpg	Ivap	lvap	Ivpi	lxka	9wga	lamo	1fb3
	1419	1419	1419	1419	1419	1419	1419	1421	1421
		1tpg         220         297         4.5e-15         -0.31         0.18         T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN: NULL; 1TPG 8	1tpg         220         297         4.5e-15         -0.31         0.18         FI-G; 1TPG 7 CHAIN: NULL;           1tpg         29         109         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR           1tpg         29         109         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR           1tpg         29         109         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR           1tpg         30         100         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR           1tpg         30         100         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR           1tpg         30         100         7.5e-19         0.14         -0.01         100	Itpg         220         297         4.5e-15         -0.31         0.18         F1-G; ITPG 7 CHAIN; NULL;           Itpg         29         109         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN; NULL;           Ivap         A         145         273         9e-16         0.02         -0.19         PHOSPHOLIPASE A2; CHAIN; A, B;	1tpg         220         297         4.5e-15         -0.31         0.18         F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8           1tpg         29         109         7.5e-19         0.14         -0.01         T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8           1vap         A         145         273         9e-16         0.02         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B; A, B; A, B;           1vap         A         81         236         7.5e-16         0.04         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B; A, B;	14pg         220         297         4.5e-15         -0.31         0.18         F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8           14pg         29         109         7.5e-19         0.14         -0.01         F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8           1vap         A         145         273         9e-16         0.02         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B;           1vap         A         81         236         7.5e-16         0.04         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B;           1vpi         81         204         3e-16         0.07         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B;           1vpi         81         204         3e-16         0.07         -0.19         PHOSPHOLIPASE A2; CHAIN: A, B;	14pg   220   297   4.5e-15   -0.31   0.18   T-PLASMINOGEN ACTIVATOR   F1-G; 1TPG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   F1-G; 1TpG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   F1-G; 1TpG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   F1-G; 1TpG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   F1-G; 1TpG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   F1-G; 1TpG 7 CHAIN: NULL;   17pG 8   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINOGEN ACTIVATOR   T-PLASMINO	14pg   220   297   4.56-15   -0.31   0.18   FI-G; ITPG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   11PG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 7 CHAIN; NULL;   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8   1TPG 8	1   1   1   1   1   1   1   1   1   1

PDB annotation			OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE	OXIDOREDUCTASE FNK; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDE 2 TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
Coumpound		OXIDOREDUCTASE (NADP+(A),FERREDOXIN(A)) FERREDOXIN:NADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, 1FNB 3 FLAVOENZYME) (E.C.1.18.1.2) 1FNB 4 1FNB 72	FLAVIN REDUCTASE; CHAIN: A, B, C, D;	FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	FERREDOXINNADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEOFOL	D score	·					80.07
PMF	score	0.01	0.07	0.43	-0.03	-0.12	
Verify	score	0.09	-0.07	-0.14	90.00	0.00	
Pei Rlact		3.4e-55	3.4e-31	1.7e-54	3.4e-49	3.4e-57	1.5e-45
UNU	¥¥	538	510	537	538	502	347
CLLAD	TAA	252	246	252	258	244	265
1400	NID		А	A			A
and	<b>a</b> a	1fnb	1qfj	1qfz	Ique	2cnd	1a1h
<b>C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E C E E C E E C E E C</b>	A C	1421	1421	1421	1421	1421	1426

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PDI: annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (77N/C FINICED (1984))	COMPLEX (TRANSCRIPTION	REGULATION/I)NA) COMPLEX (TRANSCRIPTION	REGULATION/I)NA), RNA	POLYMERASE III, 2 TRANSCRIPTION INITIATION. ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONINA) YING-YANG 1;	TRANSCRIPTION INITIATION,	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(Inclusional Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulation Regulatio	BOTENIANA SHE ENICES	GLI, ZINC FINGIR, COMPLEX (DNA-	BINDING PROTITIN/DNA)	COLUMN TAY / THE LANGEST THE COLUMN TAY IN TO COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE COLUMN TAY IN THE CO	FACTOR/DNA) TRANSCRIPTION	FACTOR, PROTEIN-DNA COMPLEX,	CYTOKINE 2 ACTIVATION,	FACTOR/DNA)	LIPID BINDING PROTEIN APO-E3:
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S	KIBOSOMAL RNA GENE; CHAIN: B, C, E, F;				YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATION ELEMENT DNA;	(1, C), D,			ZINC FINGER PROTEIN GLII; CHAIN: A: DNA: CHAIN: C D:	(16) (Mary 5:11)		STATES CHAIN A. 18 MED	DESOXYOLIGONUCLEOTIDE:	CHAIN: B;			APOLIPOPROTEIN E; CHAIN: A;
SEQFOL D score		103.77		99.56	-				88.81	_		*****		93.51								
PMF score																	0.27	į		-		0.13
Verify score																	0.41					0.25
Psi Blast		16-51		1.7e-38				;	0e-54					69-99			0.00034					1.7e-05 (
END AA		318		402				0.0	318				!	347			320			•		304
STAR T AA		236		236					7117				-00	. 702			191					187
CHAI N ID		O		A A	_	_			ر					₹			A					A
PDB ID		Imey		1tf6				111	pont				:	- Zgii			1bg1				$\dashv$	1bz4
SEQ ID NO:		1426		1426				7071	074				1400	1470			1434					1434

10	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
,	NID	TAA	AA		score	score	D score		
									LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
			514	1.5e-27			115.08	COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
	4	127	372	7.5e-11	0.07	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
	A	228	430	3e-10	0.28	0.00	-	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
	<b>∀</b>	253	475	3e-11	0.10	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
	⋖	389	494	90-99	0.40	0.40		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
	В	296	481	6e-11	0.05	0.18		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
	4	316	449	1.5e-08	0.18	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

CHAI STAR END Psi Biast Verify PMF SEQFOL NID TAA AA score score D score	END Psi Blast Verify PMF AA score score	Verify PMF score	PMF	-	SEQFOL D score	}	Coumpound	PDI3 annotation
0.36	1 50.08 0.35 0.02	0.36	600			1	O a t tation the man	BUNDLE
400 1.36-08 0.30 -0.02	1.36-08	0.30	-0.02		X —————	S	SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BINDI P
2 514 3e-20 104.88 SC TR	36-20	104.88				S # 5	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A:	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
228 464 1.5e-18 0.21 0.27 H	1.5e-18 0.21 0.27	0.21 0.27	0.27		H	ΞZ	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
481 1.2e-09 0.25 -0.17	1.2e-09 0.25 -0.17	0.25 -0.17	-0.17		H 4	<b>∄</b> ₹	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
512 3e-09 89.88	3e-09	89.88				≥ 22	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGILLATION
293 514 3e-09 0.14 0.21 R	3e-09 <u>0.14</u> 0.21	0.14 0.21	0.21		S. S.	⊠ 22 N	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMATO, RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
	-					ı		
1315 1.5e-53 105.03	1.5e-53	105.03				12	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC:42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP. SIGNAL-TRANSIDICTION
1129 1329 4.5e-58	4.5e-58					14 E 2	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
	7							
7   299   0     431.20   7	0 431.20	431.20					ANNEXIN IV; 1ANN 5 CHAIN:	CALCIUM/PHOSPHOLIPID-BINDING

PDB annotation	PROTEIN 32.5 KD CALELECTRIN, ENDONEXIN I, 1ANN 7 32.5KD CALELECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II		RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TKA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,
Coumpound	NULL; 1ANN 6	OXIDOREDUCTASE(ACTING ON NADH OR NADPH) DIHYDROPTERIDINE REDUCTASE (DHPR) (E.C.1.6.99.10) COMPLEX 1DHR 3 WITH NADH 1DHR 4	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP* UP*UP*UP*UD-CHAIN: P, Q;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D,
SEQFOL D score		304.31			51.11	52.06	
PMF			0.54	0.99			0.80
Verify			0.38	0.38			0.27
Psi Blast		6.8e-55	3.4e-33	6.8e-21	6.8e-21	3.4e-46	3.4e-46
END		213	151	230	252	156	157
STAR T AA	·	6	_	57	73	-	2
CHAI N ID			A	¥.	A	<b>∀</b>	<
PDB		1dhr	1b7f	1b7f	1b7f	lcvj	1cvj
SEQ U	NO:	1447	1452	1452	1452	1452	1452

<del></del>	<del></del>	· r · · · · · ·		-γ	
PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/INA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA (COMPLEX, GENE REGULATION/RNA	GENE REGULA/TON/RNA POLY(A) BINDING PROTISIN 1, PABP 1; RRM, PROTEIN-RNA (SOMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A.3'); CHAIN: M, N, O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3); CHAIN: M, N, O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AD*AP*AP*AP*AP*AP* AP*AP*AP*A)-3); CHAIN: M, N, O, P. O, R. S. T:	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P. O, R, S. T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, Q, R, S, T;
			•		
	0.31	0.59	0.15	1.00	0.19
	0.02	0.25	0.08	0.74	-0.03
	5.1e-24	6.8e-40	1.7e-21	1.7e-19	1.7e-31
	256	137	230	159	130
	77	5	77	77	જ
	<b>V</b>	В	В	ഥ	н
	1cvj	1cvj	levj	1cvj	lcvj
	1452	1452	1452	1452	1452
	E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	E, F, G, H; RNA (5- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	1cvj   A   77   256   5.1e-24   0.02   0.31   POLYDENYLATE BINDING   PROTEIN I; CHAIN: M, N, O, P, Q, R, S, T;   POLYDENYLATE BINDING   PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R, AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	Icvj   A   77   256   5.1e-24   0.02   0.31   POLYDENYLATE BINDING	Icvj   A   77   256   5.1e-24   0.02   0.31   POLYDENYLATE BINDING   POLYDENYLATE BINDING   POLYDENYLATE BINDING   POLYDENYLATE BINDING   P. G. H. RNA (5. T. R. A.P.*A.P.*A.P.*A.P.*A.P.*A.P.*A.P.*A.P

PDB annotation	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3
Coumpound	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3'); CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HNRNP A1; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score					50.59		
PMF score	1.00	1.00	0.07	1.00		0.64	0.04
Verify	0.81	0.73	0.06	0.87		0.28	0.13
Psi Blast	1.7e-19	1.7e-21	1.7e-35	1.7e-21	3.4e-19	1.2e-36	3.4e-32
END	159	153	151	157	158	155	144
STAR T AA	11	73	-	75	74	1	-
CHAI N ID	江	¥			₹	4	∢
PDB ID	lcvj	1d8z	lhal	lha1	2u2f	2up1	3sxl
SEQ	1452	1452	1452	1452	1452	1452	1452

PDIs annotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT;
Соитроиид		SEX-LETHAL; CHAIN: A, B, C;	SEX-LETHAL; CHAIN: A, B, C;	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B:	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A);
SEQFOL D score			53.30				
PMF score		0.69		0.87	0.84	0.99	66.0
Verify score		0.20		-0.04	-0.17	-0.09	-0.06
Psi Blast		1,4e-20	3.4e-32	3.4e-85	5.1e-88	0	1.7e-91
END AA		230	146	899	899	899	129
STAR T AA		76	7	345	346	345	341
CHAI N ID		Ą	∢	∢	В	В	∢
PDB ID		3sxl	3sxl	lc0t	1c0t	1616	1c9r
SEQ ID NO:		1452	1452	1454	1454	1454	1454

PDB annotation	HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M1841, TRANSFERASE/IMMUNE 3 SYSTEM/DNA	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M1841, TRANSFERASE/IMMUNE 3 SYSTEM/DNA		REVERSE TRANSCRIPTASE	REVERSE TRANSCRIPTASE	NUCLEOTIDYL TRANSFERASE HIV-1 RT; IRTH 6 HIV-1 REVERSE TRANSCRIPTASE IRTH 15	NUCLEOTIDYLTRANSFERASE HIV-1 RT; IRTH 6 HIV-1 REVERSE
Coumpound	CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P.	HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEA VY CHAIN: T; DNA (5'- CHAIN: P;	REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO- TERMINAL HALF) (FINGERS 1HAR 3 AND PALM SUBDOMAINS) (RT216) (E.C.2.7.7.49) 1HAR 4	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4
SEQFOL D score					199.34		
PMF score		0.99	1.00	1.00		1.00	1.00
Verify		-0.13	0.05	0.36		0.00	-0.17
Psi Blast		8.5e-98	3,4e-65	1e-59	le-59	0	0
END		899	551	570	571	899	899
STAR T AA		341	341	326	326	341	345
CHAI N ID		Δ.				4	В
PDB ID		1c9r	Ihar	lmml	1mml	1rth	1rth
SEQ ID	NO.	1454	1454	1454	1454	1454	1454

PDE annotation	TRANSCRIPTA SE 18TH 15	NICLEOTINY TRANSEED ASE UTY 1	TO THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE TANK OF THE	NI ICI EOTIDVI TRANSEEDASE UTV. 1	RT: 1VRT 6 HIV-1 REVERSE	TRANSCRIPTAGE IVET 15							STRUCTURAL (JENOMICS HYPOTHETICAL PROTEIN,	METHANOCOCCUS JANNASCHII					•		GROWTH FACTOR INSULIN-LIKE	GROWTH FACTOR-1, GROWTH	FACIOK, NMK, PROTEIN 2	STRUCTURE, DISTANCE	GEOMETRI	OXIDOREDHCTASE	FERROCYTOCHROME CI:OXYGEN
Coumpound	CHAIN: A. B. 1RTH 5	HIV-1 REVERSE	TRANSCRIPTASE; 1VRT 4 CHAIN: A. B: 1VRT 5	HIV-1 REVERSE	TRANSCRIPTASE; 1VRT 4	CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE	REVERSE TRANSCRIPTASE	(E.C.2.7.7.49) 3HV 1 3	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE	(2: C: 2: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7: 7:	ACTOROGO CITATORY	MJU882; CHAIN: A;			GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) 1IGL 3 (NMR, 20	STRUCTURES) 11GL 4 11GL 78	GROWTH FACTOR INSULIN-	II, IGF-2) IIGL 3 (NMR. 20	STRUCTURES) 11GL 4 11GL 78	INSULIN-LIKE GROWTH	FACTOR I; CHAIN: A;				CYTOCHROME COXIDASE:	CHAIN: A, B, C, D, E, F, G, H, I, J,
SEQFOL D score									01,70	84.10								108.25					_				-
PMF score		1.00		1.00			99.0			· <u></u>		000	0.0-			90:1					1.00					1.00	
Verify score		-0.04		-0.09			-0.11					000	2		22.5	0.37					-0.15		_			0.33	
Psi Blast		0		0			3.4e-100		2 40 100	0.1-54-100		5 10-13			20.00	0.06-22		6.8e-25			4.5e-25					6.8e-37	-
END		899		899			899		673	7,0		135	)		6	<u> </u>	7	4¢		18	56				-	132	1
STAR T AA		345		345			342		342	1		9	,		25	3	į	3			9		•			46	
CHAI N ID		4		Д			<b>2</b> 0		Н	1		Ą									<		-			ш	
PDB ID		lvrt		lvrt			3hvt		3hvt			1dus			ligil	b	1	181		21-15	LIIC					20cc	
SEQ ID NO:		1454		1454			1454		1454			1455			1456		1456	00+1		7371	1430					1458	

PDB annotation	OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE	OXIDOREDUCTASE FERROCYTOCHROME C\:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE; CYTOCHROME(C)-OXYGEN, CYTOCHROME C2 OXIDASE	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON	
Coumpound	K, L, M, N, O, P, Q,	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	TROPONIN C; CHAIN: A, B;	ITK; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	SPECTRIN ALPHA CHAIN; CHAIN: A;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED
SEQFOL D score		115.24						
PMF			1.00	0.29	0.87	0.92	0.54	0.13
Verify			0.64	0.01	-0.14	0.28	-0.25	-0.16
Psi Blast		6.8e-37	0.009	3e-11	1e-18	3.4e-16	3e-12	4.5e-11
END		132	640	408	365	341	392	408
STAR		46	601	332	248	248	334	340
CHAI	3	IŊ	\ ∀		A	A	A	4
PDB	3	20cc	lavs	1awj	1b8q	1be9	1g2b	1gbr
SEQ	NO:	1458	1459	1459	1459	1459	1459	1459

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PDIs annotation					CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMA IN	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, PREFAT
Coumpound	WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) IGFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRICTTIBEN I GEC	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH IGKY 3 GUANOSINE MONOPHOSPIATE IGKY 4	TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1GKY 3 GUANOSINE MONOPHOSPHATE 1GKY 4	NTERLEUKIN 16; CHAIN:	HCASK/LM-2 PROTEIN; CHAIN: A, B;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;
SEQFOL D score			146.00					
PMF score		0.66		1.00	0.95	1.00	86.0	0.96
Verify score		0.36		0.80	0.31	0.19	0.07	0.19
Psi Blast		16-10	1e-68	le-68	1.1e-16	3e-17	3.4e-16	3.4e-14
END		408	663	799	345	337	338	342
STAR T AA		349	479	480	253	254	257	253
CHAI N ID							A	
PDB ID		1gfc	lgky	lgky			Ikwa	1pdr
SEQ ID NO:		1459	1459	1459	1459	1459	1459	1459

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CTD OTH A D DEPAY IT ANT PWT.	CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-	PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON		TRANSFERASE ATP:AMP-
A PATE A CHILOTHERY CITABLE	ALPHA SPECIKIN; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	ALPHA II SPECTRIN; CHAIN: A;	TYROSINE-PROTEIN KINASE BTK; CHAIN: A;		SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	ALPHA-SPECTRIN; CHAIN: NULL;	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 1UKZ 3.	ADENYLATE KINASE; CHAIN:
D score					,				,	
score	0.58	86.0	1.00	0.48	0.47		0.41	0.40	69.0	0.22
score	0.46	0.13	0.24	0.10	0.41		-0.10	0.22	0.10	0.02
	4.5e-11	1.5e-17	4.5e-16	3e-11	1.3e-10		1.5e-10	6e-13	1.4e-07	1.2e-05
AA	408	362	336	408	408		408	392	659	662
TAA	347	254	250	350	349		350	334	477	482
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<u> </u>	Ipwt	lqau	1qav	1qkw	1qly		1sem	1tud	lukz	1zak
Аÿ	1459	1459	1459	1459	1459		1459	1459	1459	1459
	ID NID TAA AA score score Decore	ID   N   ID   T   AA   AA   Score   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Score   D   Scor	ID   N   ID   T   AA   AA   Score   Score   Score   D   Score   D   Score   ALPHA SPECTRIN; CHAIN:   NULL;   NULL;   State   362   1.5e-17   0.13   0.98   SYNTHASE (RESIDUES 1-130);   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A; 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CHAIN:   1qau   A   254   362   1.5e-17   0.13   0.98   SYNTHASE (RESIDUES 1-130);   CHAIN: A;   ALPHA-I SYNTROPHIN   1qav   A   250   336   4.5e-16   0.24   1.00   (RESIDUES 1-130);   CHAIN: A;   Iqkw   A   350   408   3e-11   0.10   0.48   ALPHA-I ISPECTRIN; CHAIN: B;   Iqky   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   BTK; CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CH	TAA   AA   Store   Store   Store   ALPHA SPECTRIN; CHAIN:     1pwt   347   408   4.5e-11   0.46   0.58   ALPHA SPECTRIN; CHAIN:     1qau   A   254   362   1.5e-17   0.13   0.98   SYNTHASE (RESIDUES 1-130);     1qav   A   250   336   4.5e-16   0.24   1.00   (RESIDUES 77-171); CHAIN: A;     1qkw   A   350   408   3e-11   0.10   0.48   ALPHA II SPECTRIN; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   TYROSINE-PROTEIN KINASE     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   1.3e-10   0.41   0.47   BTK; CHAIN: A;     1qty   A   349   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408   408	Ipwt   347   408   4.5e-11   0.46   0.58   ALPHA SPECTRIN; CHAIN:   19mt   347   408   4.5e-11   0.46   0.58   NULL;   NULL;   1	Ipwt   347   408   4.5e-11   0.46   0.58   ALPHA SPECTRIN; CHAIN: 1   1   1   1   1   1   1   1   1   1	IDPW   NB   TAA   AA   Store   Store   District   Store   Store   Store   District   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store   Store

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PDE annotation	PHOSPHOTRANSFERASE, TRANSFERASE		HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING	KINASE KINASE, PHOSPHOTRANSFERASE	TRANSFERASE ATP:DTMP PHOSPHOTRANSFERASE		HEXOKINASE ATP/:D-HEXOSE-6- PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE	HEXOKINASE ATP/:D-HEXOSE-6- PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTR ANSFERASE	TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS	SERINE PROTEASE SERINE	PROTEINASE, TRYPSIN, HYDROLASE	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROI ASE	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER,	HEPARIN, ALLERGY, 2 ASTHMA SERINE PROTEINASE TRYPSIN-I IKF
Coumpound	A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	TYROŚINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	THYMIDYLATE KINASE; CHAIN: A. B. C. D. E. F. G. H:	THYMIDYLATE KINASE; CHAIN: A;		HEXOKINASE; CHAIN: A, B;	HEXOKINASE; CHAIN: A, B;	HEXOKINASE TYPE I; CHAIN: N;	TRYPSIN; CHAIN: A, B, C, D;		TRYPSIN; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A, B, C, D;	BETA-TRYPTASE; CHAIN: A. B.
SEQFOL D score								459.01				104.84		97.00
PMF score		0.98	1.00	0.04	0.19		1.00		1.00	1.00			1.00	
Verify score		0.12	0.32	0.28	-0.03		1.13		1.07	0.88		-	0.50	
Psi Blast		90-96	1.5e-13	9e-10	7.5e-16		0	0	0	1.4e-80		1.4e-80	1.7e-74	1.7e-74
END AA		662	332	999	662		498	499	501	239		239	233	239
STAR T AA		475	253	479	478		<b>,</b>	-	-	30		30	30	30
CHAI N ID			А	၁	А		A	<b>A</b>	z	ď		∢	¥	Ą
PDB ID		3adk	3pdz	3tmk	4tmk		1bg3	1bg3	lcza	1a0j		1a0j	1a01	1a01
SEQ ID NO:		1459	1459	1459	1459		1461	1461	1461	1464		1464	1464	1464

PDB annotation	SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL			
Coumpound	С, D;	ELASTASE; CHAIN: P;	ELASTASE; CHAIN: P;	TRYPSIN; CHAIN: NULL;	PR3; CHAIN: A, B, C, D;	COMPLEX(PROTEINASE/INHIB ITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	COMPLEX(PROTEINASE/INHIB ITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (HNE)) IPPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY IPPF 4 OVOMUCOID INHIBITOR (OMTKY3) IPPF 5
SEQFOL D score			115.93	98.94	200.42		103.86	315.52
PMF score		1.00				1:00		
Verify score		0.64				0.74		
Psi Blast		1.7e-75	1.7e-75	1.7e-79	6e-71	8.5e-83	8.5e-83	le-65
END		239	239	239	237	239	239	237
STAR T AA		30	30	30	30	30	30	30
CHAI N ID		Ъ	Ъ		<b>∀</b>	A	A	ш
PDB		Ibru	1bru	1dpo	1fuj	lmct	lmct	1ppf
SEQ	SO.	1464	1464	1464	1464	1464	1464	1464

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PDI annotation	HYDROLASE MICROPLASMINOGEN, SERINE PROTEASE, ZYMOGEN, CHYMOTRYPSIN 2 FAMILY,	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE	GROWTH FACTIOR 7S NGF; GROWTH FACTIOR 7S NGF; HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE	COMPLEX (SERINE PROTEASE/MHBITOR) TRYPSIN INHIBITOR; SEIUNE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE- SUBSTRATE INTERACTIONS, 3	METALLOFKOJEINS	
Coumpound	PLASMINOGEN; CHAIN: A, B, C, D;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL. FLUOROPHOSPHOFLUORIDAT E (DFP) ITRN 4 HUMAN	HYDROLASE (SERINE PROTEINASE) TRYPSIN
SEQFOL D score	117.30		97.78			100.94
PMF score		1.00		1.00	1.00	
Verify score		0.65		0.45	0.79	
Psi Blast	3.4e-71	3.4e-72	3.4e-72	1.7e-78	5.1e-80	5.1e-80
END	239	239	240	239	239	240
STAR T AA	12	30	30	30	30	30
CHAI N ID	∢	Ð	Ð	Д	¥.	4
PDB ID	1qrz	lsgf		1siw	1tm	1tm
SEQ ID NO:	1464	1464	1464	1464	1464	1464

PDB annotation				SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION SIGNAL TRANSDUCTION	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSDUCTION	COMPLEX (SIGNAL
Coumpound	(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL- FLUOROPHOSPHOFLUORIDAT E (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	HYDROLASE(SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH BENZAMIDINE INHIBITOR 2TBS 3	BETA TRYPSIN; CHAIN: NULL;	BETA TRYPSIN; CHAIN: NULL;	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	14-3-3 PROTEIN ZETA; CHAIN: A, B, C, D;	14-3-3 PROTEIN ZETA; CHAIN: A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	14-3-3 PROTEIN ZETA; CHAIN:
SEQFOL D score	,		97.32		99.14	234.97			284.35
PMF score		1.00		1.00			1.00	1.00	
Verify score		0.65		0.73			0.55	0.59	
Psi Blast		5.1e-79	5.1e-79	1.7e-76	1.7e-76	1.7e-98	1.7e-98	0	0
END		237	239	239	239	229	230	232	232
STAR T AA		30	30	30	30	3	3	m	3
CHAI N ID						∢	A	4	A
PDB ID		2tbs	2tbs	5ptp	5ptp	1a40	1a40	1qja	Iqja
SEQ ID		1464	1464	1464	1464	1470	1470	1470	1470

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TRANSDUCTICIN/PEPTIDE) COMPLEX, 14-3-3, PHOSPHOPEPTIDE, SIGNAL TRANSPHOPEPTIDE,	TOTAL DOCUMENT	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION,	TRANSMEMBRANE 2 PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SUBCITE IN ALBITA	HELICAL LINKER REGION, 22	TANDEM 3-HEI,IX COILED-COILS.	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SECTION AT MILE	HELICAL LINKER REGION 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COLLED-COLLS, STRICTIR AT PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, 1/35A, THREE HELIX	CONTRACTILE PROTEIN TRIPLE-	HELIX COILED COIL,
A, B; PHOSPHOPEPTIDE; CHAIN: Q, R		COLICIN IA; CHAIN: NULL;	TATAL CONTRACTOR	ALFHA SFECTKIN; CHAIN: A, B. C:				ALPHA SPECTRIN; CHAIN: A, B. C:				ALPHA SPECTRIN; CHAIN: A,	B, C;			SYNTAXIN-1A; CHAIN: A, B, C:				SYNTAXIN-1A; CHAIN: A, B, C;			HUMAN SKELETAL MUSCLE	ALFRA-ACTININ 2; CHAIN: A;
		133.38															-							,
	_		000	50.5				71.0-			3	0.39				-0.13			,				0.11	
			-0.15	3	•		12	71.0			200	0.05				0.19			100	70.0			0.02	
		3.4e-08	6-15	;			7 50 1K	01-20-7			001	75-20				1.5e-09			1		•			
		621	322				363	3			240	0+7				139			214	;		,	426	
		48	117				152	1			30	ŝ	-			23			95				196	
			A				A				4	-				~_							<b></b>	
		lcii –	lcun				lcun				+				+				$\dagger$		•	+		
		1471	1471				1471				1471	:			į	14/1			╁			_		
		A, B; PHOSPHOPEPTIDE; CHAIN: Q, R	A, B; PHOSPHOPEPTIDE; CHAIN: Q, R 621 3.4e-08 133.38 COLICIN IA; CHAIN: NULL;	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cii   A   117   322   6e-15   -0.15   0.03   0.1211, 0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015   0.015	1cii   48   621   3.4e-08   3.3.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B.C.	1cii   48   621   3.4e-08   3.3.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;	1cii   48   621   3.4e-08   3.3.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;	1ci   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;   Cun   A   157   363   7 6 16   0.13   C.	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;   B, C;   Clum   A   152   363   7.5e-16   0.12   -0.17   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   C, C, C, C, C, C, C, C, C, C, C, C, C,	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL; CHAIN   A   117   322   6e-15   -0.15   0.03   B. C;   B. C;   B. C;   B. C;   B. C;   Cum   A   152   363   7.5e-16   0.12   -0.17   B. C;   B. C;   B. C;   C.	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   152   363   7.5e-16   0.12   -0.17   B, C;   B, C;   B, C;   B, C;   B, C;   C, C, C, C, C, C, C, C, C, C, C, C, C,	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   152   363   7.5e-16   0.12   -0.17   B, C;   B, C;   CHAIN: CHAIN: A, B, C;   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Chain   Cha	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C, C, C, C, C, C, C, C, C, C, C, C, C,	1   1   1   1   4   8   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1   1   2   2   6   1   5   1   2   3   3   2   4   3   2   4   3   2   4   3   2   4   3   2   4   3   4   3   4   3   4   4   4   4	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   152   363   7.5e-16   0.12   0.03   B, C;   B, C;   B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cun   A   117   322   6e-15   -0.15   0.03   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   Cun   A   38   248   3e-20   0.05   0.39   B, C;   B, C;   B, C;   B, C;   B, C;   Cun   Chain: A, B, C;   Cun   A   38   248   3e-20   0.05   0.39   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, B, C;   Cun   Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A, Chain: A	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: Q, R     1cun   A   152   363   7.5e-16   0.12   -0.17   B, C;     1cun   A   38   248   3e-20   0.05   0.39   B, C;     1cun   A   38   248   3e-20   0.05   0.19   -0.13   SYNTAXIN-IA; CHAIN: A, B, C;     1cun   A   38   248   3e-20   0.05   0.19   SYNTAXIN-IA; CHAIN: A, B, C;     1cas   A   23   139   1.5e-09   0.19   -0.13   SYNTAXIN-IA; CHAIN: A, B, C;	1   1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL; CHAIN: Q, R   1   1   1   322   6e-15   -0.15   0.03   B, C; CHAIN: CHAIN: A, B, C; CHAIN: CHAIN: A, B, C; CHAIN: CHAIN: A, B, C; CHAIN: CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN: A, CHAIN	1cii	1   1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL; Claim   A   117   322   6e-15   -0.15   0.03   ALPHA SPECTRIN; CHAIN: A, B, C; Claim   A   152   363   7.5e-16   0.12   -0.17   B, C; Claim   A   38   248   3e-20   0.05   0.39   B, C; Claim   A   38   248   3e-20   0.05   0.19   -0.13   SYNTAXIN-1A; CHAIN: A, B, C; Claim   A   38   1.5e-09   0.19   -0.13   SYNTAXIN-1A; CHAIN: A, B, C; Claim   A   34   35   1.5e-09   0.19   -0.13   SYNTAXIN-1A; CHAIN: A, B, C; Claim   A   36   24   24   24   25   24   25   24   25   24   25   24   25   24   25   24   25   24   25   24   25   24   25   25	1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL;   2.015   0.03   2.015   0.03   2.015   0.03   2.015   0.03   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017   2.017	1   1cii   48   621   3.4e-08   133.38   COLICINIA; CHAIN: MULL;   1   1cii   A   117   322   6e-15   -0.15   0.03   ALPHA SPECTRIN; CHAIN: A, B, C;   15e-16   0.12   -0.17   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;	1   1cii   48   621   3.4e-08   133.38   COLICIN IA; CHAIN: NULL; CHAIN: Q, R   1   1cii   A   117   322   6e-15   -0.15   0.03   ALPHA SPECTRIN; CHAIN: A, B, C;   1   1cii   A   152   363   7.5e-16   0.12   -0.17   B, C;   B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, B, C;   CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, CHAIN: A, C, C	1   1cii

PDB annotation	CONTRACTILE PROTEIN	CONIRACTILE PROTEIN INTELEMENTS COLLED COLL,	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION		COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COLLS.	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS,
Coumpound		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	ALPHA SPECTRIN; CHAIN: A, B, C;		ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				:			•			
PMF score		-0.02	0.03		0.04	0.15		0.19	0.55	0.35
Verify		60.0	-0.11		-0.56	-0.18		-0.12	-0.05	0.19
Psi Blast		1.5e-15	60-99		0.0045	3e-06		9e-13	1.5e-15	4.5e-15
END		487	307		77	337		458	687	724
STAR T AA		217	32		23	150		241	460	506
CHAI N ID		A			Ħ	A	··-·	A	V V	Ą
PDB		1quu	lsig		Infi	1cun		1cun	1cun	lcun
SEQ ID	NO:	1471	1471		1475	1476		1476	1476	1476

TT -		-γ	<del></del>	<del></del>		·	<del></del>	·
STRUCTURAL PROTEIN STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS.	STRUCTURAL PROTEIN STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COLLED-COLLS,	STRUCTURAL PROTEIN STRUCTURAL PROTEIN TWO REPEATS OF SIECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS,	SIRUCTURAL PROTEIN ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMMISCY MITHER STREET	COMPLETA, MOLITI-SUBONITI ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX MILITI-SUBINITY	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGNIN ASSOCIATED 35
ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B; C;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B.	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN IA; CHAIN: B:	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;
0.42	0.09	-0.14	-0.05	0.01	0.06	0.03	0.03	-0.06
0.15	0.08	-0.00	0.03	-0.30	-0.21	-0.19	-0.26	0.00
96-17	1.2e-13	6e-12	6e-16	1.5e-16	6e-18	6e-13	3e-07 ,	1.5e-11
794	850	916	423	597	711	911	363	719
583	632	721	216	380	503	700	256	593
A	∢	∢	В	В	g e			A
lcun	1cun	1cun	ldn1				·•·	lez3 ,
1476	1476	1476	1476					1476
	1cun         A         583         794         9e-17         0.15         0.42         ALPHA SPECTRIN; CHAIN: A, B, C;	lcun         A         583         794         9e-17         0.15         0.42         ALPHA SPECTRIN; CHAIN: A, B, C;           lcun         A         632         850         1.2e-13         0.08         0.09         ALPHA SPECTRIN; CHAIN: A, B, C;	lcun         A         583         794         9e-17         0.15         0.42         ALPHA SPECTRIN; CHAIN: A, B, C;           lcun         A         632         850         1.2e-13         0.08         0.09         ALPHA SPECTRIN; CHAIN: A, B, C;           lcun         A         721         916         6e-12         -0.00         -0.14         ALPHA SPECTRIN; CHAIN: A, B; C;	1cun A 583 794 9e-17 0.15 0.42 ALPHA SPECTRIN; CHAIN: A, B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; B, C; CHAIN: A, B, C; CHAIN: A, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B, CHAIN: B,	1cun A	1cm   A   583   794   9e-17   0.15   0.42   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;   B.C;	1cun A   583   794   96-17   0.15   0.42   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   B, C;   C, C, C, C, C, C, C, C, C, C, C, C, C,	Icum         A         383         794         9e-17         0.15         0.42         ALPHA SPECTRIN; CHAIN: A, B, C;           Icum         A         632         830         1.2e-13         0.08         0.09         ALPHA SPECTRIN; CHAIN: A, B, C;           Icum         A         721         916         6e-12         -0.00         -0.14         ALPHA SPECTRIN; CHAIN: A, B, C;           Idul         B         216         423         6e-16         -0.00         -0.14         ALPHA SPECTRIN; CHAIN: A, SYNTAXIN IA;           Idul         B         216         423         6e-16         0.03         -0.05         SYNTAXIN BINDING PROTEIN           Idul         B         597         1.5e-16         -0.30         0.01         SYNTAXIN BINDING PROTEIN           Idul         B         503         711         6e-18         -0.21         0.06         SYNTAXIN BINDING PROTEIN           Idul         B         700         911         6e-18         -0.21         0.06         SYNTAXIN BINDING PROTEIN           Idul         B         700         911         6e-18         -0.21         0.06         SYNTAXIN BINDING PROTEIN           Idul         B         700         911         6e-18

PDB annotation	KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN		IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN,
Coumpound		SYNTAXIN-1A; CHAIN: A, B, C;	SSOI PROTEIN; CHAIN: A;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1; CHAIN: A:	RNA-BINDING
SEQFOL D score											
PMF score		0.19	0.15	0.59	0.00	0.06	0.54	0.21	0.12	0.82	0.96
Verify score		0.28	0.17	-0.29	-0.19	-0.29	-0.02	0.07	-0.07	0.62	0.19
Psi Blast		4.5e-10	9e-10	0.0001	4.5e-22	3e-26	6e-24	1.5e-24	0.00017	0.00015	0.00075
END		822	648	711	573	640	749	790	555	199	299
STAR T AA		704	491	548	320	390	480	528	464	609	609
CHAI N ID		V	∢	U	4	A	A	A	A	A	A
PDB ID		lez3	1fio	1fxk	Iquu	1quu	Iquu	lquu	1ses	1dt4	1dtj
SEQ ID	ÖZ	1476	1476	1476	1476	1476	1476	1476	1476	1479	1479

			<del></del>	т —		<del></del>		
PD13 annotation	AT DITA TOTAL ATTOR ATTACA	ALFHA-BEIA FOLD KNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA FOLD RNA-BINDING MOTIF	IMMUNE SYSTEM KH DOMAIN, ALPHA-BETA 1'OLD RNA-BINDING MOTIF	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP:GTP 2 DIPHOSPHOTRANSFERASE, RNA	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHORYLASE, ATP-GTP DIPHOSPHORYLANSFERASE, 2 RNA	RNA BINDING PROTEIN/RNA ASTROCYTIC NOVA-LIKE RNA- BINDING PROTEIN; KH DOMAIN, ALPHA-BETA FOLD, RNA-BINDING MOTH, PROTEIN/RNA 2	SIKUCI UKE RNA BINDING IROTEIN KH3; HNRNP K, KH DOMAIN, THREE- DIMENSIONAI STRICTI DE MA
Coumpound	NET IR CONCOL OCITIVAT	VENTRAL ANTIGEN 2; CHAIN: A, B, C, D;	RNA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A B C D:	NA-BINDING NEUROONCOLOGICAL VENTRAL ANTIGEN 2; CHAIN: A R C D:	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	RNA-BINDING PROTEIN NOVA-2; CHAIN: A, B; 20-MER RNA HAIRPIN; CHAIN: C, D;	HNRNP K; CHAIN: A;
SEQFOL D score	21035							
PMF			0.94	. 68.0	1.00	1.00	0.72	0.36
Verify			0.59	0.60	0.75	0.49	0.50	0.36
Psi Blast			36-06	1e-05	0	0	0.00014	0.0014
END			667	299	613	739	675	129
STAR T AA			609	609	51	51	609	610
CHAI N ID			ن ن	D	٧	A	A	<b>∀</b>
PDB ID			latj	1dtj	1e3h	1e3p	lec6	1khm
SEQ ID	NO:	5	14/9	1479	1479	1479	1479	1479

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PDB annotation		C-MYC, 2 DIPOLAR COUPLING, DNA-BINDING, RNA-BINDING 3 PROTEIN	S1 RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, S1 RNA-BINDING DOMAIN, POLYNUCLEOTIDE PHOSPHORYLASE 2 (PNPASE)	RIBONUCLEOPROTEIN RNA- BINDING PROTEIN 1VIG 19	GENE REGULATION APO PROTEIN	GENE REGULATION APO PROTEIN	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITATION 2 FACTOR, CELL CYCLE CONTROL FACTOR	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, ATP- 2 BINDING, DNA- BINDING	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORYLATION	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN
Coumpound			PNPASE; CHAIN: NULL;	VIGILIN; 1VIG 5 CHAIN: NULL; 1VIG 6	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	PCRA (SUBUNIT); CHAÎN: A; PCRA (SUBUNIT); CHAÎN: B; PCRA (SUBUNIT); CHAÎN: C; PCRA (SUBUNIT); CHAÎN: D;	T-FIMBRIN; CHAIN: NULL;	DYSTROPHIN; CHAIN: A, B, C, D;
SEQFOL	D score									
PMF	score		1.00	0.30	0.00	0.03	0.54	0.83	0.96	0.68
Verify	score		0.78	0.46	-0.14	-0.21	-0.14	-0.19	0.28	0.54
Psi Blast			5.1e-21	1e-06	1.7e-06	0.009	0.00015	1.5e-11	6.8e-26	5.1e-28
END	AA		751	199	528	602	492	524	122	120
STAR	TAA		675	603	442	447	427	444	4	2
CHAI	QI N				A_	A	A	۷.		∢
PDB	А		lsro	lvig	1d9x	149x	1fm	lqhg	laoa	1dxx
SEO	a ș		1479	1479	1480	1480	1480	1480	1484	1484

PDI: annotation	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN		COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGIL A TION/DNA) PNA	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2	IKANSCRIPTION REGULATION		LIGASE CBL, UISCH7, ZAP-70, E2, UBIQUITIN, E3,	PHOSPHORYLATION, 2 TYROSINE	RINASE, OBIQUITINATION, PROTEIN DEGRADATION.		METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING
Coumpound	UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS.	1 (CSHC4, OK KING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP-	70 PEPTIDE; CHAIN: B;	ENZYME E12-18 KDA UBCH7;	CHAIN: C;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI;
SEQFOL D score												<del></del>		
PMF score	0.39		0.01		0.41		0.00	0.29		0.15			- 6	79.0
Verify score	0.33		-0.10		0.08		-0.38	-0.35		-0.24				0.20
Psi Blast	3.4e-26		0.0045		0.00045		0.0001	3.4e-10		5.1e-09			1	3.16-00
END	121	3	953		926		377	378		381	-		207	787
STAR T AA	5	,,,,	800		873		339	336		336			336	3
CHAI N ID	¥.		∢		K		-			∢			<b>A</b>	
PDB ID	1qag	73*1	011		2gli		Ibor	lchc		lfbv /	<del></del>		1025	
SEQ ID NO:	1484	1406	1490		1486		1487	1487		1487	<del></del>		1487	

0 40	4	TATIO	CT A TO	END	Dei Rlact	Varify	PMR	SEOFOL	Coumpound	PDB annotation
3 8 5	E C	NID	TAA	A A		score	score	D score		
į									CHAIN: A;	FINGER (C3HC4)
1487	1rmd		320	387	3.4e-09	0.10	90.0		RAGI; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING
			·							PROTEIN 1; RAG1, V(D)J
								*		RECOMBINATION, ANTIBODY,
										MAD, KING FINGER, ZZINC BINITITEAR CLIISTER ZINC
										FINGER, DNA-BINDING PROTEIN
1400	1405	<	909	787	1 2e-11	0.11	-0.18		N-ETHYLMALEIMIDE-	HEXAMERIZATION DOMAIN
1430	11771	4	2	}					SENSITIVE FUSION PROTEIN;	HEXAMERIZATION DOMAIN,
									CHAIN: A;	Alfast, indicatori
1490	1694	EI.	339	434	8.5e-12	10.0	-0.13		HEAT SHOCK PROTEIN HSLV;	CHAPERONE HSLV; HSLU
2	}	1	<u>.</u>						CHAIN: A, B, C, D; HEAT	CHAPERONE, HSLVU, CLPUY, AAA-
									SHOCK PROTEIN HSLU;	ATPASE, ATP-DEPENDENT 2
									CHAIN: E, F;	PROTEOLYSIS, PROTEASOME
1490	1,04	Į,	330	634	1.5e-12	-0.20	0.05		HEAT SHOCK PROTEIN HSLV;	CHAPERONE HSLV; HSLU
2		)							CHAIN: A, B, C, D; HEAT	CHAPERONE, HSLVU, CLPQY, AAA-
									SHOCK PROTEIN HSLU;	ATPASE, ATP-DEPENDENT 2
									CHAIN: E, F;	PROTEOLYSIS, PROTEASOME
1400	16/18	<b>A</b>	\$	514	0.0015	-0.39	0.28		ARSENITE-TRANSLOCATING	HYDROLASE ARSA ATPASE; P-
1430	1140	¢	70	;		}			ATPASE; CHAIN: A;	LOOP, ANTIMONITE BINDING SITE,
										ATP BINDING SITE
1490	1fnn	A	344	629	1.2e-15	0.15	0.45		CELL DIVISION CONTROL	CELL CYCLE CDC6P; CDC6, CDC18,
		:							PROTEIN 6; CHAIN: A, B;	ORCI, AAA PROTEIN, DNA
										REPLICATION INITATION 2
-			-,-							FACTOR, CELL CYCLE CONTROL
										FACTOR
1490	1g41	Ą	330	599	1.2e-37	0.46	0.94		HEAT SHOCK PROTEIN HSLU;	CHAPERONE AAA-ATPASE, CLPY,
									CHAIN: A;	Alf-Dereinden in in in or or or
1490	1g41	Ą	339	618	1.2e-17	-0.11	0.04	The south of	HEAT SHOCK PROTEIN HSLU; CHAIN: A:	CHAPERONE AAA-A IPASE, CLF I, ATP-DEPENDENT PROTEOL YSIS
1400	10h/		360	306	1 5e-05	-0.53	0.49		SHIKIMATE KINASE; CHAIN:	TRANSFERASE SHIKIMATE KINASE,
1470	41101	¢	<u>}</u>	)		;			A, B;	PHOSPHORYL TRANSFER, ADP,

	7	T	Т	1	T		<del>T-</del>	т
PD]3 annotation	SHIKIMATE 2 PATHWAY, P-LOOP	PROTEIN, TRANSPORT FIFTY-FOUR PROMOLOG, P48; FFH, SRP54, SIGNAL RECOGNITION PARTICLE, GTPASE, M DOMAIN, 2 RNA-BINDING, SIGNAL SEQUENCE-BINDING, HELIX-TURN-HELIX, 3 PROTEIN TARGETING, PROTEIN TRANSPORT		COMPLEX (INFIBITOR/NUCLEASE) COMPLEX (INFIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR FECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	TRANSCRIPTION RNAIP; RANGAP; TRANSCRIPTION RNAIP; RANGAP; GTRASE-ACTIVATING FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	MERCHEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
Coumpound		FFH; CHAIN: A, B, C;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;		LITHOSTATHINE; CHAIN: NULL
SEQFOL D score		·						
PMF		0.01		0.94	0.18	0.65		1.00
Verify score		-0.24		0.10	0.03	0.33		0.82
Psi Blast		1e-05		1.5e-48	6.8e-27	3.4e-43		le-42
END		537		394	391	393		991
STAR T AA		347		178	178	178		36
CHAI N ID	,	<		∢	. ·			
PDB ID		2ffh		1a4y	lyrg	2bnh		1111
SEQ ID NO:		1490		1491	1491	1491		1495

PDB annotation	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	PROTEIN TRANSPORT HELIX- TURN-HELLX TPR-LIKE REPEAT, PROTEIN TRANSPORT	HYDROLASE SERCAI; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC,
Coumpound	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: NULL	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	LITHOSTATHINE; CHAIN: A;	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;
SEQFOL D score		212.11			226.04				
PMF	1.00		1.00	1.00		-0.17	0.46	0.96	0.83
Verify	0.82		0.77	0.77		0.14	-0.16	0.20	-0.10
Psi Blast	7.5e-43	7.5e-43	1e-44	6e-47	6e-47	1.1e-13	0	16-12	1.4e-19
END	166	166	166	166	991	634	713	540	516
STAR T AA	36	36	23	23	23	489		393	448
CHAI N ID			A	А	A	A	₹	Ą	A
PDB ID	Ħ	ĮĮ.	1qdd	1qdd	1qdd	1qqe	leul	1040	1c4o
SEQ	NO: 1495	1495	1495	1495	1495	1497	1498	1499	1499

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PDI3 annotation	HELICASE, 2 HYDEDTHEDMOSTANT FINANCIERS	HYDROLASE (IVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN	GENE REGULATION APO PROTEIN	GENE REGULA TION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A. FIF4A: HFI ICASF	INITIATION FACTOR 4A, DEAD-BOX	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A,	TRANSLATION EUKARYOTIC INTITATION FACTOR 44; IF44,	HELICASE, DEAD-BOX PROTEIN HELICASE HELICASE, RNA,	HEPATITIS, HCV, ATPASE, NTPASE GENE REGULA'TION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE,	DEAD BOX 2 PROTEIN FAMILY HELICASE RNA HELICASE, HEPATITIS C VIRUS, HCV, INWINDING MECHANISM	WOLLD TANK	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTISIN, 2 CALCIUM- BINDING PROTISIN
Coumpound	CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B: CHAIN: A:	EXCINUCLEASE ABC SUBUNIT	EXCINUCLEASE UVRABC	EXCINUCLEASE UVRABC	EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	RNA HELICASE; CHAIN: NULL		PROTEIN KINASE C (BETA); CHAIN: A, B;
SEQFOL D score														77.04
PMF score		0.19	0.80	60.0	0.76	0.86		1.00	1.00	0.22	1.00	0.04		
Verify score		-0.57	0.17	-0.16	0.39	0.26		0.83	0.47	-0.18	0.55	-0.59		
Psi Blast		0.00068	8.5e-13	9e-29	3.4e-16	1.2e-43		3.4e-59	0	0.0003	5.1e-56	1.5e-53		9e-25
END		223	540	531	528	558		340	558	325	340	522		137
STAR T AA		144	393	258	380	376		127	127	158	127	158		12
CHAI N ID		∢	∢_	A	٧	¥		∢	В	4	Ą			∢
PDB ID		1d2m	Id2m	1d9x	149x	1 fuk		ng I	1fuu	Ihei	1qde	80hm	+	1a25
SEQ NO:		1499	1499	1499	1499	1499		1499	1499	1499	1499	1499	1500	7007

PDB annotation		CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLAZ; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	HYDROLASE CPLAZ; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
Coumpound		PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
SEQFOL	D score								
PMF	score	0.54	1.00	0.90	0.35	0.10	0.65	0.45	0.24
Verify	score	-0.05	0.42	0.62	0.04	0.36	0.07	0.29	0.34
Psi Blast		1.5e-26	9e-25	1.4e-24	3.4e-30	1.7e-28	1.3e-29	7.5e-24	3.4e-22
END	ΑA	287	131	117	287	122	338	184	302
STAR	TAA	167	17	18	167	19	184	22	183
CHAI	N II	A	4	<b>∀</b>	¥	A	4	A	∢
PDB	A	1a25	1a25	1a25	1byn	1byn	lejy	lejy	1djx
SEO	'e Ş	1502	1502	1502	1502	1502	1502	1502	1502

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PDB annotation	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1;	HYDROLASE HYDROLASE LIPID	DEGRADATION, 2 TRANSDICER	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	TRANSFERASE CALCIUM++,	PHOSPHOLIPIL) BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	KINASE C	TRANSFERASE CALCIUM++,	PHOSPHOLIPIE) BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	KINASE C	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINIONG 2 PROTEIN,	PHOSPHATIDY, LSERINE, PROTEIN	KINASE C	HYDROLASE CALB DOMAIN;	HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE CALB DOMAIN
Coumpound		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A,	B;					PHOSPHOINOSITIDE-SPECIFIC PHOSPHOI IDASE CHAIN: A	B;					PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;				PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;				PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;				PHOSPHOLIPASE A2; CHAIN:	NOLL;	PHOSPHOLIPASE A2; CHAIN:
SEQFOL D score																						-									51.76
PMF score		0.16						0.21						1.00				100	0.0				900	0.88 -		•		300	0.28		
Verify score		0.49					000	0.20				*****		0.52				;	-0.13				42	0.47							
Psi Blast		6.8e-23					2 42.00	27-24.0	-					le-24				\$ 10.00	2.15-26				2000	0.06-27	, <del></del>			60.00	67-20		4.5e-25
END		121					202	202						137				200	727				117	<u> </u>				226	0/7		145
STAR T AA		27					183	103					ļ	17				183	601				81	9				101	+ 0 1		20
CHAI N ID		⋖					a	3						¥.				4	¢				4	¢							
PDB ID		Idjx					1 div							Idsy				1dev	<u></u>			-	Idev					1rlw			Irlw
SEQ ID NO:		7061					1502	7001					200	7001				1502	100				1502			_		1502	70.7	_	1502

PDB annotation	HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN				ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION
Coumpound	NULL;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	SYNAPTOTAGMIN III; CHAIN: A;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA;
SEQFOL D score				•	59.11				
PMF score		0.93	0.48	0.21		0.34	0.19	1.00	96'0
Verify score		0.78	0.18	0.36	·	0.00	-0.57	0.40	0.29
Psi Blast		4.5e-25	3.4e-30	1.7e-28	1.7e-28	1.2e-26	6.8e-53	1.5e-26	1.2e-29
END		143	284	122	130	294	223	861	828
STAR T AA		30	167	61	2	168	144	693	694
CHAI N ID						₹		മ	В
PDB		Irlw	lrsy	Irsy	Irsy	3rpb		lawc	1awc
SEQ	Ö	1502	1502	1502	1502	1502	1502	1503	1503

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REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGILLATION(DAY) GARPAI PHA:	GABPBETAI; COMPLEX	(TRANSCRIPTION	REGULATION/JONA), DNA-BINDING,	ANKVEN PEPPATS	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/I)NA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/INA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA; GABPBETA1: COMPLEX
CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B:
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			9.0						0.72							5	70.0								0.08	
			5.1e-38						7.5e-34							1 20 21	1.25-27.1							2.4-00	3.46-29	
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			748						779							780	3							2770	·	
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			Iawc						lawc							lawe	2							lawe	2	
		1502	1505					1,500	50051							1503	}							1503	3	
			CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	N: B;	CHAIN: A; GA BINDING	lawc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E;	CHAIN: A; GA BINDING	1awc B 748 895 5.1e-38 0.68 1.00   CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E; CHAIN: B; DNA; CHAIN: B, BROTEIN BETA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E;	lawc B 748 895 5.1e-38 0.68 1.00 GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E; CHAIN: B; DNA; CHAIN: D, E; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E;	1awc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E;	1awc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E;           1awc         B         779         936         7.5e-34         0.72         1.00         GA BINDING PROTEIN ALPHA; CHAIN: D, E; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	lawc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: B; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; 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CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA;	1awc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B, E, E, B, E, E, E, E, E, E, E, E, E, E, E, E, E,	lawc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D; E;	Tawc   B   748   895   5.1e-38   0.68   1.00   GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: B, E; CHAIN: B, E; CHAIN: B, E; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B, CHAIN: B; CHAIN: B; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E;	Iawc         B         748         895         5.1e-38         0.68         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D; B; DNA; CHAIN: D; B; DNA; 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GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; GHAIN: A; GA BINDING PROTEIN ALPHA; 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PDB annotation	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
Coumpound	DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score							
PMF score		-0.11	0.98	1.00	0.99	0.76	1.00
Verify		0.05	0.26	09:0	0.37	0.07	0.64
Psi Blast		1.7e-29	3.4e-26	4.5e-32	1.1e-26	1.46-24	7.5e-33
END		1045	862	937	898	862	941
STAR T AA		088	269	776	695	697	779
CHAI N ID		Д			В	В	В
PDB ID		lawc	1bd8	1bd8	161x	1blx	1blx
SEQ	Ö	1503	1503	1503	1503	1503	1503

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PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPISNDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPRINDENT KINASE	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	SIGNAL ING PROTEIN HEL IX-TIBN-	HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC- BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING PROTEIN	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANN YKIN KEPEA1, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CIILL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANK YRIN REPEAT, 2 CDK 4/6 INHIRITOR	TRANSCRIPTION FACTOR P65:	P50D; TRANSCRIPTION FACTOR, IKBNPKR COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D SUBUNIT: CHAIN: C: 1-KAPPA-
SEQFOL D score					****										• • • • •						
PMF score		0.84		66'0			0.77	1.00		9.65		1.00				1.00				0.31	
Verify score		0.42		0.39			0.23	0.81		-0.07		0.22				0.52				0.21	
Psi Blast		3.4e-31		6.8e-32			3e-19	1.2e-32		1.4e-21		1.7e-30				6.8e-32		·		1.7e-31	
END AA		867		894			833	606		881		998				894				812	
STAR T AA		697		748			693	776		589		169				748				640	
CHAI N ID		∢		⋖˙			4	A		∢		Ą				⋖				Ω	
PDB ID		1bu9		1bu9			Sep I	1d9s		Ideq		lihb				1ihb				1ikn	
SEQ ID NO:		1503		1503			1503	1503		1503		1503				1503				1503	

PDB annotation			TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMFLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YKIN Z KEPEAT HELIA	COMPLEX (TRANSCRIPTION	KEG/ANK KEPEAI) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX
Coumpound		B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNII; CHAIN: C; I-KAFFA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ij.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	F;		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	Ĕ.		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL	D score																		··· ¥									
PMF	score		1.00		1.00		1.00			1.00			0.88	ļ 				1.00					1.00					1.00
Verify	score		0.10		0.37		0.52			0.37			0.15	}				0.43					0.42					0.50
Psi Blast			3e-34		3.4e-38		3e-41			3e-38			1 7e-31	• • •				7.5e-34					8.5e-38					3e-35
END	¥		912		882		947			983		,	812	! 5				606					882					982
STAR	T AA		693		722		747			776			640	2				693					721					776
CHAI	a N		Q		D		D			Q			ū	3				Ξ					Ξ					Ξ
PDB	<u> </u>		1ikn	-	1ikn		1 iku			1ik			1,000	1	_			1nfi					1nfi					lnfi
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PDI annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX		TRANSFERASE PARP-CF, POLY(ADP-RIBOSE) TRANSFERASE,	POLY TRANSFERASE, GLYCOSYLTRANSFERASE, NAD(+)	2 ADP-RIBOSYLTRANSFERASE	TRANSFERASE PARP-CF, POLY(ADP-RIBOSE) TRANSFERASE	POLY TRANSFIRASE,	GLYCOSYLTRANSFERASE, NAD(+) 2 ADP-RIBOSYI TRANSFERASE	COMPLEX (TRANSCRIPTION	REGULATION/INA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION(I)NA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION(I)NA) GABPALPHA;	GABPBETAI; COMPLEX	(IKANSCRIPTION	KEGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/ENA) GABPALPHA;	GABPBETAI; COMPLEX (TRANSCRIPTION
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, F;		POLY (ADP-RIBOSE) POLYMERASE; CHAIN: NULL;		DOI W/ARD PERSON	POLY (ADP-KIBOSE) POLYMERASE; CHAIN: NULL;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DINA; CHAIN: D, E;				OA DINIDAG OR CHOING	CHAPING PROTEIN ALPHA;	DE OTTEN BETA 1. CITABLE	TNO LEIN BETA I; CHAIN: B; DNA: CHAIN: D. E.	DIAN, CITAIN: D, E;				or or and and and	GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	FROIEIN BEIA I; CHAIN: B; DNA; CHAIN: D. E;
SEQFOL D score	·											•								-	-						<del>-</del> -
PMF score		0	0.52		0.16	0.10			1.00							1 00	3.						•	200	0.90		
Verify		0.01	10:0		PC 0-	±7.0-			0.46							0.22	77:0							0.15		-	
Psi Blast		16.35	16-33		1 7e-08	200			3.4e-35			_				6 86-39			-					1 70-36			-
END		1170	1170		1127				296							329	<u></u>		-					357	<u> </u>		
STAR T AA		050	900		994				128							185	•		-					215	)		
CHAI N ID									<u></u>							В								В	)		
PDB ID		1926			1a26	)		-	lawc							lawc								lawc			
SEQ ID NO:		1504	}		1504				1504			-				1504								1504			

PDB annotation	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score					
PMF score	,	1.00	1.00	1.00	0.95
Verify score		0.62	0.75	0.69	0.17
Psi Blast		3e-43	1.5e-39	1.2e-33	1.26-37
END		164	176	482	578
STAR T AA		25	56	335	402
CHAI N ID		æ	В	В	В
PDB ID		lawc	lawc	lawc	lawc
SEQ ID	Oz	1504	1504	1504	1504

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ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPISATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/NA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/INA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGIL ATTOMINA) CARBAI BUA	GABPBETAI; COMPLEX	TRANSCRIPTION BEGIN ATTOMASMA	2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 2 EACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	PROTEIN: BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B; DNA: CHAIN: D. E:			
							105.28		_								
	1.00		1.00		-		·					1.00					
	0.04	-	0.49				-					0.47					
	3.4e-33		4.5e-47				4.5e-47					8.5e-39	•	•••••			
	611		644				644					640					
	437		491				491					496					
	Д		щ				eq.					м					
	lawc	,	lawc				Iawc					1awc					
	1504		1504				1504					1504					
		B 437 611 3.4e-33 0.04 1.00 GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN B; DNA; CHAIN: B; DNA; CHAIN: D, E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING PROTEIN B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B;         PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING         PROTEIN BETA 1; CHAIN: B;         DNA; CHAIN: D, E;         DNA; CHAIN: D, E;           lawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING         CHAIN: A; GA BINDING         CHAIN: A; GA BINDING	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B;           lawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D; E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING         PROTEIN BETA 1; CHAIN: B;           DNA; CHAIN: D, E;         DNA; CHAIN: B;           Iawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING         PROTEIN BETA 1; CHAIN: B;         DNA; CHAIN: D, E;         DNA; CHAIN: D, E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DINA; CHAIN: B; DINA; CHAIN: B; DINA; CHAIN: D, E;           lawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DINA; CHAIN: D, E; DINA; CHAIN: D, E; DINA; CHAIN: D, E; CHAIN: A. GA BINDING PROTEIN ALPHA; CHAIN: A. GA BINDING PROTEIN ALPHA; CHAIN: A. GA BINDING PROTEIN ALPHA; CHAIN: A. GA BINDING PROTEIN ALPHA; CHAIN: A. GA BINDING	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: B; CHAIN: CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHA	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: B; CHAIN: CHAIN: CHAIN: B; CHAIN: CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D; E;	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA; GABINDING PROTEIN ALPHA; GABINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; 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CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: B; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; DNA; CHAIN: D, E; 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          lawc         B         491         644         4.5e-47         105.28         GA BINDING PROTEIN ALPHA;           lawc         B         496         640         8.5e-39         0.47         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         496         640         8.5e-39         0.47         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING PROTEIN ALPHA;         CHAIN: A; GA BINDING         DNA; CHAIN: B;         0	lawc         B         437         611         3.4e-33         0.04         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         491         644         4.5e-47         0.49         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         491         644         4.5e-47         105.28         GA BINDING PROTEIN ALPHA;           lawc         B         496         640         8.5e-39         0.47         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         496         640         8.5e-39         0.47         1.00         GA BINDING PROTEIN ALPHA;           lawc         B         496         640         8.5e-39         0.47         1.00         CHARIN: A; GA BINDING PROTEIN B;           lawc         B         496         640         8.5e-39         0.47         1.00         CHARIN: A; GA BINDING PROTEIN ALPHA;           characteristics         CHARIN: A; GA BINDING PROTEIN BETA I; CHAIN: B;         DINA; CHAIN: B;         DINA; CHAIN: B;

SRQ         PDB         CFHAI         STAR         END         Faster         SEQPOL         Columpound         PDB anmothtion           150         130         130         150         CABINDING PROTEIN ALPHA;         COMPLEX (TRANSCURTION           1504         1awc         B         645         784         3-42         0.64         1.00         CHAIN: A; GA BROING         CRAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAI													_										_				-	
TAA   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation	COMBI EX (TB ANSCBIBLION	REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX	(IRAINSCRIF IJON REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	INAINSCALE HOLY STREET ON	COMPLEX (IRANSCKIPITON REGULATION/DNA) GABPALPHA:	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRAINSCRIP A SE DECEDIOD	I TYROSINE KINASE, PROTEIN
PDB         CHAI         STAR         END         Psi Blast         Verify         PMF           lawc         B         645         784         3c-42         0.64         1.00           lawc         B         660         797         3.4c-38         0.49         1.00           lawc         B         683         817         1.2c-35         0.28         1.00           lawc         B         89         296         1.4c-40         -0.00         1.00           lawc         B         89         296         1.4c-40         -0.00         1.00           lbbx         A         877         933         9e-07         1.27         1.00	Coumpound	OA BERTELE DE CATERIA AT DITA.	GA BINDLING FROIEIN ALFRA, CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DIM, CILIM, D, L,			GA BINIDING PROTEIN AI PHA:	CHAIN: A: GA BINDING	PROTEIN BETA I; CHAIN: B;	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;				H doo dry dondarona ,	EPHA4 RECEPTOR 1 YROSINE KINASE; CHAIN: A;
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PDB         CHAI         STAR           Iawc         B         645           Iawc         B         660           Iawc         B         683           Iawc         B         89           Iawc         B         89           Ibox         A         877	Psi Blast		3e-42				3.4e-38						10-05	1.26-33							1.4e-40							9e-07
PDB CHAI  I awc B  I awc B  I awc B  I awc B  I awc B	END		784		-		797	· ·		• .				81/							296							933
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PDB annotation	INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN,	SIGNAL TRANSDUCTION SAM DOWARN, EPH RECEPTOR, SIGNAL TRANSDUCTION OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE S	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TO AMENICATION OF 1000 FT.	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANK YR IN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	TUMOR SUPPRISSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANK VB IM MOTIFE	TUMOR SUPPRISSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	TUMOR SUPPRISSOR TUMOR SUPPRISOR, CDK4/6 INHIBITOR,	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,
Coumpound		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;
SEQFOL D score											
PMF score		1.00	0.99	0.99	1.00	1.00	1.00	0.98	1.00	1.00	1.00
Verify score		1.08	0.82	0.72	0.43	0.67	0.67	0.13	0.14	0.82	60:0
Psi Blast		3.4e-06	0.00014	4.5e-10	4.5e-36	3e-39	1e-28	3e-34	7.5e-39	1.5e-42	1.5e-41
END		941	935	933	317	164	483	581	614	643	701
STAR T AA		877	875	877	179	24	332	402	433	492	525
CHAI N ID		<b>4</b>	A	Ą							
PDB ID		1b0x	1b4f	1b4f	1bd8	1bd8	1bd8	1bd8	1bd8	1bd8	15d8
SEQ NO:		1504	1504	1504	1504	1504	1504	1504	1504	1504	1504

PDB annotation		ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANK YRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF			COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
Coumpound			P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL	D score										
PMF	score		1.00	0.94	1.00	1.00	0.99	0.53	1.00	0.01	1.00
Verify	score		0.31	0.09	0.50	0.51	0.47	-0.32	0.45	-0.31	0.60
Psi Blast			6e-41	4.5e-39	3e-41	1e-28	1.4e-28	1.2e-37	1.5e-35	1.26-31	1.5e-39
END	AA		167	266	784	800	818	299	317	459	164
STAR	T AA		594	62	644	099	683	95	179	248	26
CHAI	N ID								æ	В	В
PDB	A		1bd8	1bd8	1bd8	1bd8	1bd8	1bd8	1blx	1blx	1blx
SEO	ΑŞ		1504	1504	1504	1504	1504	1504	1504	1504	1504

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PDI: annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHIBITOR PROTEINKINASE)	COMPLEX (INFIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INFIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITÓR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	COMPLEX (PRINETAGE)	PROTEIN/FINASEN INTIDITOR	PROTEIN CVC! IN. DEPENDENT	KINASE, CELL CYCLE 2 CONTROL.	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;		CYCLIN-DEPENDENT KINASE	B;			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;			CYCLIN-DEPENDENT KINASE	6: CHAIN: A: PI9INK4D: CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;				CYCLIN-DEPENDENT KINASE
SEQFOL D score																									
PMF score		1.00		0.99				00.1			_		1.00						00.					5	1.00
Verify score		0.49		0.34				0.72					0.17			-		9	65.0					100	0.04
Psi Blast		4.5e-30		1.5e-41				7.5e-42					4.5e-45					3,	<b>ye-4</b> 0					0 50 00	07-20
END		483		618				643					771					, 65	†ø/					000	3
STAR T AA		332		435				494					594					640	040					660	3
CHAI N ID		<b>a</b>		B				В		-			В					٥	۵				-	ď	7
PDB ID		1blx		Ibix				lblx					1blx					17.	٠					1hly	1
SEQ ID NO:		1504		1504				1504					1504				•	1504	1202					1504	1

PDB annotation	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- NK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
Coumpound	6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE
SEQFOL D score								
PMF score		66:0	0.92	1.00	1.00	1.00	1.00	1.00
Verify score		0.30	0.28	0.85	0.64	0.57	0.63	0.27
Psi Blast		1.4e-28	1.7e-36	1.2e-35	1.4e-32	5.1e-33	6e-35	3e-35
END		818	334	176	640	802	617	164
STAR T AA		683	182	28	496	663	485	49
CHAI N ID		В	A	⋖	Ą	A	Ą	4
PDB ID		1blx	1bu9	15u9	1bu9	1bu9	149s	1d9s
SEQ EQ		1504	1504	1504	1504	1504	1504	1504

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PDE annotation	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HEI IX ANKYPIN PEPEAT	SIGNALING PROTEIN HELIX-TURN-HELIX ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18.	INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6),	ANK I KIN KEPISA I, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE INHIBITOR 818: INF 4C(INK)	ANKYRIN REPLAT. 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	NK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKI KIN KEPEAI, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	I KAINSCKIPTION FACTOR F65;	IXBAFKB COMPLEX		TRANSCRIPTION FACTOR P65	P50D; TRANSCRIPTION FACTOR.	IKB/NFKB COMPLEX	The Association of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of th
Coumpound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B. CHAIN: A:	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: 4:	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;		CYCLIN-DEPENDENT KINASE	o infibil OK; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			NE VADDA D DZE SIBIRITE.	CHAIN: A: NF-KAPPA-B P50D	SUBUNIT; CHAIN: C: I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	D-ALFHA; CHAIN: D;
SEQFOL D score								*										· •								
PMF		1.00	0.45	1.00			1.00				1.00				1.00				90	3			0:30			1 00
Verify score		0.32	0.17	0.40			0.84				89.0				0.47		_		-018	·			-0.38			0.36
Psi Blast		7.5e-38	6e-37	8.5e-36			1.2e-35				1.4e-32				1.7e-32				1 2e-35				1.7e-33			1 5e-48
END		643	770	333			176				640				801				366	) ) )			403			240
STAR T AA		517	585	182			28			,	496				693				156	,			210		<del></del>	28
CHAI N ID		∢	Ą	Ą			∢				∢				Ą	•		-	Ω				Ω			D
PDB ID		ld9s	1d9s	1ihb			lihb				qui				lihb		-		likn			7	likn			likn
SEQ NO:		1504	1504	1504			1504				1504				1504				1504				1504			1504

<b>-</b>		ACTOR,	R P65;	ACTOR,		R P65;	ACTOR,		R P65;	ACTOR,			R P65;	ACTOR,			R P65;	ACTOR,			R P65;	'ACTOR,			IR P65;	ACTOR,			HIN, VK-REPEAT	HIN,
PDB annotation		P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR, IKBANFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN
		P5C IKI	TR			T.			TR	P5(			TR	P5(			TR			1	<u> </u>				TR		_	-	<u> </u>	¥
Coumpound		CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL
		CHAI SUBI B-AL	NF-K	CHA	SUBU B-AL	NF-K	CHA	B-AL	NF-K	CHA	SUBI	B-AI	NF-K	CHA	SUBI	B-AI	NF-K	CHA	SUB	B-AL	NF-K	CHA		B-AI	NF-K	CHA	SUB	B-A1	MYC	MYC
SEQFOL	D score																			_										
PMF	score		0.30			90.0			0.55				0.25				0.92				08.0				0.12				0.98	1.00
Verify	score		-0.26			-0.26			-0.05				-0.36				0.20				-0.05				-0.19				60.0	0.57
Psi Blast			1.4e-30			5 1e-34			6e-60				1.7e-36				1.7e-36				8.5e-40				4.5e-40				3e-35	6e-30
END	Ψ¥		562	}		715	}		775				748	)			817	;			296				396				317	482
STAR	TAA		399	<u>`</u>		505	}		528	)     			558	}			672	;			8				91				213	365
CHAI	NID		0	1		6	j			1			C	1				1			Ω				Ω					
PDB	A		1 iku			1:12			1:ki	į			1.ikm	<u> </u>			1 ikn				1ikn				1 ikn	,			1myo	lmyo
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PDB annotation	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMB. ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ANK-REPEAT MYOTROPHIN,	ANK-REPEAT MYOTROPHIN,	COLOR TWO CTR AND AND THE PEAL	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YKIN Z KEI'EAT HELLIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT), ANKYRIN 2 REPRAT HEI IV	COMPLEX (TRANSCRIPTION	DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG/ANT/ DEG	REGIAIN REFEAT) COMPLEX	REGULATION/ANK REPEAT).	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	OPEGIT ATTOM/ANY PERFATE	REGOLATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
Coumpound		MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NE-K APPA B P65. CUANT. A C.	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	F;	A TO IN A DO A TO A COLUMN TO THE	MF-NAFFA-B F05; CHAIN: A, C;	INF-KAPPA-B P30; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	· · ·	NF-KAPPA-B P65: CHAIN: A. C.	NF.K APPA.B PS0: CHAIN: B.:	I-KAPPA-B-ALPHA; CHAIN; E.	F;		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	···		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B PSO; CHAIN: B, D;	F: F: F: F: F: F: F: F: F: F: F: F: F: F	•
SEQFOL D score																				. 1								
PMF score	,	1.00	1.00	1.00	0.86	0.58				0.03	2				0.36					0.96					0.41			
Verify score		0.51	0.03	99.0	0.57	-0.11				-0.17					-0.34				,	-0.01				90	0.08			
Psi Blast	00	3e-39	1.5e-38	7.5e-39	6.8e-25	6.8e-36				1.56-40					1.2e-44				+	5.1e-33				Ť	1.36-30			
END	777	044	165	794	799	366				424	·				458				,67	504				637	770			
STAR T AA	903	976	- 61	681	684	154				154					208				000	503				375	3			
CHAI N ID						Ε				Е	_	•			ш				p	<u></u>				ц	,			
PDB ID	1 man	oć ililiyo	Imyo	1myo	lmyo	Infi				lnfi			_		Infi				1.00					Infi				
SEQ ID NO:	1504	+ OC 1	1504	1504	1504	1504				1504					1504				1504	-				1504				

PDB annotation	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
Coumpound	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;
SEQFOL D score							
PMF score	0.95	1.00	66:0	1.00	0.49	1.00	0.98
Verify score	0.08	0.35	0.34	-0.06	-0.13	0.22	0.12
Psi Blast	3e-45	5.1e-37	1.7e-32	6e-57	1.3e-54	1.7e-36	6.8e-40
END	643	628	682	777	307	817	296
STAR T AA	429	463	490	528	19	672	88
CHAI N ID	ம	ഥ	ជា	ជា	ជ	ш	旦
PDB	1nfi	lnfi	Infi	Infi	Infi	Infi	Infi
SEQ US	1504	1504	1504	1504	1504	1504	1504

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PDB annotation	ANKYRIN 2 REPEAT HELIX	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION,	EPH RECEPTORS, TYROSINE 2	TRANSPHORYLATION, SIGNAL	PROTEIN 3 KINASE	TYROSINE-PROTEIN KINASE NMR,	RECEPTOR OLIGOMERIZATION, FPH PECEPTOR'S TYPOGENERS	PHOSPHOP VI ATION STONAL	TRANSDUCTION, TYROSINE.	PROTEIN 3 KINASE	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MOIATION, 3	ONCOGENE/ANKYRIN REPEATS)
Coumpound		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;				EPHRIN TYPE-B RECEPTOR 2;	CHAIN: NULL;				REGULATORY PROTEIN SWI6;	CHAIN: A, B;		P53; CHAIN: A; 53BP2; CHAIN:	B;								Pos; CHAIN: A; 53BP2; CHAIN:	B;						
SEQFOL D score												-				•														
PMF score		0.84				0.59					0.18		, , ,	U.84								5	90.1					··		·
Verify score		0.65				0.78					-0.22				-							0.03								
Psi Blast		0.00034				1.5e-09					be-3/		60.30			•	-			-		1 50.40								
END		935			000	933				,	+8/		260	5						-	· <del>-</del>	777	!					-		
STAR T AA		875			2000	//8				203	170		366	2					•			828	)							
CHAI N ID										_	₹		THE STREET	·								B	····							
PDB ID		Isgg			1995	9881				1000	OM C		lvcs	-								lycs	_							
SEQ ID NO:		1504			1507	+ OC -				1504			1504									1504								

PDB annotation	CONTENT TO VANITE	COMPLEA (AN II- COMPLEA (AN II- CONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	HYDROLASE TETRATRICOPERTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION			CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL
Coumpound	**************************************	P53; CHAIN: A; 53BP2; CHAIN: B;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN:
SEQFOL	D score							
PMF	score	0.76	0.05	0.13	0.82	-0.03	0.31	-0.02
Verify	score	0.01	-0.10	-0.76	-0.25	0.02	0.05	0.00
Psi Blast		7.5e-39	1.7e-29	3e-14	6e-14	3.46-14	6.8e-22	1.5e-11
END	AA	254	190	262	262	191	161	110
STAR	TAA	29	39	218	221	40	39	24
CHAI	OL N	m .				М	⋖	A
PDB	e	1ycs	1a17	1bor	Ichc	1e96	1efr	lelw
SEO	A Ö	1504	1507	1507	1507	1507	1507	1507

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PDI3 annotation	REPEAT, HSC70, 2 HSP70, PROTEIN	CHAPERONE F.OP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL PEPTING T. HSC70, 2 HSP70, PROTEIN	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER CALLON	DNA-BINDING PROTEIN V(D)J DNA-BINDING PROTEIN V(D)J PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC	FINGER, DNA-131NDING PROTEIN	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGE N) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGE N) PHETIN/ATCHE	ANTIBODY COMPLEX	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,	HOMOPHILIC ADHESION INSECT IMMUNITY INSECT	IMMUNITY, LPS-BINDING, HOMOPHILIC A DHESTON	INSECT IMMUNITY INSECT
Coumpound	C, D;	TPR I-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	RAGI; CHAIN: NULL;		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;		HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;		HEMOLIN; CHAIN: A, B;
SEQFOL D score												124.44
PMF score		0.24	0.37	0.84		0.64		0.39	0.49	96.0		
Verify score		0.13	-0.20	0.13		-0.07	,	× I.O	0.34	0.29		
Psi Blast		1.4e-21	4.5e-13	9e-17	$\Pi$	8.5e-18	7	5.Ie-43	1.5e-43	1.7e-50 (		1.7e-50
END		153	262	302		531	007	070	721	812		813
STAR T AA		39	221	210		352	750	707	350	449		450
CHAI N ID		¥	A		,	<b>-</b>		:	∢	V		∢
PDB ID		lelw	1g25	Irmd	$\vdash$	jadq	17:17		1bih	1bih	$\dashv$	Ioin
SEQ ID NO:		1507	1507	1507	1600	8061	1508		1508	1508	$\dashv$	1300

PDB annotation		HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHLIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD,	TRANSMEMBRANE,	LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL ADHESION	CELL ADHESION NEURAL CELL
Coumpound			HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	HEMOLIN; CHAIN: A, B;	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN:	NULL;		AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;	AXONIN-1; CHAIN: A;
SEQFOL	D score																
PMF	score		-0.07	0.36	0.49	0.21	0.42			0.53	0.41	0.62	-0.01	0.84	0.70	-0.08	-0.02
Verify	score		0.00	0.15	0.06	0.18	0.42			-0.05	0.07	0.15	0.08	0.26	0.24	0.05	0.07
Psi Blast			5.1e-37	6.8e-40	4.5e-37	3.4e-46	1.5e-15			8.5e-49	1.5e-49	5.1e-63	1e-44	3.4e-55	5.1e-49	6.8e-37	7.5e-39
END	· AA		335	1073	447	1184	723			535	628	721	347	813	897	448	448
STAR	TAA		4	726	74	816	557			178	262	348	3	449	536	64	74
CHAI	OI N		A	A	A	A				Ą	⋖	A	A	V V	A	A	A
PUB	1		1bih	1bih	1bih	1bih	1cdy			1cs6	1cs6	1cs6	1cs6	1cs6	1cs6	1cs6	1cs6
OAS	j e ș	Ö	1508	1508	1508	1508	1508			1508	1508	1508	1508	1508	1508	1508	1508

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PDB annotation	ADHESION	CELL ADHESION NEURAL CELL ADHESION	GROWTH FACTOR/GROWTH	IMMUNOGIORII IN-I IKE SIGNAI	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	TRANSDICTION 2 DIVERIZATION	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	Chowing a constant	GROWIH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	TB ANEDITOTION OF THE CONTROLL OF THE CONTROLL OF THE CONTROLL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF	GROWTH EACTION, 2 DIMERIZATION,	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEP'TOR FGF, FGFR.	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH
Coumpound		AXONIN-1; CHAIN: A;	FIBROBLAST GROWTH FACTOR 2: CHAIN: A B:	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FACTOR RECEPTOR 1. CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	رن ن	FIBEOBI A ST CBOWNEY	FACTOR 2: CHARLA P.	FIREORI AST GROWTH	FACTOR RECEPTOR 1: CHAIN:	C. D.		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;	To the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of th	FIBROBLAST GROWTH
SEQFOL D score																			•	-	•								
PMF		0.24	-0.01				-0.19					0.30					-0.15	;					0.21					750	0.04
Verify score		0.04	0.13				80.0				,	-0.16					0.23	}					0.17		_			50.0	
Psi Blast		8.5e-48	1.7e-38				5.1e-21					6.8e-21					3.4e-17						5.1e-23			•••		8 5p. 38	1
END		1185	1184				1260				246	340					146						535					863	777
STAR T AA		829	1009			,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1096				170	0/1	-				2	~		-			361		-			450	
CHAI N ID		A	ပ			(	ر.					<del></del>			-		C					,	 رد					U	
PDB ID	,	lcs6	Icvs				ICAS		<del>-</del>	<del></del>	10.00						lcvs	-				十	SASI			•		lcvs (	1
SEQ NO:		1508	8061			1508	9000				1508	200					1508					1500	900					1508	1
																	_	_											

PDB annotation	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR/GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH
Coumpound	FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;
SEQFOL D score						
PMF		0.27	0.21	-0.05	-0.15	90.0
Verify score		-0.10	-0.42	0.07	0.05	0.23
Psi Blast		5.1e-24	8.5e-36	1.7e-24	1.7e-37	5.1e-34
END		260	812	968	966	1184
STAR T AA		61	642 .	737	813	1009
CHAI N ID		U	O	ပ	U	Q
PDB		lcvs	lcvs	lcvs	lcvs	lcvs
SEQ ID		1508	1508	1508	1508	1508

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PD/3 annotation	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	I RAINSDOCTION, Z DIMEKIZATION, GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL TP ANSPHICTION 2 DIMEBITA THOSE	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEIPTOR FGF, FGFR,	IMMUNOGLOBULIN-LIKE, SIGNAL	TRANSDUCTION, 2 DIMERIZATION,	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR	GROWTH FACTOR/GROWTH	FACTOR RECEITOR FGF, FGFR,
Coumpound		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH FACTOR RECEPTOR 1. CHARI.	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH FACTOR RECEPTOR 1: CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:	C, D;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B;	FIBROBLAST GROWTH	FACTOR RECEPTOR 1; CHAIN:			FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH
SEQFOL D score															•		-													
PMF score		0.82				0.01					-0.05					200	0.25											1	0.30	
Verify score		-0.19				0.15					0.19					01.0	61.0					500	-0.02		,	-		,	61.0	
Psi Blast		1.2e-21			1	1.7e-33				,	6.8e-19					0 50 75	0.36-23		_			3 10 35						$\dagger$	77-97.1	
END		346			1	447				<u>``</u>	140	-				252	CCC				•	809	070					000	707	
STAR T AA		178				271				,	7					361	100					450	2					17	<del></del>	
CHAI N ID	_	a			4	a					<b>a</b>					-	j					2	1					-	<u> </u>	
PDB ID		Icvs			1	ICVS				13.52	ICVS					1 cve	2	-				lcvs	2					10.70		
SEQ ID NO:	3000	8000			1500	1208				1500	000					1508	3					1508	3					1508	2	

PDB annotation		GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR			GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR		YIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS,
Coumpound	FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2;
SEQFOL D score							
PMF score		0.00	0.04	-0.11	0.00	0.03	0.16
Verify score		-0.31	0.11	0.04	0.20	-0.35	-0.09
Psi Blast		1.2e-36	1.7e-25	3.4e-34	3.4e-23	6e-22	1.3e-23
END		812	968	966	1082	810	688
STAR T AA		642	737	813	911	602	641
CHAI N ID		Q	Ω	Q	Q	ಜ	M.
PDB ID		lcvs	lcvs	lcvs	lovs	1dgi	1dgi
SEQ ID	2	1508	1508	1508	1508	1508	1508

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PD 8 annotation	ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRTISIVIR AT PROTEIN PECEPTOP	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2	POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN RECEPTOR	CELL ADHESTON NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULN FOLD,	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	CELL ADHESION NCAM; NCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCAM, INCA	CELL ADHESION NCAM; NCAM,	GLY COPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN GROWTH FACTOR/GROWTH FACTOR PECENTOR FORM
Coumpound	CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4;	CHAIN: 4;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2: CHAIN: A B C D:
SEQFOL D score												
PMF		0.00		0.30	0.42	0.22	0.92	0.07	66.0	0.01	0.75	0.24
Verify score		-0.36		0.02	0.11	0.09	0.34	0.23	0.02	0.16	0.25	-0.16
Psi Blast		3.4e-18		6.8e-17	5.1e-28	3.4e-17	3e-24	3.4e-25	1.7e-20	4.5e-22	6.8e-19	1e-29
END		1184		346	433	517	645	722	798	766	982	447
STAR T AA		902		178	266	354	452	539	644	815	818	271
CHAI N ID		<b>ಜ</b>		₹	A	A	A	A	A	Ą	V.	E
PDB ID		Idgi	,	lepf	1epf	lepf	lepf	lepf	lepf	lepf	lepf	lev2
SEQ ID NO:		1508		1508	1508	1508	1508	1508	1508	1508	1508	1508

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PDB annotation	IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBUL.N (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;
SEQFOL D score						
PMF score		0.04	0.07	-0.11	0.01	0.43
Verify score		0.10	-0.05	90.0	0.10	0.02
Psi Blast		5.1e-22	le-33	1.7e-31	5.1e-35	8.5e-21
END		535	628	966	1188	350
STAR T AA		361	454	825	1009	178
CHAI N ID	3	ம்	ш	ம	Ð	g
PDB ID		lev2	lev2	lev2	lev2	lev2
SEQ	SON SON	1508	1508	1508	1508	1508

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PDB annotation	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B. TUBEDIL FOR D	GROWTH FACTION FOLD GROWTH FACTION GROWTH FACTOR RECEIPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B-TREEDIL FOLD	GROWTH FACTION GROWTH FACTOR RECEIPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELCONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEITOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BEL()NGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTOR/GROWTH GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELCINGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B. TEFFOI FOIL	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBIJLIN (IG)LIKE DOMAINS BELONGING TO THE I.
Coumpound	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN:
SEQFOL D score						
PMF	-0.05	0.18	69.0	0.06	0.53	0.17
Verify score	0.01	0.13	0.41	-0.02	0.23	0.12
Psi Blast	8.5e-18	1.2e-32	6.8e-24	6.8e-34	1.7e-23	1.2e-21
END	152	451	538	628	724	264
STAR T AA		271	361	454	549	19
CHAI N ID	Ð	Ö	_D	Ð	ڻ ن	D
PDB ID	1ev2	lev2	lev2	1ev2	1ev2	lev2
SEQ ID NO:	1508	1508	1508	1508	1508	1508

PDB annotation	Like a CA Constant	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FOF 2; FOF RZ;	IMIMONOGLOBOLIN (19)LINE	CET 2 CITIES DELCINOLING TO THE 1-	DOMAINS B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH	FACTOR RECEPTOR FGF2; FGFR2;	IMMUNOGLOBULIN (IG)LIKE	DOMAINS BELONGING TO THE I-	SET 2 SUBGROUP WITHIN IG-LIKE	DOMAINS, B-TREFOIL FOLD	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1;
Coumpound		Е, Ғ, G, Н;	FIBROBLAST GROWTH FACTOR 2: CHAIN: A. B. C. D:	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	r, r, g, ri,	FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROW IH	FACTOR RECEPTOR 2; CHAIN:	ָּהָ הָיָלְיּהָיּ הַיִּילִי	RIBPORT AST GROWTH	FACTOR 2: CHAIN: A. B. C. D:	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH	FACTOR 2; CHAIN: A, B, C, D;	FIBROBLAST GROWTH	FACTOR RECEPTOR 2; CHAIN:	E, F, G, H;		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B;
SEQFOL	D score																													
PMF	score		0.15				0.23					130						-0.15						-0.01						0.33
Verify	score		-0.35				0.08					9	0.10					0.04						0.02						-0.26
Psi Blast			6.8e-34				3.4e-25					00	1.58-22					1 7e-33						6.8e-22						5.1e-21
END	AA		816				900					9.50	607			_		1000	}					1087						346
STAR	TAA		651				737						4/					825	3					911	:					178
CHAI	N ID		U				Ð						<u>ت</u>					و	,					ď	)					U
PDB	А		lev2				lev2						lev2					101/2	7647					1ev2	2					1evt
SEO	e è		1508				1508						1508					1500	200					1508	200					1508

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PDE annotation	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B-TREFOII FOID	GROWTH FACTOR/GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTOR/GROWTH FACTOR RECEITOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELÜNGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTIOR/GROWTH FACTOR RECEITOR FGF1; FGFR1; IMMUNOGLOB'ULIN (1G) LIKE DOMAINS BELONGING TO THE 1- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELCINGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELCNGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS B TREEDIT FOR I
Coumpound	FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR I; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR I; CHAIN: C, D;
SEQFOL D score						
PMF score			-0.09	0.18	0.19	0.04
Verify score		0.01	0.23	-0.15	-0.01	0.16
Psi Blast		8.5e-32	3.4e-19	3.46-33	3e-16	1.2e-22
END		447	146	628	703	260
STAR T AA		271	2	450	552	61
CHAI N ID		ပ	ပ	ن ن	U	O
PDB ID		levt	levt	levt		levt
SEQ ID NO:		1508	1508	1508	1508	1508

PDB annotation	HEART GOT GOTO LE TIMINO CO.	GROWTH FACTORGROW IN FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	GROW IN FACTOR/GROW IN FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD	IMMUNE SYSTEM FC-EFSILON KI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EFSILON KI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON KI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD,
Coumpound		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON
SEQFOL	D score	·							
PMF	score	0.11	-0.03	0.06	0.48	0.92	0.63	0.17	0.12
Verify	score	-0.32	0.05	0.14	0.32	0.26	-0.01	0.05	0.04
Psi Blast		1.4e-35	1.2e-24	1.5e-17	3e-21	1.5e-20	9e-18	1.7e-21	3e-19
END	AA —	812	968	538	153	539	727	795	006
STAR	TAA	642	737	349	39	415	909	646	611
CHAI	N N	U	U	A	A	Ą	4	4	A
PDB	<u>e</u>	levt	levt	1£2q	1£2q	129	1f2q	1f2q	1f2q
SEQ	ΑŞ	1508	1508	1508	1508	1508	1508	1508	1508

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PDJ3 annotation	GLYCOPROTEIN, RECEPTOR, IGE-	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD.	GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SÝSTEM HIGH AFFINITY IGE-FC RECEP/FOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD,	GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIRODY 1GR-FC	IMMUNE SYSTEM HIGH AFFINITY	IGE-FC KECEP LOK, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD.	GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTIEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON)	IGE-FC; IMMUNIOGLOBULIN FOLD, GILYCOPROTEIN RECEPTOR 1GE	BINDING 2 PROTEIN, IGE	MMUNE SYSTEM HIGH AFFINITY	IGE-FC RECEPTOR, FC(EPSILON)	GLYCOPROTEIN RECEPTOR ICE	BINDING 2 PROTEIN, IGE	ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR FOCEPSII ON
Coumpound	RECEPTOR CHAIN: A;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG	EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG	EFSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY	RECEPTOR CHAIN: A; IG	EPSILON CHAIN C REGION; CHAIN: B, D;		HIGH AFFINITY IMMUNOGLOBULIN EPSILON	RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION:	CHAIN: B, D;	HIGH AFFINITY	IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A: 10	EPSILON CHAIN C REGION:	CHAIN: B, D;	HIGH ARRESTEN	HIGH AFFINITY IMMUNOGLOBULIN EPSILON
SEQFOL D score																		
PMF score		0.01		-0.02		0.30	•		,	0.24			0.70				200	
Verify score		-0.01		60.0		0.16			200	0.35			0.21	<del> :</del> -			0.37	
Psi Blast		3.4e-19		3.4e-17		6e-21			000		<del></del>		7.5e-19				7.5e-19	
END		430		938		152			530	occ			645		•		726	
STAR T AA		258	0.50	346		36			415	?			451				566	
CHAI N ID		∢		€		<del></del> -			4				A				A	
PDB ID		1f6a	239-1			Iroa	- <u> </u>		1669				1f6a   1			··	1f6a /	_
SEQ ID NO:		1508	1500	8000	002	8007			1508				1508				1508	

PDB annotation	G logic man room as on so.	IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE-ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE- BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR,
Coumpound		RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;
SEQFOL	D score							
PMF	score		-0.11	0.11	0.10	0.65	0.55	0.86
Verify	score		0.20	-0.14	0.27	0.11	0.38	0.28
Psi Blast			1e-16	1.4e-20	1.5e-19	1.5e-15	1.2e-17	3e-19
END	AA		152	795	006	666	534	148
STAR	T AA		\$	646	740	821	349	37
CHAI	N ID		A	4	4	K	4	A
PDB	<u>e</u>		1f6a	1f6a	1f6a	1f6a	1fcg	1fcg
SEQ	ВŞ		1508	1508	1508	1508	1508	1508

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PDE annotation	IMMUNOGLOULIN, LEUKOCYTE,	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE,	IMMUNOGLOULIN, LEUKOCYTE,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN DAMENOGLOBULIN FOLD, BETA	CONTRACTILE PROTEIN CONTRACTILE PROTEIN DAMENOGLOBULIN FOLD, BETA	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-	LINE, NECETIOR IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN- 1 RF PECEPTOR	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN- BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4	GLICOSTLAIED PROTEIN
Coumpound		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	TELOKIN; CHAIN: A	TELOKIN; CHAIN: A	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: 4.	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: 4:	ENVELOPE PROTEIN B120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3
SEQFOL D score									
PMF score		0.43	0.53	0.03	0.00	0.54	0.41	0.60	90.0
Verify score		0.02	-0.26	0.20	-0.28	0.29	0.03	0.17	-0.34
Psi Blast	·	6e-19	6.8e-17	8.5e-16	8.5e-17	3e-18	3.4e-16	1.7e-15	6e-19
END		645	266	1186	447	148	796	518	703
STAR T AA		456	820	1085	347	36	646	352	557
CHAI N ID		Ą	¥	A	Ą	¥	¥.	J	A
PDB ID		1fcg	1fcg	1fhg	1fhg	Iful	IÆ.	lgc.l	1hng
SEQ ID NO:	,	1508	1508	1508	1508	1508	1508	1508	1508

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		COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN		
. Motoritation and an observed	T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	TWITCHIN; CHAIN: NULL;	LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	IMMUNOGLOBULIN
D score							104.67	
score	0.17	0.18	0.09	0.55	0.59	09:0		0.23
score	90.0	-0.02	0.42	0.10	0.14	0.20		-0.05
	9e-15	1.5e-20	3e-20	1.7e-15	3.4e-14	8.5e-16	5.1e-17	1.5e-17
AA	966	679	966	994	1185	531	543	884
TAA	825	462	740	747	1084	355	143	538
e E Z	۲ '	В	В	д		A	Н	H
<u>a</u>	Ihng	litb	litb	litb	Ikoa		1mco	1mco
АŞ	1508	1508	1508	1508	1508	1508	1508	1508
	ID NID TAA AA score score D score	ID   N ID   T AA   AA   Score   Score   D Score   D Score   D SCORE   T LYMPHOCYTE ADHESION   GLYCOPROTEIN CD2 (RAT)   1 HNG 3	D	Ihrig   A   825   996   9e-15   0.06   0.17   TLYMPHOCYTE ADHESION   GLYCOPROTEIN CD2 (RAT)   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3   IHNG 3	Ihrig   A   825   996   96-15   0.06   0.17   TLYMPHOCYTE ADHESION   GLYCOPROTEIN CD2 (RAT)   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3   IHRIG 3	Ihng   A   825   996   9e-15   0.06   0.17   TLYMPHOCYTE ADHESION   CLYCOPROTEIN CDZ (RAT)   IHNG   THNG   TLYMPHOCYTE ADHESION   CLYCOPROTEIN CDZ (RAT)   IHNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG   THNG	Ihng   A   825   996   96-15   0.06   0.17   TLYMPHOCYTE ADHESION   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   IHNG   GLYCOPROTEIN CD2 (RAT)   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYCOPROTEIN CD3   GLYC	Ihr   B   740   996   9-17   0.06   0.17   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION   CLYMPHOCYTE ADHESION

		<del></del>								_														
PDB annotation		MUSCLE PROTISIN CONNECTIN,	GLYCOPROTEIN,	TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD.	ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTIEN	MUSCLE PROTIIN CONNECTIN,	NEXTMS; CELL ADHESION,	TRANSMEMBRANE, REPEAT	BRAIN, 2 IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING, SIGNAL, 3	MISCIE PROTEIN CONNECTES	NEXTM5: CELL ADHESION	GLYCOPROTEIN,	TRANSMEMBRANE, REPEAT,	BRAIN, 2 IMMUNOGLOBULIN FOLD,	ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN	MUSCLE PROTEIN CONNECTIN,	NEXTMS; CELL ADHESION,	TO ANGMENTE DEPENDE	BRAIN 2 IMMINOGIODETT IN ECT.	ALTERNATIVE (SPLICING, SIGNAL, 3	MUSCLE PROTEIN	INHIBITORY RECEPTOR KILLER	CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR NATIRAL
Coumpound	IMMUNOGLOBULIN GI (IGGI) (MCG) WITH A HINGE DELETION IMCO 3	TITIN; CHAIN: NULL;				TITIN; CHAIN: NULL;					TITIN: CHAIN: NITI.1:						TITIN; CHAIN: NULL;						P58-CL42 KIR; CHAIN: NULL;	
SEQFOL D score									•								-		•	-				
PMF score		0.53				0.00					-0.12						0.04						-0.07	
Verify score		0.58				-0.53					0.16						0.46				•	;	11.0	
Psi Blast		1.7e-14	•			3.4e-11					5.1e-15					1	1.7e-13					1	3.4e-10	
END		1185				262					449						721					5	149	
STAR T AA		1086				178					349						643					70	3	
CHAI N ID						_												-						
PDB ID		Inct				Inct					lnct						1301					125	1	
SEQ ID NO:		1508			900	1208					1508					1500	9061					1508	3	

PDB annotation	KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD					CELL ADHESION PROTEIN VCAM- D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	CELL ADHESION PROTEIN VCAM-
Coumpound		P58-CL42 KIR; CHAIN: NULL;	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	MUSCLE PROTEIN TITIN MODULE MS (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	HUMAN VASCULAR CELL
SEQFOL D score								
PMF score		0.13	0.35	0.00	-0.15	0.04	0.72	0.00
Verify score		-0.01	0.63	-0.22	0:30	0.50	-0.05	-0.15
Psi Blast		1.7e-23	1.7e-14	3.4e-11	1.5e-09	1.7e-13	4.5e-15	4.5e-13
END		995	1185	262	19	721	538	089
STAR T AA		813	1088	178	7	643	397	557
CHAI N ID							A	A
PDB ID		Inkr	ltnm	Ltnm	1tmm	ltnm	lvca	Ivca
SEQ		1508	1508	1508	1508	1508	1508	1508

								.,												
DI,2; IVCA 6 INIMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD,	TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC I IPOPROTEIN POI VAZORPHISM	GLYCOPROTEIN CD4;	IMMONOGLOBULIN FOLD, TRANSMEMBRANE,	GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM	CELL ADHESION ICAM-2;	IMMUNOGLOBULIN FOLD, CELL	ADHESION, GLYCOPROTEIN, 2 TRANSMEMBRANE, REPEAT.	SIGNAL	IMMUNE SYSTIM P58 NATURAL	KILLER CELL RECEPTOR; KIR,	NATOKAL KILLEK KECEPTOK,	IMMUNOGLOBIJLIN	IMMUNE SYSTEM P58 NATURAL	KILLER CELL RECEPTOR; KIR,	NATURAL KILLER RECEPTOR,	INHIBITORY RECEPTOR, 2	IMMUNE SYSTEM P58 NATURAL
ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN:	A, B;	T-CELL SURFACE	GET COPROTEIN CD4; CHAIN: A, B;		INTERCELLULAR ADHESION	MOLECULE-2; CHAIN: NULL;			MHC CLASS I NK CELL	KECEFIOR PRECURSOR;	Circuit: A,		MHC CLASS I NK CELL	RECEPTOR PRECURSOR;	CHAIN: A;	•	MHC CLASS I NK CELL
				-								-						-		
	0.41		0.13	-	0.68			0.05				-0.09				0.05				0.19
	0.09		-0.11		90.0			-0.09				0.19				0.28				0.00
	1.2e-26		6e-26		6e-23			1.5e-16				1.2e-19				4.5e-24				3e-16
	703		882		1068			1000				534				643				723
	364		552		740			821			2,5	347				451	-		•	536
	∢		∢		Ą							∢				∢	•			A
	1wio		Iwio		lwio			1zxq			:::0	 II ₀ 7		•		Zdlı				2dli
	1508		1508		1508			1508			96.56	onci				8061				1508
	ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	A 364 703 1.2e-26 0.09 0.41 T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5  A 364 703 1.2e-26 2.09 0.41 T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	1 wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;	Iwio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           Iwio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           6LYCOPROTEIN CD4; CHAIN:         A, B;           7-CELL SURFACE         GLYCOPROTEIN CD4; CHAIN:         A, B;	Iwio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           Iwio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;           A, B;         CLYCOPROTEIN CD4; CHAIN:           A, B;         A, B;	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1xq         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1xq         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           3xq         A         3xq         3xq         3xq         3xq         3xq           1xq         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1xq         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1xq         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1xq         A         740 </th <th>1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;           1zxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           1xxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           1xxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION</th> <th>1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;         A, B;           1zxq         821         1000         1.5e-16         -0.09         0.05           1zxq         MOLECULE-1; CHAIN: NULL;         MOLECULE-2; CHAIN: NULL;         1.5e-16         -0.09         0.05</th> <th>Iwio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           Iwio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;           Izxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           Au         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           Au         MOLECULE-2; CHAIN: NULL;         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION</th> <th>1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.18         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1zxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           2dir         A         347         534         1.2e-19         0.19         -0.09         0.09</th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE</th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5    </th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE    </th> <th>  Iwio   A   364   703   1.26-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5   1.26-26   0.011   0.13   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; B; B; B; B; B; B; B; B; B; B; B; B;</th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5    </th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; IVCA 4 CHAIN: A, B; IVCA 5 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; 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IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA</th> <th>  Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   1.VCA 4 CHAIN: A, B; 1VCA 5     Iwio   A   552   882   6e-26   -0.11   0.13   T-CELL SURFACE     Iwio   A   740   1068   6e-23   0.06   0.68   T-CELL SURFACE     Iwio   A   740   1068   6e-23   0.06   0.08   T-CELL SURFACE     Iwio   A   740   1.5e-16   -0.09   0.05   INTERCELLULAR ADHESION     Izxq  </th>	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;           1zxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           1xxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           1xxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;         A, B;           1zxq         821         1000         1.5e-16         -0.09         0.05           1zxq         MOLECULE-1; CHAIN: NULL;         MOLECULE-2; CHAIN: NULL;         1.5e-16         -0.09         0.05	Iwio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           Iwio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           Iwio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           GLYCOPROTEIN CD4; CHAIN:         A, B;         A, B;           Izxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           Au         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           Au         MOLECULE-2; CHAIN: NULL;         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION	1wio         A         364         703         1.2e-26         0.09         0.41         T-CELL SURFACE           1wio         A         552         882         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.13         T-CELL SURFACE           1wio         A         740         1068         6e-26         -0.11         0.18         T-CELL SURFACE           1wio         A         740         1068         6e-23         0.06         0.68         T-CELL SURFACE           1zxq         821         1000         1.5e-16         -0.09         0.05         INTERCELLULAR ADHESION           2dir         A         347         534         1.2e-19         0.19         -0.09         0.09	Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A   B; IVCA 5   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE   CELL SURFACE	Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5	Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE	Iwio   A   364   703   1.26-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5   1.26-26   0.011   0.13   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; B; B; B; B; B; B; B; B; B; B; B; B;	Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; 1VCA 5	Iwio   A   364   703   1.2e-26   0.09   0.41   T-CELL SURFACE   1.2e-26   0.09   0.41   T-CELL SURFACE   GLYCOPROTEIN CD4; CHAIN: A, B; IVCA 4 CHAIN: A, B; IVCA 5 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A, B; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; IVCA 6 CHAIN: A; 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PDB annotation	KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITOR Y RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM PS8 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR,
Coumpound	RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;	FC GAMMA RIIB; CHAIN: A;
SEQFOL D score												
PMF score		0.23	-0.06	-0.06	-0.02	0.27	0.75	0.65	0.65	0.47	0.00	-0.05
Verify		0.20	0.22	0.17	0.01	0.25	0.28	-0.04	0.19	0.38	0.04	0.08
Psi Blast		3e-21	1.2e-09	5.1e-22	7.5e-15	3.4e-18	7.5e-21	3e-20	1.2e-16	3e-20	3.4e-17	4.5e-19
END		256	148	991	349	537	151	536	724	868	666	866
STAR T AA		19	7	813	152	349	37	415	528	740	820	825
CHAI N ID		А	4	Æ	A	₹.	A	<b>∀</b>	A	A	A	Ą
PDB ID		2dli	2dli	2dli	2fcb	2fcb	2fcb	2fcb	2fcb	2fcb	2fcb	2fcb
SEQ ID	.OX	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508	1508

PDIs annotation	FC, CD32, IMMUNE SYSTEM	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL	TOTAL STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE		HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY 2 PMR FESTER A SEE	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA	HYDROLASE HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMBR, 2 EIYDROLASE FOLD,	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
Coumpound		FC GAMMA RIIB; CHAIN: A;	NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGGI (LAMBDA, HIL) 8FAB 3		PARA-NITROBENZYL ESTERASE; CHAIN: A;	ACETYLCHOLINESTERASE; CHAIN: A;	ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	CHOLESTEROL ESTERASE; CHAIN: NULL;
SEQFOL D score									
PMF score		0.70	0.12	0.47		0.22	0.12	0.43	0.06
Verify score		0.00	0.42	0.05		-0.24	-0.23	-0.29	-0.50
Psi Blast		3e-18	1.7e-12	5.1e-18		9e-13	1e-21	5.1e-22	3.4e-19
END	,	9801	722	529		64	73	73	74
STAR T AA		716	642	353		4	೮	E.	3
CHAI N ID		∢ .	<	A		<b>V</b>	∢	∢	
PDB ID	1-30	7ICD	3ncm	8fab		16/j	lea5	Imaa	2bce
SEQ ID NO:	1500	1500	1508	1508		0161	1510	1510	1510

PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	PRO REGION PRO REGION, FOI DASP PROTEIN FOI DING.	SERINE PROTEASE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX	BUNDLE	COMPLEX (INHIBITOR/NUCLEASE),	COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE),	MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
Coumpound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	ADR1; CHAIN: NULL;	ADR1; CHAIN: NULL;	ALPHA-LYTIC PROTEASE;	Chaint A, B, C,	SYNTAXIN-1A; CHAIN: A, B, C;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN;	CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN;	CHAIN: B, E;
SEQFOL D score												
PMF score	-0.11		0.03	-0.20	-0.19		60:0		1.00		1.00	
Verify score	0.14.		-0.78	60.0	0.03		-0.01		0.21		0.34	
Psi Blast	3.4e-08		5.1e-11	1.7e-11	4.5e-10		4.5e-09		5.1e-25		3e-34 ·	
END AA	274		39	446	166		543		200		469	
STAR T AA	241			403	81		432		164		243	
CHAI N ID	Ð				A		A		₽		Ą	
PDB OI	Imey		2adr	2adr	2pro		lez3		la4y		1a4y	
SEQ ID NO:	1512		1512	1512	1514		1515		1521		1521	

PDl3 annotation	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (INHIBITORNUCLEASE) COMPLEX (INHIBITORNUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB
SEQFOL D score			113.01				
PMF score	1.00	0.95		0.90	0.48	0.39	0.19
Verify score	0.51	0.05		-0.03	-0.27	-0.30	0.07
Psi Blast	3e-35	3.4e-24	6.8e-32	6.8e-32	1.2e-23	1.7e-21	1.7e-10
END	469	407	496	471	438	495	474
STAR T AA	282	2	2	986	267	316	350
CHAI N ID	<b>4</b>	٧	¥	A	∢	A	4
PDB ID	1a4 <i>y</i>	la4y	1a4 <i>y</i>	la4y			1dce
SEQ ID NO:	1521	1521	1521	1521	1521	1521	1521

PDB annotation	ATM IA THE CHIMEN AND A PARTY	FORM YLME I HIONINE, ALFRA SUBUNIT, BETA SUBUNIT	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION RNAIP; KANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL MEROHEDRY	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN
Coumpound		GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;
SEQFOL	D score					•		
PMF	score		0.39	0.28	0.03	0.51	0.55	0.98
Verify	score		-0.04	-0.07	0.00	0.08	-0.08	0.17
Psi Blast			1.5e-06	1.5e-06	1.7e-12	8.5e-13	6.8e-19	5.1e-21
END	AA		471	471	512	514	814	474
STAR	T AA		401	401	254	323	157	215
CHAI	OI N		A	В	A	Ą	A	A
PDB	А		1fo1	1f01	1fqv	1fs2	lyrg	lyrg
SEO	A S		1521	1521	1521	1521	1521	1521

<del>T</del>				
FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, MEROHEDRAL TWINNING,	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL	TRANSCRETTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, 3 HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLESNI/ANGIOGENIN INHIBITOR ACETYLATION,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE//ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;
			109.97	
	0.55	0.28		0.81
	0.11	0.10		0.12
	4.5e-30	3.4c-09	8.5e-46	8.5e-46
	469	508	491	511
	243	348	42	68
	A	∢		
	l yrg	lyrg	2bnh	2bnh
	1521	1521	1521	1521
		Jyrg A 243 469 4.5e-30 0.11 0.55   GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	Lyrg   A   243   469   4.5e-30   0.11   0.55   GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A,	1   1yrg   A   243   469   4.5e-30   0.11   0.55   GTPASE-ACTIVATING CHAIN: A, B;

PDB annotation	A CAMPAGE OF STREET	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2
Coumpound		TROPOMYOSIN; CHAIN: A, B, C, D	COLICIN IA; CHAIN: NULL;	SYNTAXIN-1A; CHAIN: A, B, C;	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHI.; CHAIN: C, F, I, L;
SEQFOL	D score								
PMF	score	-0.20	-0.20	-0.14	-0.20	1.00	0.62	0.99	1.00
Verify	score	0.46	0.36	0.36	0.11	0.78	0.21	0.48	0.76
Psi Blast		4.5e-08	1.5e-08	1.1e-12	4.5e-08	1.7e-24	1.7e-24	1.7e-24	3.4e-16
END	¥	142	142	143	142	82	82	82	08
STAR	TAA	54	50	20	20	17	17	17	17
CHAI	A E	Ą		∢	▼	a	В	Д	В
PDB	A	1c1g	1cii	lez3	lreq	Ifqv	1fs1	1fs2	1vcb
SEQ	<u>a ş</u>	1522	1522	1522	1522	1523	1523	1523	1523

		_	<del></del>	<del></del> _		
TRANSCRIPTION,	TRANSCRIPTION TUMOR BETA SANDWICH, 2 TRANSCRIPTION, ELONGATION TRANSCRIPTION, ELONGATION		PHOSPHOTRANISFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSINICTION	PHOSPHOTRANISFERASE RHOGAP DOMAIN; PHOSPHOTRANISFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSI'HOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL	TRAINING CITION PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL	PHOSPHOTERASE RHOGAP PHOSPHOTRANSFERASE DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2
	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;		PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;	PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;
	52.02				67.87	
			0.63	0.1		0.76
			0.10	0.57		0.09
	3.4e-16		6.8e-19	4.5e-35	3e-36	6.8e-19
	84		291	304	312	291
	17		122	125	107	122
	В		4	<b>A</b>	æ	В
	lvcb		Ipbw	1pbw	Ipbw	1pbw
	1523		1524	1524	1524	1524
	TRANSCRIPTION, TELEPHONIAL EL CALCALTION	1vcb         B         17         84         3.4e-16         52.02         ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; YHL; CHAIN: C, F, I, L;	1vcb B 17 84 3.4e-16 52.02 ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	1vcb         B         17         84         3.4e-16         52.02         ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN: C, F, I, L; VHL; CHAIN	1vcb         B         17         84         3.4e-16         52.02         ELONGIN B; CHAIN: A, D, G, J; ELONGIN B; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;           1pbw         A         122         291         6.8e-19         0.10         0.63         PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;           1pbw         A         125         304         4.5e-35         0.57         1.00         PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	Iveb         B         17         84         3.4e-16         52.02         ELONGIN B; CHAIN: A, D, G, J, ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;           Ipbw         A         122         291         6.8e-19         0.10         0.63         PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;           Ipbw         A         125         304         4.5e-35         0.57         1.00         KINASE; CHAIN: A, B;           Ipbw         B         107         312         3e-36         67.87         PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;

PDB annotation	DOMAIN, 3 SIGNAL TRANSDUCTION	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP,	CDC42, 2 PHOSPHOINOSITIDE 3- KINASE, SH3 DOMAIN, SH2	DOMAIN, 3 SIGNAL TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION	G-PROTEIN CDC42 GTPASE-	ACTIVATING PROTEIN; G-PROTEIN, GAP. SIGNAL-TRANSDUCTION	COMPLEX(GTPASE	ACTIVATN/PROTO-ONCOGENE)	GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	GTPASE, 2 TRANSITION STATE, GAP	COMPLEX(GTPASE	GTPASE-ACTIVATING PROTEIN	RHOGAP; COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE),	GTPASE, 2 TRANSITION STATE, GAP	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)	GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE
Coumpound		PHOSPHATIDYLINOSITOL 3- KINASE; CHAIN: A, B;			RHOGAP; CHAIN: NULL;		RHOGAP; CHAIN: NULL;		RHOGAP; CHAIN: NULL;		P50-RHOGAP; CHAIN: A;	TRANSFORMING PROTEIN	RHOA; CHAIN: B;			P50-RHOGAP; CHAIN: A;	RHOA: CHAIN: B:				P50-RHOGAP; CHAIN: A;	RHOA; CHAIN: B;
SEQFOL D score			•						92.76										-		107.06	
PMF score		0.95			1.00		0.54				100					1.00						
Verify score		0.44	•	<del>-</del> -	0.77		0.08				0.88					0.18						
Psi Blast		3e-36			1.5e-37		1e-29		1.5e-37		7.56-39	2				1.7e-29					7.5e-39	
END		311			308		277		308		308	8				304					308	
STAR T AA		125			112		88		88		112	!				16					91	
CHAI N ID		В									4	<b>t</b>		•		A					¥	
PDB ID		1pbw			Irgp		Irgp		1rep		14v4					1tx4					1tx4	
SEQ D		1524			1524		1524		1524		1524	777				1524					1524	

	T	Т	T	Т	Т							,		T	7										
PDB annotation	ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE. GAP		UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING	LIGASE E6AP: UBCH7: BIT OBAT	STRUCTURE, ELONGATED SHAPE,	E3 UBIQUITIN LIGASE, E2 2	UBIQUITIN CONJUGATING ENZYME	LIGASE E6AP; UBCH7; BILOBAL	STRUCTURE, ELONGATED SHAPE,	E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONFIGATING ENZYME	LIGASE UBIQUITIN, UBIQUITIN-	CONJUGATING ENZYME, YEAST	LIGASE UBIQUITIN, UBIQUITIN-	CONJUGATING ENZYME, YEAST	UBIQUITIN-CONJUGATING	ENZYME UBIQUITIN-	CONJUGATING ENZYME;	ODICOLLIN-COMPORALING	ENZYME, UBIQUITIN-DIRECTED 2	PROTEOLYSIS, CELL CYCLE	CONTROL, LIGASE	UBIQUITIN-CONJUGATING	ENZYME UBIQUITIN-	CONJUGATING ENZYME; UBIQUITIN-CONJUGATING
Coumpound			UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN-PROTEIN LIGASE	E3A; CHAIN: A, B, C;	UBIQUITIN CONJUGATING	ENZ YME E2; CHAIN: D;	UBIQUITIN-PROTEIN LIGASE	ESA; CHAIN: A, B, C;	ENZYME E2; CHAIN: D;	UBIQUITIN CONJUGATING	ENZYME; CHAIN: A;	UBIQUITIN CONJUGATING	TEOC OIL BY	OBCY; CHAIN: NULL;						* * * * * * * * * * * * * * * * * * *	OBC9; CHAIN: NOLL;		
SEQFOL D score			92.22					60.00	80.53	•				106.20						_		77 11	/3.11		
PMF score				1.00	0.99							1.00			5	3							**	_	
Verify				0.61	0.36							0.57			0.83	6.0	•	•							
Psi Blast			1e-40	1e-40	8.5e-33			0 50 22	0.75-33			3.4e-51	;	3.4e-51	3 40-38	200						3 40-38	90-24-0		
END AA			134	128	129			120	7			130		131	130	2					*	131	-		
STAR T AA				4	5			8	,			_		4	-	•						-		•	
CHAI N ID			∢	٧	Д			6	1					<	A							A	:		
PDB ID			layz	layz	lc4z			10.47				Iqeq	100	hoh i	1u9a	!				•	-	1u9a			
SEQ ID NO:		101	1525	1525	1525			1525				1525	1505	1361	1525				_			1525			

PDB annotation	ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE	UBIQUITIN CONTUGATION UBC1; UBIQUITIN CONTUGATION, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
Coumpound		UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score		96.00		82.57		77.96	5		67.17
PMF score			1.00		1.00		1.00	0.03	
Verify			0.49		0.66		0.80	-0.14	
Psi Blast		1.2e-41	1.2e-41	1.5e-37	1.5e-37	1.7e-36	1.7e-36	5.1e-19	3.4e-18
END		126	127	132	124	132	128	338	473
STAR T AA		-	-		E	2	3	01	10
CHAI N ID								A	4
PDB ID		2aak	2aak	2e2c	2e2c	2ucz	2ucz	1a4y	la4y
SEQ ID	2	1525	1525	1525	1525	1525	1525	1527	1527

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PDB annotation	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIROMICT FORDOTERN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SYRND P. BROWLICE EXPROSERY	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SURVEY, ALBONOCLEOPROTEIN COMPLEX (NUCLEAR NUCLEAR PROTEIN/RNA), SOMPLEX SURNP, RIBONUCLEOPROTEIN SURNP, RIBONUCLEOPROTEIN
Coumpound	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	UZ RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;
SEQFOL D score							
PMF score	0.68	0.76	0.99	09.0	0.01	0.22	0.13
Verify score	0.07	0.27	0.36	0.50	0.25	0.36	0.18
Psi Blast	9e-28	3.4e-18	1.5e-34	3e-25	7.5e-24	1.5e-14	3.4e-07
END	335	415	309	284	291	326	339
STAR T AA	134	25	99	140	164	212	232
CHAI N ID	Ą	A	A	٧	<b>V</b>	₹	4
PDB ID	la4y	la4y	1a4y			1a9n	la9n
SEQ ID NO:	1527	1527	1527	1527	1527	1527	1527

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PDB annotation	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
Coumpound	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B";
SEQFOL D score									
PMF score	0.68	0.98	0.43	0.45	0.27	0.00	0.43	0.96	0.70
Verify score	0.42	0.15	0.23	0.25	0.37	0.03	0.36	0.37	0.16
Psi Blast	1.7e-07	1.5e-24	3e-26	4.5e-26	9e-15	3.4e-05	1.7e-07	3e-24	le-24
END	146	187	234	290	326	95	146	187	215
STAR T AA	43	51	22	140	212	23	43	51	89
CHAI N ID	Ą	Ą	A	ပ	၁	ပ	ပ	ပ	ပ
PDB ID	la9n	la9n	la9n	1a9n	1а9п	1a9n	1a9n	1a9n	la9n
SEQ ID NO:	1527	1527	1527	1527	1527	1527	1527	1527	1527

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PDB annotation	(NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONICI EODDOTEN	COMPLEX (NUCLEAR DECTENTIONAL COMPLEX	(NUCLEAR PROTEIN/RNA), RNA, SNEW, PROTEIN/RNA), RNA, SNEW, PROTEIN/RNA), RNA, SNEW, PROSITION FOR STATES	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH	ADHESION	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE.	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	KICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE.	CYINDER DYNEW 2	CHLAMYDOMONAS, FLAGELLA
Coumpound	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R: 112 A': CHAIN: A C: 112 B".	CHAIN: B, D;	INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;		INTERNALIN B; CHAIN: A;		RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; KAB	GERANYLGERANYLTRANSFE	RASE BEIA SUBUNII; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN:	A;		OTITED ABM DISHER! CITYER!	OUTER ARM DYNEIN; CHAIN:	<b>.</b>		Olitep APM DWEEL CHAP	A:		
SEQFOL D score												-							†	<u> </u>					·	
PMF score		69.0		0.99		0.10		0.70		0.15						90.0			000	20.0			0.23	}		
Verify score		0.43		0.35		-0.07		0.12		0.31						-0.40			0 12	71.0			-0.08	·		
Psi Blast		3e-26		8.5e-24		3.4e-18	1	3.4e-23		1.2e-10						1.5e-18			5.1e-15				1e-09		<u> </u>	
END		234		311		377	00.	88		121						291			338	)			145			
STAR T AA		92		129		228	,	4		7.1						167		•	217				43			
CHAI N ID		ပ		A		¥	•	₹ .		∢									A				A			
PDB ID		la9n		90P1		140b	107	ann		Idce		<del></del>				lasy		_	1ds9				1ds9			
SEQ ID NO:		1527		1527		1527	1507	/761		/701					1,507	7701			1527				1527			

PDB annotation	THOUTH I THEIR IS ASSESSED IN COLUMN	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP,
Coumpound		OUTER ARM DYNEIN; CHAIN: A;	NUCLEAR RNA EXPORT FACTOR I; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
SEQFOL	D score							
PMF	score	0.15	0.01	0.30	0.36	-0.03	0.04	-0.03
Verify	score	-0.39	-0.15	0.16	-0.05	0.21	0.00	0.16
Psi Blast		1,4e-11	3.4e-07	3.4e-07	1.5e-15	1.3e-20	5.1e-12	6.8e-12
END	AA	235	308	308	347	334	311	360
STAR	T AA	73	227	227	134	125	171	62
CHAI	9 2	A	A	В	⋖	<b>«</b>	A	A
PDB	 8	1ds9	1fo1	1fo1	1fqv	1fs2	1fs2	l yrg
SEQ	Αÿ	1527	1527	1527	1527	1527	1527	1527

PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL   Coumpound			<del></del>	γ		·	 			
2 PDB CHAI STAR END Psi Blast Verify PMF SEQFOL.  1 Jyrg A 86 265 1e-30 0.11 0.15  2 bnh 25 413 1.2e-22 0.08 0.74  2 bnh 64 312 1.2e-40 0.01 0.81  1 a68 117 207 1.5e-13 0.66 0.86  1 exb E 117 200 1.2e-11 0.48 0.41	PDB annotation	LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRAY	TRANSCRIPTION RNA IP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA IP, RANGAP, LER, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, 3 HEMIHEDRAL TWINNING, 3	MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE INHIBITOR,	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LELICINE-RICH REPRATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, I HICONE-BICH REPEATS	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL,	ASSEMBLY DOMAIN, IETRAMER METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE-
2 PDB CHAI STAR END Psi Blast Verify PMF score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score score s	Coumpound		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR;	CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL;	KV BETA2 PROTEIN; CHAIN: 4; POTASSIUM CHANNEL KVI.1;	KVI.2 VOLTAGE-GATED
2 PDB CHAI STAR END Psi Blast Verify score  1 D N ID TAA AA AA Score  2 bnh 25 413 1.2e-22 0.08 0  2 bnh 64 312 1.2e-40 0.01 0  1 a68 117 207 1.5e-13 0.66 0  1 exb E 117 210 1.2e-11 0.48 0	SEQFOL D score									
2 PDB CHAI STAR END PSi Blast ID N ID TAA AA AA AA AA AA AA AA AA AA AA AA AA	PMF score		0.15	0.74		0.81	0.86	0.28	0.41	0.43
2 PDB CHAI STAR END PSi Blast 1 D N ID TAA AA AA AA AA AA AA AA AA AA AA AA AA	Verify score		0.11	0.08		0.01	99.0	60.0	0.48	0.48
2 PDB CHAI STAR  1 D N ID TAA  2 bnh 25 4  2 bnh 64 3  1 a 68 117 2  1 a 68 117 2	Psi Blast		16-30	1.2e-22		1.2e-40	1.5e-13	7.5e-12	1.2e-11	3e-12
2 PDB CHAI	END		265	413	_	312	207	204	210	208
2 PDB 1 DB 2 Dnh 2 Dnh 2 Dnh 1 a 68 1 a 68 1 a 68 1 a 68 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1 a 64 1	STAR T AA		98	25		64	117	117	117	117
PDB  D  D  D  D  D  D  D  D  D  D  D  D	CHAI N ID		٧ ·					A	8	A
	PDB ID		lyrg	2bnh		2bnh	1a68		<del> </del>	Iqdv
	SEQ ID NO:		1527	1527		1527	1528	1528	1528	1528

PDB annotation	GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE: NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER	GENE REGULATION SON OF SEVENLESS PROTEIN; GUANINE
Coumpound	POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KV1.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C,	REGULATOR OF CHROMOSOME CONDENSATION 1; CHAIN: A, B, C;	HUMAN SOS I; CHAIN: A;
SEQFOL D score					97.41		
PMF score		0.45	0.62	-0.08		0.22	0.22
Verify score		0.26	0.59	0.04		-0.01	-0.03
Psi Blast		1.3e-11	6e-15	1.7e-49	1.7e-49	6.8e-91	3e-16
END		204	217	704	741	415	1001
STAR T AA		117	117	346	354	6	695
CHAI N ID		<b>∀</b>		<b>4</b>	<b>4</b>	<b>4</b>	Ą
PDB ID		1114	3kvt	la12	1a12	1a12	1dbh
SEQ ID	Š	1528	1528	1529	1529	1529	1529

	<del></del>	<del></del> _					
PDI: annotation	NUCLEOTIDE EXCHANGE FACTOR, GENE REGIL ATTOM	SIGNATURE PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN,	SIGNALING PROTEIN SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECK STRIN, 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN,		SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN- BINDING PROTISIN, POLY-L- 2 PROLINE BINDING PROTEIN,	CONTRACTILE PROTEIN CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-
Coumpound		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHHH)) (NMR,	SOS 1; CHAIN: NULL;	PROFILIN II; CHAIN: A, B, C, D;	PROFILIN II; CHAIN: A, B, C, D;
SEQFOL D score					-		
PMF score		0.33	0.35	0.93	-0.02	1.00	1.00
Verify		-0.27	0.02	0.38	0.32	1.32	1.32
Psi Blast		7.5e-07	3e-07	0,0003	1.5e-09	6.8e-52	9e-63
END		1006	1007	1007	1004	138	138
STAR T AA		930	930	935	897	2	2
CHAI N ID		∢ .	¥	,		∢	A
PDB ID		Ifao	1fb8	1pls	Ipms	141j	ldlj
SEQ ID NO:		1529	1529	1529	1529	1530	1530

PDB annotation	BINDING PROTEIN, POLY-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY	PROTEIN BINDING ACETYLATION, ACTIN-BINDING PROTEIN, MULTIGENE FAMILY			CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L- 2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN ACIDIC PROFILIN ISOFORM, ACTIN-BINDING PROTEIN, POLY-L-2 PROLINE BINDING PROTEIN, CONTRACTILE PROTEIN			MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE
Coumpound		PROFILIN; CHAIN: NULL;	PROFILIN; CHAIN: NULL;	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	PROFILIN II; CHAIN: A, B, C, D;	PROFILIN II; CHAIN: A, B, C, D;	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	ACTIN BINDING PROTEIN PROFILIN 1PNE 3	KINESIN; CHAIN: NULL;	KINESIN; CHAIN: NULL;
SEQFOL D score			167.69		167.40				133.14		
PMF		1.00		1.00		1.00	1.00	1.00		1.00	1.00
Verify score		1.04		0.92		0.75	0.71	0.64		-0.22	-0.15
Psi Blast		1.7e-52	1.7e-52	1.7e-52	1.7e-52	1.7e-42	4.5e-52	1.5e-42	1.5e-42	3e-68	6.8e-35
END		140	140	140	140	122	122	124	124	176	176
STAR T AA		2	2	2	2	2	2	2	2	73	2
CHAI N ID						٧	A				
PDB ID		1161	161	lpne	1pne	141j	141j	Ipne	1pne	1bg2	1bg2
SEQ ID	NO:	1530	1530	1530	1530	1531	1531	1531	1531	1534	1534

		NCD,		REAMILY,	PROTEIN,	PROTEIN.	•	CINESIN,	EN.	7.403		SE, P-	DING	PROTEIN,		PROTEIN,					<u></u>	-		RIDOXAL
PDB annotation	ASSOCIATED	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL	PROTEIN; NCD CRYSTAL	MOTORS, KINESIN 2 SUPERFAMILY,	MOTOR PROTEIN MOTOR PROTEIN,	MOTOR PROTEIN MOTOR PROTEIN.	CYTOSKELETON	CONTRACTILE PROTEIN KINESIN,	NCD, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN	KINESIN-RELATED PROTEIN.	MOTOR 2 PROTEIN, ATPASE, P-	LOOP, MICROTUBULE BINDING PROTEIN	MOTOR PROTEIN MOTOR PROTEIN,	CYTOSKELETON	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON							AMINOTRANSFIRASE	AMINOTRANSFIERASE, PYRIDOXAL ENZYME
Coumpound		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C,	Ď		KINESIN; CHAIN: A, B;	KINESIN; CHAIN: A, B;		KINESIN MOTOR NCD; CHAIN: A:		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL:			-	KINESIN HEAVY CHAIN;	CHAIN: A, B, C, D;	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;		TRANSFERASE(AMINOTRANSF FP ASE) ASPABTATE	AMINOTRANSFERASE	(E.C.2.6.1.1) COMPLEXED WITH	1ARS 3 PYRIDOXAL-5'-	PHOSPHATE IARS 4	ASPARTATE	AMINOTRANSFERASE; CHAIN: A, B;
SEQFOL D score												-						-						
PMF score		0.10			0.83	1.00		0.54		99.0				86.0	0.71	1.71		0.07					c.7.0	
Verify score		-0.36			0.03	-0.17		-0.24		-0.30				-0.25	777	1		-0.22				1	0.17	
Psi Blast		1e-17			3e-40	6.8e-19	,	6.8e-18		1.7e-21				1.5e-38	1 76-20	07-20-1		6.8e-13	-	-		6 1- 01	3.1e-81	
END		170			186	199		0.7	ļ	172				186	230		2,5	309	·			970	202	
STAR T AA		4			101	101		4						105	105		1.6		•			-		
CHAI N ID		¥			В	В		€						— Д	В							<		
PDB ID		1cz7			2kin	2kin	7	71100		3Kar				3kin	3kin		1010	2 2				1hiw		
SEQ ID NO:		1534			1534	1534	1524	1034	1631	1334				1534	1534		1536	2				1536	2	

PDB annotation	TRANSFERASE AONS, 8-AMINO-7- KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7- KETOPELARGONATE 3 SYNTHASE, TRANSFERASE	TRANSFERASE AONS, 8-AMINO-7-KETOPELARGONATE SYNTHASE; PLP-DEPENDENT ACYL-COA SYNTHASE, BIOTIN BIOSYNTHESIS, 8-2 AMINO-7-OXONANOATE SYNTHASE, 8-AMINO-7-KEŢOPELARGONATE 3 SYNTHASE, TRANSFERASE	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C- 2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM, DECARBOXYLATION 2 INHIBITOR, LYASE	LYASE DGD; ENZYME COMPLEXES, CATALYTIC MECHANISM,
Coumpound	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	8-AMINO-7-OXONANOATE SYNTHASE; CHAIN: A;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	MALY PROTEIN; CHAIN: A, B;	2,2-DIALKYLGLYCINE DECARBOXYLASE (PYRUVATE); CHAIN: A;	2,2-DIALKYLGLYCINE DECARBOXYLASE
SEQFOL D score	69.72					169.86	
PMF score		0.12	0.16	0.25	-0.05		1.00
Verify score		0.32	0.09	-0.03	0.10		0.72
Psi Blast	1.7e-41	1.7e-41	6.8e-54	1.7e-18	3.4e-21	3.4e-63	3.4e-63
END	375	365	373	373	373	372	372
STAR T AA	1	47	-	89	25	<b>,</b>	46
CHAI N ID	¥	⋖	4	¥	<b>4</b>	Α	A
PDB ID	1bs0	1bs0	1bw0	1c7n	1d2f	1d7u	1d7u
SEQ UD	1536	1536	1536	1536	1536	1536	1536

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PDB annotation	DECARBOXYLATION 2 INHIBITOR, 1.YASF	TRANSFERASE GABA-AT; PLP-DEPENDENT ENZYME, AMINOTRANSFERASE, 4-AMINOBUTYRIC ACID, 2	AN IEFILEF III. DRUG IARGEI TRANSFERASE GABA-AT; PLP. DEPENDENT ENZYME, AMINOTRANSFERASE, 4- AMINOBUTYRIC ACID, 2	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXALS'-PHOSPHATE, BIOTIN	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SEMIALDEHYDE AMINOMUTASI; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'-	CHLOROPHYLL BIOSYNTHESIS GLUTAMATE SISMIALDEHYDE AMINOMUTASE; CHLOROPHYLL BIOSYNTHESIS, PYRIDOXAL-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'- PHOSPHATE, 2 PYRIDOXAMINE-5'-	AMINOTRANSFERASE AMINOTRANSFERASE AMINOTRANSFERASE, 5- FLUOROMETHYLORNITHINE, PLP- DEPENDENT 2 ENZYME,	AMINOTRANSFERASE
Coumpound	(PYRUVATE); CHAIN: A;	4-AMINOBUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	4-AMINOBUTYRATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	7,8-DIAMINOPELARGONIC ACID SYNTHASE; CHAIN: A, B;	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	GLUTAMATE SEMIALDEHYDE AMINOTRANSFERASE; CHAIN: A, B;	ORNITHINE AMINOTRANSFERASE; CHAIN: A, B, C;	ORNITHINE
SEQFOL D score					90.43		130.71	
PMF score		1.00	1.00	1.00		1.00		1.00
Verify score		0.71	0.47	0.54		0.25		0.57
Psi Blast		1.5e-70	1.7e-53	6.8e-64	1.26-72	1.2e-72	1.7e-62	1.7e-62
END		370	373	371	372	372	372	369
STAR T AA		49	53	40	-	5	7	40
CHAI N ID		<b>4</b>	⋖	A	A	А	¥	A
PDB ID		1gtx	lgtx	1qj5	2gsa	2gsa	20at	20at
SEQ ID NO:		1536	1536	1536	1536	1536	1536	1536

PDB annotation	AMINOTRANSFERASE, 5- FLUOROMETHYLORNITHINE, PLP- DEPENDENT 2 ENZYME, PYRIDOXAL PHOSPHATE	HYDROLASE SERCAI; ION PUMP, CALCIUM, MEMBRANE PROTEIN, P- TYPE ATPASE, ACTIVE 2 TRANSPORT	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SIGNALLING COMPLEX RACI; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,
Coumpound	AMINOTRANSFERASE; CHAIN: A, B, C;	CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC CHAIN: A;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEQFOL D score								
PMF score		0.04	0.77	0.15	0.29	0.54	0.19	0.52
Verify score		-0.16	0.06	-0.35	-0.12	0.21	0.00	0.26
Psi Blast		0	3.4e-23	1e-10	1.5e-13	16-12	16-18	1e-18
END		916	247	253	230	961	231	167
STAR T AA		91	135	179	102	101	139	19
CHAI N ID		A			Ф	A	∢	A
PDB ID		leul	1a17	1a17	1e96	1elr	leir	1elr
SEQ ID		1539	1541	1541	1541	1541	1541	1541

Т	T	т	1	<del></del>	<del></del>	<del></del>	<del></del>	
PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BENEAU.	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMFLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN RIDDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL PROTEIN PROTEIN PROTEIN PROTEIN	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR,	A HELICAL KEFEAT PROTEIN TRANSPORT HELIX- TURN-HELIX TIR-LIKE REPEAT, PROTEIN TRANSPORT	TRANSFERASE METHYLTRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN
CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR 1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	VESICULAR TRANSPORT PROTEIN SEC17; CHAIN: A;	GLYCINE N. METHYLTRANSFERASE; CHAIN: A. B. C. D.	MJ0882; CHAIN: A;
						63.04		
	0.53	0.01	0.46	0.37	0.18		-0.09	0.37
	-0.04	0.30	0.73	0.35	90.0-		0.55	0.57
	1.7e-20	3.4e-15	16-14	3.4e-13	8.5e-35	3.4e-07	3.4e-16	3.4e-09
	250	133	175	202	252	254	061	187
	133	28	49	86	9	2	65	72
	٧	¥	∢	Ą	A	4	A	4
	lelw	lelw	lelw	Ielw		Iqqe	1d2h ,	ldus
	1541	1541	1541	1541	1541	1541	1	1542
	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	Ielw         A         133         250         1.7e-20         -0.04         0.53         TPR1-DOMAIN OF HOP; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: C. D;	lelw         A         133         250         1.7e-20         -0.04         0.53         TPR1-DOMAIN OF HOP; CHAIN: B;           lelw         A         28         133         3.4e-15         0.30         0.01         TPR1-DOMAIN OF HOP; CHAIN: C, D;           lelw         A         28         133         3.4e-15         0.30         0.01         TPR1-DOMAIN OF HOP; CHAIN: C, D;	1elw         A         133         250         1.7e-20         -0.04         0.53         TPR1-DOMAIN OF HOP; CHAIN: B;           1elw         A         28         133         3.4e-15         0.30         0.01         TPR1-DOMAIN OF HOP; CHAIN: C, D;           1elw         A         28         133         3.4e-15         0.30         0.01         TPR1-DOMAIN OF HOP; CHAIN: C, D;           1elw         A         64         175         1e-14         0.73         0.46         TPR1-DOMAIN OF HOP; CHAIN: C, D;           A, B; HSC70-PEPTIDE; CHAIN: C, D;         C, D;         C, D;         C, D;	Ielw   A   133   250   1.7e-20   -0.04   0.53   TPR1-DOMAIN OF HOP; CHAIN: B; HSC70-PEPTIDE   CHAIN: B; HSC70-PEPTIDE; CHAIN: C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;   C, D;	Ielw   A   133   250   1.7e-20   -0.04   0.53   TPR1-DOMAIN OF HOP; CHAIN: B; C, D; C, D; D; D; D; C, D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; D; C, D; D; D; C, D; D; D; C, D; D; D; D; C, D; D; D; D; D; D; C, D; D; D; D; D; D; D; D; D; D; D; D; D;	1elw   A   133   250   1.7e-20   -0.04   0.53   TPR1-DOMAIN OF HOP; CHAIN: B; B; B; B; B; B; B; B; B; B; B; B; B;	1elw   A   133   250   1.7e-20   -0.04   0.53   TR1-DOMAIN OF HOP; CHAIN: B;     1elw   A   28   133   3.4e-15   0.30   0.01   TR1-DOMAIN OF HOP; CHAIN: C, D;     1elw   A   28   133   3.4e-15   0.30   0.01   TR1-DOMAIN OF HOP; CHAIN: C, D;     1elw   A   64   175   1e-14   0.73   0.46   TR1-DOMAIN OF HOP; CHAIN: C, D;     1elw   A   64   175   1e-14   0.73   0.46   TR1-DOMAIN OF HOP; CHAIN: C, D;     1elw   A   64   252   8.5e-35   -0.06   0.18   TR1-DOMAIN OF HOP; CHAIN: C, D;     1fch   A   6   2.52   8.5e-35   -0.06   0.18   TR1-DOMAIN OF HOP; CHAIN: C, D;     1dqe   A   2   2.54   3.4e-07   63.04   VESICULAR TRANSFORT     1ddh   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1d2h   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   3.4e-16   0.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   10.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   A   65   190   10.55   -0.09   GLYCINE N-TRANSFERASE;     1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap   1dap

PDB annotation	METHANOCOCCUS JANNASCHII	TRANSFERASE RRNA METHYLTRANSFERASE ERMC', COFACTOR ANALOGS	METHYLTRANSFERASE GNMT, S- ADENOSYL-L-METHIONINE\: GLYCINE METHYLTRANSFERASE	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM	METHYLTRANSFERASE TRANSFERASE, METHYLTRANSFERASE, RESTRICTION SYSTEM	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	
Coumpound		ERMC' METHYLTRANSFERASE; CHAIN: A;	GLYCINE N- METHYLTRANSFERASE; CHAIN: A, B;	ADENINE-N6-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	ADENINE-N6-DNA- METHYLTRANSFERASE TAQI; CHAIN: A, B;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 IAHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR,
SEQFOL D score								58.51
PMF score		0.00	-0.13	-0.14	0.16	0.28	0.25	
Verify score		0.27	-0.00	0.14	-0.29	-0.10	0.17	-
Psi Blast		3e-06	3.4e-17	5.1e-11	7.5e-06	1.5e-06	4.5e-06	5.1e-32
END AA		200	190	192	337	58	83	291
STAR T AA		72	21	99	99	<b></b>	2	228
CHAI N ID		A	A	A	A		A	മ
PDB ID		Iqam	Ixva	2adm	2adm	1a17	1fch	1ahd
SEQ NO:		1542	1542	1542	1542	1544	1544	1545

		T						
PDI: annotation			COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUTARY, CPHD, 2 POU DOMAIN,	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING	PROTEIN, PROTEINDNA PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING	PROTEIN, PROTEINDNA PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING	TRANSCRIPTIONDNA TRANSCRIPTIONDNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS
Coumpound	1AHD 4 16 STRUCTURES) 1AHD	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 14HD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B;	HOMEOBOX PROTEIN B; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D: DNA CHAIN: E.	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'-	ULTRABITHORAX HOMEOTIC ULTRABITHORAX HOMEOTIC HOMEOBOX PROTEIN EXTRADENTICLE: CHAIN: R:
SEQFOL D score			·	78.21			55.32	
PMF score		1.00	0.59		1.00	1.00		1.00
Verify score		0.01	-0.40		0.40	0.40		0.49
Psi Blast		5.16-32	4.5e-22	3e-28	3e-28	5.1e-26	5.1e-27	5.1e-27
END		294	286	290	290	290	287	287
STAR T AA		229	212	224	233	233	226	233
CHAI N ID		ъ	¥.	¥	A	A	A	A
PDB ID		lahd	lau7	1672	1b72	1672	168i	168i
SEQ NO:		1545	1545	1545	1545	1545	1545	1545

PDB annotation	Thurst out of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the section of the sec	DEVELOPMENT, 2 SPECIFICITY				ŕ									COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) HD;	HOMEODOMAIN, COMPLEA (DNA-BINDING PROTEIN/DNA)	COMPLEX (ZINC FINGER/DNA)
Coumpound		DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MOTALLY WITH CYS 39 ISAN 3 REPI ACED RV SER AND	RESIDUES 1-6 DELETED (C39S.DEL 1-6) ISAN 4 (NMR. 20	STRUCTURES) 1SAN 5	DNA-BINDING PROTEIN	AN I ENNAFEDIA FRO I EIN (HOMEODOMAIN) MUTANT	WITH CYS 39 1SAN 3	REPLACED BY SER AND	RESIDUES 1-6 DELETED	STRUCTURES) 1SAN 5	ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C,	D, E, F;	ANTENNAPEDIA PROTEIN;	CHAIN: A, B; DNA; CHAIN: C,	D, E, F;	QGSR ZINC FINGER PEPTIDE;
SEQFOL	D score		59.53		57.26													61.44			
PMF	score			0.92					1.00						1.00						1.00
Verify	score			-0.12					0.30	·				. 11724	0.42						0.19
Psi Blast			8.5e-28	8.5e-28	1.4e-29				1.4e-29						1.7e-29			1.7e-29			1.4e-27
END	ΑA		296	294	291				294				- <u> </u>		288			288			92
STAR	T AA		227	229	234			,	235						233		,	233			12
CHAI	N E														A			Ą			А
PDB	<u> </u>		1ffz	1ftz	Isan				lsan						9ant			9ant			lalh
SEQ	ΑÖ		1545	1545	1545				1545						1545			1545			1546

	Т	<del></del>		<del></del>					
PDB annotation	COMPLEX (ZRIC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PROTEIN COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, IDNA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, INA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, INA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, I'NA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTFIN, DNA
Coumpound	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	GOSR ZINC FINGER PEPTIDE; CGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCIED BINDING STE: CHAIN: B. C.	GGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZING FINGER PEPTIDE; QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING STTE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE; OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONIUCEOTIDE BINDING SITE: CHAIN: B. C.	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER
SEQFOL D score							80.58		
PMF score		1.00	0.88	1.00	0.80	1.00		0.23	1.00
Verify score		0.26	0.16	0.48	0.31	0.22		0.01	0.48
Psi Blast		8.5e-27	3e-28	1.5e-37	5.1e-22	3.4e-30	3,4e-30	1.5e-14	1e-46 (
END		249	250	277	64	361	391	185	92
STAR T AA		161	162	199	-	281	309	101	11
CHAI N ID		∢	<b>4</b>	¥	A	A	4	ပ	U
PDB ID		laih	lalh	lalh	laih	lalh		Imey	1mey
SEQ ID NO:		1546	1546	1546	1546	1546	1546	1546	1546

Image   C   125   249   66-25   -0.12   0.49   DNA; C   CONSE   PROTEIN		FUD annotation
125   249   6e-25   -0.12   0.49   130   221   1.5e-39   -0.10   0.48   160   249   5.1e-47   0.09   1.00   188   277   1.7e-47   0.57   1.00   1   64   5.1e-34   0.26   0.95   1   224   305   1e-49   0.81   1.00   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.00   1   1.		
C 125 249 6e-25 -0.12 0.49  C 130 221 1.5e-39 -0.10 0.48  C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00	PROTEIN; CHAIN: C, F, G; INTE CRY (ZIN	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
C 130 221 1.5e-39 -0.10 0.48  C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00		COMPLEX (ZINC FINGER/DNA) ZINC
C 130 221 1.5e-39 -0.10 0.48  C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00	~	FINGER, PROTEIN-DNA
130     221     1.5e-39     -0.10     0.48       160     249     5.1e-47     0.09     1.00       188     277     1.7e-47     0.57     1.00       1     64     5.1e-34     0.26     0.95       224     305     1e-49     0.81     1.00	PROTEIN; CHAIN: C, F, G; INTE	INTERACTION, PROTEIN DESIGN, 2
C 130 221 1.5e-39 -0.10 0.48  C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00	CKY (ZIŞ	CRYSIAL SIRUCIURE, COMPLEX (ZINC FINGER/DNA)
C 160 249 5.1e-47 0.09 1.00 C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	DNA; CHAIN: A, B, D, E; CON	COMPLEX (ZINC FINGER/DNA) ZINC
C 160 249 5.1e-47 0.09 1.00 C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	ER	FINGER, PROTEIN-DNA
C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00	PROTEIN; CHAIN: C, F, G;   INTE	INTERACTION, PROTEIN DESIGN, 2
C 160 249 5.1e-47 0.09 1.00  C 188 277 1.7e-47 0.57 1.00  C 1 64 5.1e-34 0.26 0.95  C 224 305 1e-49 0.81 1.00		CRYSTAL STRUCTURE, COMPLEX
C 160 249 5.16-47 0.09 1.00  C 188 277 1.76-47 0.57 1.00  C 1 64 5.16-34 0.26 0.95  C 224 305 16-49 0.81 1.00	NIZ)	(ZINC FINGER/DNA)
C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	DNA; CHAIN: A, B, D, E; COM	COMPLEX (ZINC FINGER/DNA) ZINC
C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00		INTER A CTION PROTEIN DESIGN 2
C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00		CRYSTAL STRUCTURE, COMPLEX
C 188 277 1.7e-47 0.57 1.00 C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	NIZ)	(ZINC FINGER/DNA)
C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	DNA; CHAIN: A, B, D, E; COM	COMPLEX (ZINC FINGER/DNA) ZINC
C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	CONSENSUS ZINC FINGER FINC	FINGER, PROTEIN-DNA
C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00		INTERACTION, PROTEIN DESIGN, 2
C 1 64 5.1e-34 0.26 0.95 C 224 305 1e-49 0.81 1.00	CRY	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
C 224 305 1e-49 0.81 1.00	DNA; CHAIN: A, B, D, E; CON	COMPLEX (ZINC FINGER/DNA) ZINC
C 224 305 1e-49 0.81 1.00	ER	FINGER, PROTEIN-DNA
C 224 305 1e-49 0.81 1.00	PROTEIN; CHAIN: C, F, G;   INTE	INTERACTION, PROTEIN DESIGN, 2
C 224 305 1e-49 0.81 1.00		CRYSTAL STRUCTURE, COMPLEX
C 224 305 1e-49 0.81 1.00	(ZIN	(ZINC FINGER/DNA)
CONSE		COMPLEX (ZINC FINGER/DNA) ZINC
PROTE	~	FINGER, PROTEIN-DNA
	PROTEIN; CHAIN: C, F, G;   INTE	INTERACTION, PROTEIN DESIGN, 2
	CRY	CRYSTAL STRUCTURE, COMPLEX
1mev C 224 306 18-49 DNA C	DNA: CHAIN: A B D F: CON	COMPLEX (ZINC FINGER/DNA) ZINC

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PDB annotation	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/INA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTISIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRIJCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTI:IN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/I)NA) COMPLEX (TRÁNSCRIPTION REGULATION/I)NA) COMPLEX (TRANSCRIPTION REGULATION/I)N REGULATION/I)NA), RNA POL YMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/I)NA) COMPLEX (TRANSCRIPTION
Coumpound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F:
SEQFOL D score				·			117.50
PMF		1.00	1.00	1.00	1.00	0.46	
Verify score		0.59	0.38	0.37	0.26	0.03	
Psi Blast		1.2e-49	3.4e-49	1.2e-49	3.4e-44	1.4e-31	1.5e-37
END		333	361	389	411	291	359
STAR T AA		252	280	308	336	132	196
CHAI N ID		υ	υ	U	O	∢	A
PDB ID	,	lmey	Imey	lmey	Imey	11f6	1tf6
SEQ ID NO:		1546	1546	1546	1546	1546	1546

PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	INDITION OF A VICTORIONI
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	
SEQFOL D score						
PMF score		1.00	1.00	0.75	0.96	3
Verify score		0.41	0.32	0.07	0.20	3
Psi Blast		1.5e-37	1.5e-37	1.7e-26	6.8e-31	١
END		342	403	410	249	200
STAR T AA		199	253	309	133	1,,,
CHAI N ID		K	4	4	ပ	
PDB ID		11f6	11f6	1tf6	lubd	
SEQ ID		1546	1546	1546	1546	

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PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELIEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELIMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATIONINA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	RECOLLATIONADA) COMPLEX (TRANSCRIPTION REGULATIONADA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX GTRANSCRIPTION	COMPLEX (TRANSCRIPTION REGULATION/DINA) YING-YANG 1; TRANSCRIPTION DITTATION
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INTIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA-
SEQFOL D score					
PMF score		1.00	0.81	0.16	1.00
Verify score		0.47	0.24	-0.28	-0.01
Psi Blast		5.1e-33	36-25	1.7e-23	3.4e-29
END		277	119	150	92
STAR T AA		168	16	19	-
CHAI N ID		ပ	O	ပ	S
PDB ID		lubd	lubd		lubd
SEQ ID NO:		1546	1546	1546	1546

PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN -RECOGNITION, 3 COMPLEX (TRANSCRIPTION -REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score			97.53		
PMF		1.00		1.00	1.00
Verify score		0.25		0.44	0.42
Psi Blast		7.5e-48	1.2e-50	1.2e-50	4.5e-47
END		333	334	362	389
STAR T AA		201	226	250	279
CHAI N ID		ပ	U .	ပ	ပ
PDB ID		lubd	lubd	1ubd	lubd
SEQ ID		1546	1546	1546	1546

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PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION (DAY)	COMPLEX (TRANSCRIPTION REGULATIONIDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELIEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	KEGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX (TRÁNSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION(I)NA)	COMPLEX (DNA-BINDING
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY I; CHAIN: C; ADENO- ASSOCIATED VRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE)	ZINC FINGER PROTEIN GLII;
SEQFOL D score						
PMF score		1.00	1.00	0.93	0.74	99.0
Verify score		0.35	0.11	0.16	0.24	0.09
Psi Blast		1.76-33	7.5e-46	8.56-32	le-10 (	6e-32 C
END	Coc	28.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5	417	410	122	150
STAR T AA	000	8 8 7	306	316		12
CHAI N ID		)	၁	O	4	A
PDB ID			lubd	1ubd	2drp	2gli /
SEQ NO:	1546		1546	1546	1546	1546

PDB annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score				106.53					
PMF score		0.34	0.94		1.00	0.95	1.00	1.00	0.99
Verify		-0.08	0.34		0,35	0.40	0.13	0.45	0.14
Psi Blast		3.4e-26	3.4e-32	1.2e-63	1.2e-63	3.4e-34	9e-45	6.8e-31	1.5e-42
END AA		248	304	363	391	388	418	410	279
STAR T AA		137	160	224	224	260	280	288	66
CHAI N ID		A	4	A	A	Ą	A	A	A
PDB ID		2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli
SEQ D D		1546	1546	1546	1546	1546	1546	1546	1546

PD]3 annotation	PRIDATO PROGRAMMA	BINDING FRO (BIN/DINA)	RIBOSOME 305 RIBOSOMAL SUBUNIT, RIBOSOME, ANTIBIOTIC, STREPTOMYCIN, 2	SPECTINOMYCIN, PAROMOMYCIN																	-						
Coumpound			16S RIBOSOMAL RNA; CHAIN: A; FRAGMENT OF MESSENGER RNA; CHAIN: X; 30S	RIBOSOMAL PROTEIN S2; CHAIN: B; 30S RIBOSOMAL PROTEIN S3: CHAIN: C: 30S	RIBOSOMAL PROTEIN S4;	CHAIN: D; 30S RIBOSOMAL PROTEIN S5: CHAIN: E: 30S	RIBOSOMAL PROTEIN S6;	CHAIN: F; 30S RIBOSOMAL	PROTEIN S7; CHAIN: G; 30S	KIBOSOMAL PROTEIN S8; CHAIN: H: 30s PIBOSOMAI	PROTEIN S9; CHAIN: I: 30S	RIBOSOMAL PROTEIN S10;	CHAIN: J; 30S RIBOSOMAL	PROTEIN S11; CHAIN: K; 30S	CHAPIT 1.300 PID COLOR	PROTFIN S13: CHAIN: M: 308	RIBOSOMAL PROTEIN S14.	CHAIN: N; 30S RIBOSOMAL	PROTEIN S15; CHAIN: 0; 30S	RIBOSOMAL PROTEIN S16;	CHAIN: P; 30S RIBOSOMAL	PROTEIN S17; CHAIN: Q; 30S	RIBOSOMAL PROTEIN S18;	CHAIN: R; 30S RIBOSOMAL	PROTEIN S19; CHAIN: S; 30S	RIBOSOMAL PROTEIN S20;	CHAIN: 1; 30S RIBOSOMAL PROTEIN THX: CHAIN: V
SEQFOL D score						-																	_		=	-	
PMF score			1.00																		,						
Verify score			0.78		-	17	.,				•		-												_		<del></del>
Psi Blast			1e-53				············	-																	<del></del>		
END			366											**													
STAR T AA			217		·																		-				
CHAI N ID			ET)																						_		
PDB ID			1fjg								_																
SEQ ID NO:			1547																								

PDB annotation			TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S
Coumpound	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN S5 (PROKARYOTIC) 1PKP 3	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	SP1F2; CHAIN: NULL;	SP1F2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;
SEQFOL D score	64.28		-						
PMF score		1.00	0.11	-0.20	60:0	0.18	-0.20	-0.13	0.07
Verify score		0.53	0.31	0.02	-0.41	-0.05	0.21	0.05	-0.63
Psi Blast	1e-56	1e-56	0.0045	5.1e-29	5.1e-33	1.7e-07	1.7e-10	8.5e-09	1.7e-15
END AA	357	357	219	251	169	104	203	108	130
STAR T AA	211	217	119	172	7.1	77	173	78	69
CHAI N ID			A	ບ	ပ	<b>ს</b>			٧
PDB ID	1pkp	1pkp	lerj	1mey	Imey	Imey	1sp2	1sp2	1#3
SEQ ID NO:	1547	1547	1549	1553	1553	1553	1553	1553	1553

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PDE annotation	GENE; NMR, TI-IIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION	REGULATION/JONA) COMPLEX (TRANSCRIPTION REGULATION/JONA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	KEGULATIONDINA) ZINC FINGER DNA BINDING DOMAIN DNA BINDING MOTIF, ZINC FINGER DNA BINDING	DOMAIN	COMPLEX (DNA.BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGIR, COMPLEX (DNA.	BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	LIGASE SKP2 F.BOX: SVP1. SVP1
Coumpound	CHAIN: B, F;	YY1; CHAIN: C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	SWIS; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3	DNA ZDRP 4 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	CYCLIN A/CDK2-ASSOCIATED
SEQFOL D score						54.61	
PMF score		0.24	0.00	0.36	0.03		0.41
Verify		-0.83	-0.36	0.04	-0.30		-0.10
Psi Blast		1.46-15	5.1e-06	1.7e-06	3.4e-41	3.4e-41	4.5e-07
END		130	104	130	201	229	47
STAR T AA		49	78	74	52	79	8
CHAI N ID		၁		<b>V</b>	4	4	
PDB ID		lubd	1zfd	2drp	2gli ,	2gli /	Ifsi A
SEQ ID NO:		1553		1553	1553	1553	1554

PDB annotation	SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN- DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP-BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS	COMPLEX OF TWO ELONGATION FACTORS EF-TU; EF-TS; ELONGATION FACTOR, NUCLEOTIDE EXCHANGE, GTP- BINDING, 2 COMPLEX OF TWO ELONGATION FACTORS	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL	RNA BINDING PROTEIN G-PROTEIN, BETA-BARREL	RNA BINDING PROTEIN EFTU;
Coumpound	P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	CYCLIN H; CHAIN: NULL;	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE ` PEPTIDE; CHAIN: E, F;	ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	ELONGATION FACTOR TU; CHAIN: A, B, E, F; ELONGATION FACTOR TS; CHAIN: C, D, G, H;	ELONGATION FACTOR TU (EF- TU); CHAIN: A, B, C, D	ELONGATION FACTOR TU (EF-TU); CHAIN: A, B, C, D	ELONGATION FACTOR;
SEQFOL D score					134.70		131.00	
PMF		0.24	0.28	0.78		1.00		1.00
Verify score		-0.49	-0.36	0.02		0.41		0.47
Psi Blast		3e-11	1.5e-09	0	0	0	0	0
END		99	62	541	542	548	552	541
STAR T AA		11	W	122	165	122	124	121
CHAI N ID			В	4 ·	4	Æ	A	Ą
PDB ID		1 jkw	Iqmz	laip	laip	1d2e	1d2e	1efc
SEQ ID		1558	1558	1559	1559	1559	1559	1559

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PDi3 annotation	TRANSPORT AND PROTECTION	RNA BINDING PROTEIN RNA BINDING PROTEIN EFTU; TRANSPORT AND PROTECTION	PROTEIN, RNA, BINDING PROTEIN COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT INSTABLE	ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX TWO ET ONS A TRANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FOR STANSFER FO	COMPLEX (TWO ELONGATION FACTORS) COMPLEX (TWO ELONGATION FACTORS)	ELONGATION PACTOR FOR	ELONGATION PACTOR, COMPLEX	HYDROI ASE ED A GERAGE BATA	BINDING RAS-LIKE, HYDROL ASE					TRANSLATION EF-TU; GTPASE,	MOLECULAR SWITCH, TRNA, RIBOSOME, O-BETA REPITCASE 2	CHAPERONE, DISULFIDE ISOMED ASE	TRANSLATION PROTEIN-PROTEIN
Coumpound	CHAIN: A, B;	ELONGATION FACTOR; CHAIN: A, B;	ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS: CHAIN: B, D.			GTP-BINDING PROTEIN ERA:	CHAIN: A, B;	TRANSPORT AND	PROTECTION PROTEIN FI ONGATION BACTOR TIL	(DOMAIN I) - *GUANOSINE	DIPHOSPHATE 1ETU 4	ELONGATION FACTOR TU (EF-	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)		ELONGATION FACTOR EEFIA; CHAIN: A: ELONGATION
SEQFOL D score		129.64			115.68												
PMF score			0.86	-				0.13		0.45				1.00			1.00
Verify score			-0.05		,			0.05		0.18				0.29			0.31
Psi Blast		0	0		0			1.5e-13	7	8.5e-67				0	-		0
END		542	541		542			368	245	345				541			542
STAR T AA		137	122		172		•	126	110	110				117			120
CHAI N ID		Ą	¥.		∢			¥						<del></del>			∢
PDB ID		lefc	lefu		lefu			lega /	1eti:	3				lexm 		$\neg \dagger$	0011
SEQ ID NO:		1559	1559	1	6661			1559	1559				-	1559		1,660	

PDB annotation		TRANSLATION EF-G; BENT CONFORMATION, VISIBLE DOMAIN III, MUTATION HIS573ALA	TRANSLATION TRANSLATIONAL GTPASE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN,
Coumpound	FACTOR EEF1BA; CHAIN: B;	ELONGATION FACTOR G; CHAIN: A;	TRANSLATION INITIATION FACTOR IF2/EIF5B; CHAIN: A;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR2A-DOMAIN OF HOP;
SEQFOL D score										
PMF score		0.00	0.28	0.07	0.83	0.70	0.03	0.10	0.41	0.05
Verify		-0.15	0.03	0.08	-0.01	0.01	-0.46	-0.07	0.36	-0.02
Psi Blast		1.7e-05	8.5e-62	4.5e-09	1.2e-06	1.3e-08	0.0012	0.003	0.0003	0.0001
END	Ŀ	459	553	165	105	111	401	558	119	165
STAR T AA		319	123	19	2	19	316	462	42	63
CHAI N ID		A	A			A	₹	<b>√</b>	₹	A
PDB ID		1fnm	1g7s	1a17	1a17	leir	1elr	lelr	1elr	lelr
SEQ ID NO:		1559	1559	1561	1561	1561	1561	1561	1561	1561

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PDI annotation	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL BEPTIDE-T, HSC70, 2 HSP70, PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMI'LEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMFLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPET, HSC70, 2 HSP70, PROTEIN	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN PROPER	BINDLING PROTEIN SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP. PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT. TPR.	2 HELICAL REPEAT SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT TPR
Coumpound	CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING PEPTIDE; CHAIN: C, D;	PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;
SEQFOL D score								
PMF score		86.0	0.71	0.95	0.19	0.12	0.65	0.31
Verify score		0.38	0.26	0.31	-0.68	0.41	0.25	0.34
Psi Blast		7.5e-08	5.1e-06	4.5e-07	0.00034	1.7e-05	1.3e-13	1.2e-10
END		119	123	26	472	537	252	119
STAR T AA		19	25	2	382	458	17	2
CHAI N ID		A	¥	٩	A	Ą	¥.	A
PDB ID		lelw	lelw	1elw	1elw		l fch	1fch
SEQ ID NO:		1561	1561	1561	1561	1561	1561	1561

PDB annotation	2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN- PEPTIDE COMPLEX,	TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1- BP, PEROXIN-5, PTS1 PROTEIN-	PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT	LIPID TRANSPORT APO A-1; LIPOPROTEIN, LIPID TRANSPORT,	CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION	STRIICTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35
Coumpound		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;		PEROXISOMAL TARGETING SIGNAL I RECEPTOR; CHAIN: A, B; PTSI-CONTAINING	PEPTIDE; CHAIN: C, D;	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;		AI PHA SPECTRIN: CHAIN: A	B, C;			ALPHA SPECTRIN; CHAIN: A,	î		SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;
SEQFOL D score						68.91		68 37	2									
PMF score		0.03		0.48								0.03			010	?		0.00
Verify score		0.05		0.10								0.04			-0.33			0.19
Psi Blast		3.4e-10		1.4e-11		1.4e-07		1 50 10	21.20			1.5e-10			1 50-13	2		1.5e-07
END		563		286		242		222				269			254		•	128
STAR T AA		318		31		41		101	2			61			18	2		٧.
CHAI N ID		A		¥		A			ζ			A			а	۹		∢
PDB ID		1fch		1fch		lavi		!	Ican			1cun			1dn1			1ez3
SEQ D	5	1561		1561		1563		1560	200			1563			1563	651		1563

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PDB annotation	KDA PROTEIN, P35A, THREE HELIX	PROTEIN TRANSPORT HELIX- TURN-HELLIX TPR-LIKE REPEAT, PROTEIN TO AMENODE	CONTRACTILE PROTEIN TRIPLE- HELLY COLLED CONTRACTION CONTRACTILE PROTEIN TRIPLE-	CONTRACTILE PROTEIN CONTRACTILE PROTEIN TRIPLE. HELLY COLLED COLL.	TRANSCRIPTION REGULATION SIGMA 70; TRANSCRIPTION ESIGMA FACTOR, TRANSCRIPTION REGULATION		COMPLEX (INFIBITOR/NUCLEASE) COMPLEX (INFIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-	LIGASE CYCLIN A/CDK2. ASSOCIATED PROTEIN P45: CVC1 IN
Coumpound		VESICULAR TRANSPORT. PROTEIN SEC17; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RNA PÓLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L.
SEQFOL D score		90.99	71.18							
PMF score				-0.06	0.12		0.00	0.62	-0.05	0.01
Verify score				0.01	0.09		0.06	0.50	0.04	90.0
Psi Blast		1.2e-09	4.5e-17	4.5e-17	1.2e-06			1.5e-13	6.8e-09	3.4e-15 (
END AA		283	291	246	287		143	176	133	140
STAR T AA		2	22	'n	92		_	<b>m</b>	43	3
CHAI N ID		A	A	A			∢	¥	В	4
PDB ID		lqqe	1quu	lquu	lsig			la4y	1601	1fqv .
SEQ ID NO:		1563	1563	1563	1563		5057	1565	1565	1565

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PDB annotation	A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS		
PD	A/CDK2-ASSC SKP1, SKP2, F RICH REPEAT E3, UBIQUITII	LIGASE CYCLIN A/CDK2 ASSOCIATED PROTEIN P A/CDK2-ASSOCIATED PR SKP1, SKP2, F-BOX, LRR, RICH REPEAT, SCF, UBIC E3, UBIQUITIN PROTEIN	LIGASE CYCLIN A/CDK2. ASSOCIATED P45; CYCLI ASSOCIATED P19; SKP1, BOX, LRRS, LEUCINE-RIC REPEATS, SCF, 2 UBIQUI UBIQUITIN PROTEIN LIG	ACETYLATION RNASE IN RIBONUCLEASE/ANGIOG INHIBITOR ACETYLATIO LEUCINE-RICH REPEATS	ACETYLATION RNASE IN RIBONUCLEASE/ANGIOG INHIBITOR ACETYLATIO LEUCINE-RICH REPEATS		
Coumpound	N, P;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, I, L, N, P;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 3 M AMMONIUM SULFATE, PH 7.8) 2CBA 4	LYASE(OXO-ACID) CARBONIC ANHYDRASE II (E.C.4.2.1.1) (50 MM TRIS, 2CBA 3 3 M AMMONIUM SULFATE, PH 7.8)
SEQFOL D score							403.66
PMF		0.99	0.07	0.03	0.35	1.00	
Verify score		0.74	0.23	0.01	0.18	1.12	
Psi Blast		3e-17	3.4e-15	1.5e-12	4.5e-10	0	0
END		174	140	143	176	242	242
STAR T AA		က	m	=	2	3	ဇ
CHAI N ID		V V	A				
PDB ID		1fqv	1fs2	2bnh	2bnh	2cba	2cba
SEQ		1565	1565	1565	1565	1567	1567

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PDJ8 annotation			OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN,	AKACHIDONA 1E, 2 ENDOPEROXIDE OXIDOREDUCTASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE- 2	DECOMPLEA OXIDOREDUCIASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCIASE, PEROXIDASE-2	OXIDOREDUC: FEBRACHIDONIC ACID, MEMBRANE PROTEIN, PEROXIDASE DIOXYGENA SE		OXIDOREDUCTASE ADR, NADPH: ADRENODOXIN OXIDOREDUCTASE; FLAVOENZYME, MAD ANALYSIS,	ELECTRON TRANSFERASE	CALDOREDUC LASE FLAVOPROTEIN, OXIDASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II;	REDUCTASE, COMPLEX II,	SUCCINATE DEHYDROGENASE, 2 PESDIP A TION ONLY OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STAT	ACCIDENTALION, CALLOCAEDUCIASE	
Coumpound	2CBA 4		PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9- MER; CHAIN: F;	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A;		ADRENODOXIN REDUCTASE; CHAIN: A;	SARCOSINE OXIDASE: CHAIN:	A, B;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A M: FIIMARATE	REDUCTASE IRON-SULFUR	PROTEIN; CHAIN: B, N; FIJMARATE REDITCTASE 15 KD	HYDROPHOBIC PROTEIN;	CHAIN: C, O; FUMARATE REDUCTASE 13 KD
SEQFOL D score															
PMF score			-0.11	0.19	1.00	1.00		0.00	0.81		0.03				
Verify score			0.06	-0.76	0.61	0.22		-0.65	0.31		-0.04	-			
Psi Blast			0	3.4e-41	0	0		0.0045	6.8e-37	7	8.5e-53	,		<u>.</u>	
END AA			089	241	714	680		82	430		437		,		
STAR T AA			167	139	252	167		51	62		10	-			
CHAI N ID			∢	Y	ပ	A		∢	<b>V</b>		€	_			
PDB ID			Icvu	1d2v	1d2v	1diy		ojo -	lel5	+					
SEQ NO:		7	1568	1568	1568	1568		1569	1569	$\dashv$	6001				
							_								

PDB annotation					TIME A CLASSICAL CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTR	OXIDOREDUCIASE FUMARATE REDUCIASE, SUCCINATE	DEHYDROGENASE, RESPIRATORY 2 CHAIN, CITRIC ACID CYCLE,	FLAVOPROTEIN, IRON-SULPHUR 3	PROTEIN, DIHAEM CYTOCHROME B		OXIDOREDUCTASE OXIDOREDUCTASE				ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM-	BINDING, PHOSPHORYLATION	ACTIN-BINDING PROTEIN ACTIN-	BINDING, PHOSPHORYLATION	STRUCTURAL PROTEIN CALPONIN	HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN CALPONIN
Coumpound		HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (F.C.1.8.1.4)	COMPLEX WITH 1LPF 3 FLAVIN-ADENINE-	DINUCLEOTIDE (FAD) 1LPF 4	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT;	CHAIN: A, D; FUMARATE REDITCTASE IRON-SULFUR	PROTEIN; CHAIN: B, E;	FUMARATE REDUCTASE CYTOCHROME B SUBUNIT:	CHAIN: C, F;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A. D:	OVIDOBEDIICTARE	DIHYDROLIPOAMIDE	DEHYDROGENASE (E.C.1.8.1.4)	T-FIMBRIN; CHAIN: NULL;		T-FIMBRIN; CHAIN: NULL;		UTROPHIN; CHAIN: A, B;		UTROPHIN; CHAIN: A, B;
SEQFOL	D score								<u>.</u>					,					74.32		
PMF	score		0.07			0.04					-0.09	9	0.0		0.83		0.40				1.00
Verify	score		-0.23			-0.34					0.04	000	60.0		09.0		0.54				0.84
Psi Blast			0.003			1.2e-43	·		_		8.5e-29	21000	0.0013		5.1e-24		1.5e-29		4.5e-35		1.7e-34
END	AA		82			437					434	6	2		230		230		232		232
STAR	TAA		46			61					28	1	<del>2</del>		125		127		123		126
CHAI	e z		A	,		A	_				Ą		∢						A		А
PDB	A		llpf			1qla					1408	,	Siad		laoa		1aoa		1bhd		1bhd
SEO	a Ş		1569			1569					1569	33.	1369		1571		1571		1571		1571

HOMOLOGY, ACTIN BINDING,	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRICTI BAI BOTTEN	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING	DOMAIN, CYTOSKELETON STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN-	BINDING, UTROPHIN STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRIFTI BAT 1920 CHEN	STREET WOLLING	STRUCTURE, ELONGATED SHAPE, E3 UBIQUITING LIGASE, E2 2	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONITICATING ENZYME	THE CHARLES CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL O	CELL ADHESION NOAM; NCAM,
	UTROPHIN; CHAIN: A, B;	SPECTRIN BETA CHAIN; CHAIN: A;	SPECTRIN BETA CHAIN; CHAIN: A;	DYSTROPHIN; CHAIN: A, B, C, D;	UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2: CHAIN: D.	UBIQUITIN-POTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONUGATING ENZYME E2; CHAIN: D;		NEURAL CELL ADHESION
		86.88						131.07		
	1.00		1.00	1.00	1.00		1.00			0.05
	0.85		0.86	0.69	0.68		0.24			99.0
	4.5e-35	8.5e-43	8.5e-43	le-35	5.1e-35		0	0		1e-06
	232	235	235	233	233		562	564		207
	127	126	127	126	126		202	212		115
	∢	∢	¥.	∢.	Ą		∢	4		A
	Ibhd	16kr	1bkr	Idxx	lqag	+		lc4z	,	lepf
	1571	1571	1571	1571	1571		1574	1574	7	1575
		1bhd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN: A, B;	1bhd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN; A, B;           1bkr         A         126         235         8.5e-43         86.88         SPECTRIN BETA CHAIN;           CHAIN; A;         CHAIN; A;	1bhd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN: A, B;           1bkr         A         126         235         8.5e-43         86.88         SPECTRIN BETA CHAIN;           1bkr         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           1bkr         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;	lbhd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN: A, B;           lbkr         A         126         235         8.5e-43         86.88         SPECTRIN BETA CHAIN;           lbkr         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           ldxx         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           ldxx         A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN: A, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B, C, B,	1bhd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN: A, B;           1bkr         A         126         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           1bkr         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           1dxx         A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN; A, B, C, D;           1qag         A         126         233         5.1e-35         0.68         1.00         UTROPHIN ACTIN BINDING         3           1qag         A         126         233         5.1e-35         0.68         1.00         UTROPHIN ACTIN BINDING         3	1bkd         A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN: A, B;           1bkr         A         126         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           1bkr         A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           1dxx         A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN: A, B, C, B, B, B, B, B, B, B, B, B, B, B, B, B,	1bhd   A   127   232   4.5e-35   0.85   1.00   UTROPHIN; CHAIN: A, B;   1bkr   A   126   235   8.5e-43   0.86   1.00   SPECTRIN BETA CHAIN;   CHAIN: A;   126   233   1e-35   0.69   1.00   DYSTROPHIN; CHAIN: A, B, C, D;   1dag   A   126   233   5.1e-35   0.68   1.00   UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;   1e-25   202   562   0   0.24   1.00   UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN 1.1GASE E3A; CHAIN: A, B, C,	Ibbr   A   127   232   4.5e-35   0.85   1.00   UTROPHIN; CHAIN: A, B;   Ibbr   A   126   235   8.5e-43   0.86   1.00   SPECTRIN BETA CHAIN;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	lbhd   A   127   232   4.5e-35   0.85   1.00   UTROPHIN; CHAIN: A, B;     lbkr   A   126   235   8.5e-43   0.86   1.00   SPECTRIN BETA CHAIN;     lbkr   A   126   233   1e-35   0.69   1.00   DYSTROPHIN; CHAIN; A, B, C, D;     ldxx   A   126   233   5.1e-35   0.68   1.00   DYSTROPHIN ACTIN BINDING REGION; CHAIN: A, B;     lc4z   A   202   562   0   0.24   1.00   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C, UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   0.24   1.00   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   0.24   1.00   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   564   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   242   0   BiQUITIN-PROTEIN LIGASE E3A; CHAIN: B, B;     lc4z   A   212   242   0

PDB annotation	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD		IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN IG REPEAT · 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR,
Coumpound	MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	TLYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) IHNG 3	TITIN, 127; CHAIN: NULL;	FC GAMMA RIIB; CHAIN: A;	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	SIALIDASE; CHAIN: NULL;	SIALIDASE; CHAIN: NULL;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR;
SEQFOL D score											53.09
PMF score		0.13	0.04	0.00	0.01	-0.19	-0.20	-0.20	-0.19	-0.14	
Verify score		-0.30	0.13	-0.25	0.13	0.08	0.14	0.05	0.03	0.02	
Psi Blast		3e-05	1.5e-06	1.2e-05	7.5e-06	9e-10	7.5e-10	1.5e-10	6e-10	6e-11	6e-11
END		188	212	186	206	999	643	324	476	212	224
STAR T AA		113	115	113	105	484	491	138	266	102	31
CHAI N ID		m	A		A	A	A			£	В
PDB ID		lev2	1hng	1tit	2fcb	1d0s	1d0s	1eut	1eut	1bp3	1bp3
SEQ	ë	1575	1575	1575	1575	1576	1576	1576	1576	1578	1578

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PDi3 annotation	HORMONE/GROWTH FACTOR	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN					HORMONE/GROWTH	FACTOR/HORMONE RECEPTOR 4-	HELICAL BUNDLE, ALFRA HELICAL BUNDLE TERNARY	COMPLEX, FN 2 III DOMAINS, BETA	SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING	CELL ADHESION PROTEIN CELL ADHESION PROTEIN RGD	EXTRACELLULAR MATRIX, 2	HEPARIN-BINDING,	CELL ADHESION PROTEIN CELL	ADHESION PROTEIN, RGD,	EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING
Coumpound	CHAIN: B;	TITIN; CHAIN: NULL;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A:	NEURAL ADHESION MOLECULE DROSOPHILA NET IR OCT 14 N	(CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO	AMINO PROXIMAL	REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	PLACENTAL LACTOGEN;	CHAIN: A; PROLACTIN RECEPTOR: CHAIN: B. C.	Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro			FIBRONECTIN; CHAIN: A;	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	FIBRONECTIN; CHAIN: NULL;			FIBRONECTIN: CHAIN: NI II J.		-
SEQFOL D score													56.61	200	57.30					
PMF score		-0.08	-0.09	0.04				-0.14										0.34		
Verify score		-0.00	0.08	0.09				0.23										0.30		
Psi Blast		9e-10	3e-08	6e-10				3e-10					7.5e-06	1 22 00	1.25-09	•		1.2e-09		
END		218	211	661				211					315	224	+77			199		
STAR T AA		119	124	41				124					35	3.4	÷			37		
CHAI N ID			Ą					В					∀		_					
PDB ID		1bpv	1c8p	1cfb				J9J1					1fnh	1mfn				Imfn		
SEQ ID NO:		1578	1578	1578				1578					1578	1578				1578		

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PDB annotation	GLYCOPROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX,	ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN		PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCN5-RELATED N- ACETYI TRANSFERASE, 3 COA-	BINDING	TRANSFERASE N-ACETYL TRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE	
Coumpound		TENASCIN; CHAIN: A, B;		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	FIBRONECTIN; CHAIN: A;	ARYLALKYLAMINE N- ACETYLTRANSFERASE; CHAIN: A, B;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;		SEROTONIN N- ACETYLTRANSFERASE; CHAIN: A;	HPA2 HISTONE ACETYL TRANSFERASE; CHAIN: A, B, C, D;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	
SEQFOL D score		55.27										
PMF score				0.59	0.10	0.80	0.10		0.86	0.04	0.00	
Verify score				-0.03	0.11	0.42	-0.56		0.50	-0.15	0.08	
Psi Blast		4.5e-07		1.5e-09	9e-10	8.5e-14	1.7e-10		5.1e-13	5.1e-12	1.5e-14	
END		211		199	213	627	622		627	624	633	
STAR T AA		35		124	124	511	523		511	487	537	
CHAI N ID		A			A	В	A		A	A	A	
PDB	1	1qr4		J#I	2fnb	1b6b	1bo4		1cjw	1qsm	1qsm	
SEQ ID	NO:	1578		1578	1578	1579	1579		1579	1579	1579	

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מאמ	FDE annotation	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AAC; AMINOGLYCOSIDE 6-N- ACETYLTRANSFERASE, ANTRIOTIC 2 RESISTANCE	ACETYL COENZYME A TRANSFERASE AMINOGL YCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2	AMINOGLYCOSIDE RESISTANCE, GCNS-RELATED N-	TRANSFERASE N-ACETYL TRANSFERASE	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING	PROTEIN TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX,	ACETYLTRANSFERASE TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX,	ACETYLTRANSFERASE TRANSFERASE HISTONE ACETYLTRANSFERASE, GCNS- RELATED N-	ACETYLTRANSFERASE, 2 COA BINDING PROTEIN
Commonad		ARYLALKYLAMINE N. ACETYLTRANSFERASE; CHAN: A D.	CHAIN: A, B, AMINOGLYCOSIDE N6- ACETYLTRANSFERASE TYPE 1; CHAIN: A;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;	•	SEROTONIN N. ACETYLTRANSFERASE;	P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	HPA2 HISTONE ACETYLTRANSFERASE;	HPA2 HISTONE HPA2 HISTONE COURT TRANSFERASE;	CERAIN: A, B, C, D; TGCNS HISTONE ACETYL TRANSFERASE; CHAIN: A;	
SEOFOL	D score										
PMF	score	0.83	0.16	0.04		0.63	0.10	0.64	0.00	0.48	
Verify	score	0.43	-0.18	-0.18		0.59	0.13	0.17	0.08	-0.21	
Psi Blast		3.4e-19	1.7e-11	5.1e-12		1.5e-18	1e-17	3.4e-11	1.5e-14	8.5e-16	
匚		732	749	727		732	751	729	738	749	
STAR	TAA	919	626	627		610	637	615	642	637	
CHAI	21 Z	В	¥.	A		٧	В	<b>V</b> .	∢	<b>∀</b>	
PDB	<b>a</b>	1565	1587	1504		1cjw	1cm0	lqsm	1qsm	1qst	
SEQ	e ë	1580	1580	1580		1580	1580	1580	1580	1580	
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PDB annotation	GENE REGULATION ADA4; TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N- 2 ACETYLTRANSFERASE, GCN5 RELATED N-ACETYLTRANSFERASE FAMILY, 3 GENE REGULATION	OXIDOREDUCTASE TRYPANOTHIONE REDUCTASE, FAD DEPENDENT DISULPHIDE 2 OXIDOREDUCTASE	OXIDOREDUCTASE FLAVIN- DEPENDENT AMINE OXIDASE, OXIDOREDUCTASE		RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE,
Coumpound	TRANSCRIPTIONAL ACTIVATOR GCNS; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	SMALL NUCLEAR RIBONUCLEOPROTEIN SM DI; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN
SEQFOL D score						·	·
PMF score	0.39	0.21	0.09	0.16	0.63	0.93	0.33
Verify score	-0.37	0.06	0.02	0.01	0.48	0.50	0.50
Psi Blast	5.1e-14	1.2e-06	0.00014	1.5e-07	1.4e-13	3.4e-11	1.7e-11
END	749	116	104	123	126	122	126
STAR T AA	637	65	70	19	44	40	14
CHAI N ID	A	Ą	A	A	A	В	⋖
PDB ID	lygh	laog	1537	3lad	1634	1b34	1436
SEQ ID	1580	1582	1582	1582	1587	1587	1587

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PDB annotation	RNA BINDING PROTEIN	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN	RNA BINDING I'ROTEIN D3 CORE SNRNP PROTEIN, B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING I'ROTEIN		OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN	CYTOKINE LCF. CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
Coumpound	ASSOCIATED CHAIN: B, D, F, H,	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, I, L;		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE: CHAIN: B:	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE: CHAIN: B:	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	INTERLEUKIN 16; CHAIN: NULL;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;
SEQFOL D score		·							
PMF score		0.99	0.69		0.96	0.82	1.00	0.76	0.93
Verify		0.25	0.26		0.69	0.72	0.56	0.35	0.83
Psi Blast		5.1e-24	8.5e-25		3e-14	3.4e-13	1.5e-18	1.5e-16	7.5e-15
END		134	134		80	110	98	96	82
STAR T AA	,	43	39		12	3	٧.	6	6
CHAI N ID		В	Q		¥.	<b>V</b>	<		A
PDB ID		1436	1436		1689	1b8q	1be9	1116	Ikwa
SEQ D NO:		1587	1587	3000	1388	1588	1588	1588	1588

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PDB annotation	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING	PROTEIN BINDING GATE-16; UBIQUITIN FOLD	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN
Coumpound	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	GOLGI-ASSOCIATED ATPASE ENHANCER OF 16 KD; CHAIN: A, B;	APOLIPOPROTEIN A-1; CHAIN: A, B, C, D;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score							54.19	61.70
PMF score	1.00	0.95	1.00	0.99	1.00	0.89	_	
Verify score	0.78	0.89	0.66	0.79	0.91	0.36		
Psi Blast	16-17	1.2e-14	3.4e-19	1.4e-15	1.7e-16	8.5e-34	4.5e-06	1.5e-07
END	96	96	81	83	98	187	244	248
STAR T AA	m	12	m			91	29	28
CHAI		A	A	A	A	A	Ą	A
PDB ID	1pdr	1qau	Iqav	1qlc	3pdz	1co6	1av1	lcun
SEQ ID	1588	1588	1588	1588	1588	1590	1591	1591

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PDB annotation	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN	MEMBRANE PROTEIN FOUR HELIX	CONTRACTILE PROTEIN TRIPLE- HELLY COLLED COLL,	CONTRACTILE PROTEIN TRANSPORT PROTEIN VAMP 2; MEMBRANE FUSION PROTEIN COMPLEX, TRANSPORT PROTEIN	DESIGNED HELICAL BUNDLE	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	COMPLEY (RI OD)	COAGULATION/INHIBITOR) ATTOPROTHROMBIN IA:	HYDROLASE, SERINE	PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COAGULATION/INHIBITOR)	COMPLEX (BLOOD COAGULATION/INHIBITOR)	AUTOPKOTHROMBIN IIA; HYDROLASE, SERINE	PROTEINASE), PLASMA CALCIUM BINDING 2 GLYCOPROTEIN
Coumpound	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B.	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B.	SSOI PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SYNAPTOBREVIN 2; CHAIN: A, E, I; SYNTAXIN 1A; CHAIN: B, F, J; SNAP-258; CHAIN: C, G, K; SYAP, 25B; CHAIN: C, G, K;	DHP1; CHAIN: NULL;	DHP1; CHAIN: NULL;	ACTIVATED PROTEIN C:	CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P:			A COTTAIN AFTER THE COMPANIES	CHAIN: C, L; D-PHE-PRO-MAI;	CIPAIN: F;	
SEQFOL D score				57.26	55.15									- 1	
PMF score	0.45	0.95	0.04			0.16	0.17	0.06				0.47	ì		
Verify	-0.00	0.16	0.23		-	0.49	0.17	0.21				0.32	7		
Psi Blast	3.4e-22	1.5e-38	3.4e-13	4.5e-12	9e-24	5.1e-05	3.4e-05	lc-10				4 SP-12			
END	233	233	213	251	245	73	75	324				385	}		
STAR T AA	17	19	22	28	174	30	36	249				306			
CHAI N ID	В	В	V	∢	В			ı				]			
PDB ID	1dn1	1dn1	1fio	Iquu	1sfc	4hb1	4hb1	laut				laut			
SEQ ID NO:	1591	1651	1591	1591	1591	1591	1591	1592				1592			

PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR)	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
Coumpound		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;
SEQFOL D score						
PMF		0.04	0.04	,	-0.19	0.16
Verify score		0.18	90.0	0.44	0.17	0.02
Psi Blast		1.5e-09	1.5e-14	1.4e-09	3.4e-11	3e-15
END		326	374	186	249	385
STAR T AA		246	280	109	139	253
CHAI N ID		A	A	ı	T	L
PDB		Icej	lcej	1dan	Idan	1dan
SEQ U		1592	1592	1592	1592	1592

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PDIs annotation	HYDROLASE/IYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGRCMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGR-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2	MATRIX PROTEIN MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISFASP MITATION, 2 FOR 1 TAT
Coumpound	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEDTIDE E 76. CHAIN: V, V.	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG: CHAIN: C, D;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, I, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, I, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	FIBRILLIN; CHAIN: NULL;
SEQFOL D score					
PMF score	-0.03	-0.18	0.01	-0.15	-0.05
Verify score	0.24	0.13	-0.18	0.03	0.01
Psi Blast	1.4e-09	3.4e-11	1.2e-14	8.5e-12	1.7e-09
END AA	186	249	383	402	339
STAR T AA	109	139	295	307	245
CHAI N ID	T	L	I	Н	
FDB ID	Idva	1dva	1dx5	1dx5	Iemn
SEQ ID	1592	1592	1592	1592	1592

PDB annotation	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR,
	DOM FRA(	EXTI EXTI CAL( GLY) SIGN DISE DOM	MAT EXTI CALV GLY SIGN DISE DOW	EXT. EXT. CAL GLY SIGN DON FRA	SIGN PRO PRO	BLO CON PRO BLO PRO
Coumpound		FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR:
SEQFOL D score		56.86			55.46	
PIMF score			0.55	0.13		0.03
Verify score			0.33	0.36		0.10
Psi Blast		1.7e-15	1.7e-15	8.5e-14	3e-10	1.4e-09
END		382	380	402	357	186
STAR T AA		277	302	337	194	109
CHAI					¥	T
PDB UD		1emn	lemn	lemn	lext	1fak
SEQ 1D	NO:	1592	1592	1592	1592	1592

	<del></del>	<del></del>																					
PD/8 annotation	RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	BLOOD CLOTIING COMPLEX(SERINE	PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME 3 INHIBITOR	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND),	HORMONE RECEPTOR HOPMONE	RECEPTOR, INSULIN RECEPTOR	FAMILY	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROJEIN GLYCOPROTEIN	COMPLEX (BLOOM COPROTEIN	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	BINDING HYDROI ACE 2	GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMBIES
Coumpound	CHAIN: T; SL15; CHAIN: I;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L;	BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I:		INSULIN-LIKE GROWTH	FACTOR RECEPTOR 1; CHAIN:	A;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	LAMMIN; CHAIN: NULL;	LAMMINI, CHAIN: NOLL;	I AMININI CHAIN; NULL;	I AMININ, CHAIN: NOLL;	FACTOR IXA: CHAIN: C 1 · D-	PHE-PRO-ARG; CHAIN: 1;						FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;
SEQFOL D score												70.13	70.13							<del>,</del>			
PMF score		-0.18				0.00		0.21	0.51	21.7	-0.14	-0.10	-0.14	-010	-0.12					-		-0.02	
Verify score		0.08				0.20		0.15	0.44	0.00	0.19	21.5	0 37	0.07	0.58							0.44	
Psi Blast		3.4e-11				4.5e-12		3 46-13				7.5e-19	3.4e-12		6							1.56-10	
END AA		249				380		242	281	331	382	396	193	403	173		,				8	677	
STAR T AA						246		112	146	147	230	231	27	295	109			•			955	651	
CHAI N ID		<b>-</b> 1				Ą									l,								
PDB ID		Itak				ligr		1klo	1klo	Iklo	1klo	1klo	1klo	1klo	-						$\top$		
SEQ NO:		1592				1592		1592	1592	1592	1592	1592	1592	1592	1592						1500	7	

				1		T	
PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	PLASMINOGEN ACTIVATION	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD
Coumpound		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score							
PMF score		-0.09	-0.17	-0.18	0.71	-0.05	-0.12
Verify score		0.55	0.23	0.26	0.49	0.91	0.23
Psi Blast		1.4e-09	3.4e-10	7.5e-09	1.3e-11	3e-10	3.4e-09
END		186	249	338	385	180	189
STAR T AA		109	143	253	283	128	109
CHAI N ID		٦	L	٦	7		L
PDB ID		1qfk	Iqfk	19fk	1qfk	1tpg	1xka
SEQ US	2	1592	1592	1592	1592	1592	1592

	T					-,			
COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, ISPIDERMAL 2	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, IPDERMAL 2	GNOW THE FACTOR LINE DOMAIN					CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3		DNAJ; CHAIN: NULL;
			53.26		60.84				81.78
	-0.03	0.46		-0.12		-0.19	-0.05		
	0.04	0.43		0.22		0.04	0.00		
	7.5e-09	1.2e-11	1.2e-11		1.5e-16	··	3.46-13		3.4e-28
	328	382	395	264	340	342	221		77
	255	283	305	114	152	183	25		_
,	1	J	Г	A	۷	∢	∢		
	Ixka	lxka	Ixka	9wga	9wga	ywga	9wga	  -  -	0pd I
	7661	1592	1592	1592	1592	7601	1592	203.	1393
		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	1xka         L         255         328         7.5e-09         0.04         -0.03         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.43         0.46         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.45         BLOOD COAGULATION	1xka         L         255         328         7.5e-09         0.04         -0.03         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.43         0.46         BLOOD COAGULATION         1           1xka         L         305         395         1.2e-11         53.26         BLOOD COAGULATION         1           1xka         L         305         395         1.2e-11         53.26         BLOOD COAGULATION         1           1xka         L         305         395         1.2e-11         53.26         BLOOD COAGULATION         1	1xka         L         255         328         7.5e-09         0.04         -0.03         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.43         0.46         BLOOD COAGULATION         1           1xka         L         305         395         1.2e-11         53.26         BLOOD COAGULATION         1           1xka         L         305         395         1.2e-11         53.26         BLOOD COAGULATION         1           9wga         A         114         264         3.4e-14         0.22         -0.12         LECTIN (AGGLUTININ) WHEAT         PRODLINININ WHEAT           1column         CHOOL TO SWGA 3         (ISOLECTIN 2) 9wGA 3         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00         10.00 <th>  1xka   L   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   C   C   C   C   C   C   C   C   C</th> <th>  1kka   L   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   C   C   C   C   C   C   C   C   C</th> <th>1xka         L         255         328         7.5e-09         0.04         -0.03         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.43         0.46         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.45         BLOOD COAGULATION           9wga         A         114         264         3.4e-14         0.22         -0.12         BLOOD COAGULATION           9wga         A         152         340         1.5e-16         33.26         BLOOD COAGULATION           9wga         A         114         264         3.4e-14         0.22         -0.12         GBRM AGGLUTININ           9wga         A         152         340         1.5e-16         AGGLUTININ         BECTIN (AGGLUTININ)           9wga         A         183         342         1.4e-15         0.04         -0.12         GBRM AGGLUTININ           9wga         A         183         342         1.4e-15         0.04         -0.19         GBRM AGGLUTININ           9wga         A         183         342         1.4e-15         0.004         -0.19         GBRM AGGLUTININ           9wga         <td< th=""><th>  1   1   1   1   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   2   2   3   3   3   2   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   4   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   3   3</th></td<></th>	1xka   L   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   C   C   C   C   C   C   C   C   C	1kka   L   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   C   C   C   C   C   C   C   C   C	1xka         L         255         328         7.5e-09         0.04         -0.03         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.43         0.46         BLOOD COAGULATION           1xka         L         283         382         1.2e-11         0.45         BLOOD COAGULATION           9wga         A         114         264         3.4e-14         0.22         -0.12         BLOOD COAGULATION           9wga         A         152         340         1.5e-16         33.26         BLOOD COAGULATION           9wga         A         114         264         3.4e-14         0.22         -0.12         GBRM AGGLUTININ           9wga         A         152         340         1.5e-16         AGGLUTININ         BECTIN (AGGLUTININ)           9wga         A         183         342         1.4e-15         0.04         -0.12         GBRM AGGLUTININ           9wga         A         183         342         1.4e-15         0.04         -0.19         GBRM AGGLUTININ           9wga         A         183         342         1.4e-15         0.004         -0.19         GBRM AGGLUTININ           9wga <td< th=""><th>  1   1   1   1   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   2   2   3   3   3   2   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   4   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   3   3</th></td<>	1   1   1   1   255   328   7.5e-09   0.04   -0.03   BLOOD COAGULATION   FACTOR XA; CHAIN: L, C;   2   2   3   3   3   2   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   4   1.2e-11   0.43   0.46   BLOOD COAGULATION   1   2   3   3   3   3   3   3   3   3   3

ration	OTTA DEBONE	EIN FOLDING,	ERONE HDJ-1; ERONE	ERONE HDJ-1; ERONE	ERONE HDJ-1; ERONE	-			NDING		, , , , , , , , , , , , , , , , , , , ,					VDNA LEF-1	ACTOR, DNA	ENDING,	OMAIN/DNA),	N/DNA LEF-1 ICR-A,
PDB annotation	Over Tree date 1 170	CHAPEKONE HSF 40; CHAFEKONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE				COMPLEX (DNA-BINDING	( COLUMNIA)						GENE REGULATION/DNA LEF-1	TRANSCRIPTION FACTOR,	BINDING, DNA 2 BENDING	COMPLEX (HMG DOMAIN/DNA),   GENE REGULATION/DNA	GENE REGULATION/DNA LEF- HMG; LEF1, HMG, TCR-A,
Coumpound		DNAJ; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-	BINDING IHME 3 HMG-BOX	DOMAIN B OF RAT HMG1)   (NMR, 1 STRUCTURE) 1HME 4	HUMAN SRY; 1HRY 6 CHAIN:	CHAIN: B; 1HRY 10	DNA-BINDING HIGH	(HMG1) BOX 2, COMPLEXED	WITH 1HSM 3	MERCAPTOETHANOL (NMR,   MINIMIZED AVERAGE	STRUCTURE) 1HSM 4	LYMPHOID ENHANCER-	DNA (5'- CHAIN: B; DNA (5'-	CHAIN: C;		LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A;
SEQFOL D score	31036 7		86.98					· · · · · · · · · · · · · · · · · · ·								125.69				
PMF	31016	1.00		1.00	1.00	0.43			0.24		0.75							•		1.00
Verify	SCOLE	0.84		0.97	0.97	-0.13			0.01		0.11									0.31
Psi Blast		3.4e-28	1e-33	3.4e-27	1e-33	1.4e-21			1e-27		3.4e-22					3e-22				3e-22
END	¥.¥	89	78	89	11	416			416		419					429				420
STAR	I AA	E.	7	c.	6	351			350		351					344				345
CHAI	OI N	-							A							Ą				A
PDB	a	1bq0	1hdj	1hdj	1hdj	1hme		,	1hry		Ihsm					2lef				2lef
SEQ	a ë	1593	1593	1593	1593	1594			1594		1594					1594				1594

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PDB annotation	TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGIT ATION/DNA	GENE REGULATION/DNA LEF-1 FING; LEF1, HMG, TCR-4, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA),	GENE REGULA TION/DNA	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN	COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA)	GENE REGULATIONDNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA? BENDING, COMPLEX (HMG DOMAINDNA),	GENE REGULATIONDNA GENE REGULATIONDNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANDNG RIPTION FACTOR, DNA RINDING DNA 9 PENDING
Coumpound	DNA (S'- CHAIN: B; DNA (S'- CHAIN: C;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;		NON HISTONE PROTEIN 6 A; CHAIN: A;	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: R: 1HRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B: 1HRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: R: IHRY 10	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;
SEQFOL D score						83.75		57.47	
PMF score		1.00		0.89	0.78		0.81		0.74
Verify		0.40		0.10	-0.10		0.04		-0.29
Psi Blast		3.4e-20		8.5e-21	le-21	7.5e-27	7.5e-27	66-27	8.5e-17
END		420		106	114	115	115	128	128
STAR T AA		350		31	43	43	44	43	44
CHAI N ID		∢		V	¥	A	Ą	· ·	A
PDB ID		2lef		1cg7	lhry	lhry		2lef	Zlef ,
SEQ NO:		1594		1598	1598	1598	1598	1598	1598

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IN/DNA), A	A LEF-1 A, DR, DNA NG, IN/DNA),	MOLLOTIV	.A, PP33;	CIN, BETA	SDOCIIC	PROTEIN	N, MEKA,	) NCTION		AIN, FBP.	Z.	AIN, FBP.	און אין אין אין אין אין אין אין אין אין אי	AIN, FBF.	AIN, FBP.	X.	ROTOTYP	ROTOTYF		STRUCTURAL PROTEIN EF-HAND LIKE DOMAIN, WW DOMAIN
DOMA JON/DN	TON/DN G, TCR-, N FACT S BENDI S DOMA TON/DN	TD A NCT	IA; MER	ANSDU	L IKAN	TION, G	3 VISIO	TRANSI		W DOM	DUCTIC	W DOM			W DOW	DUCTIC	E WWP	E WWP	Z	STRUCTURAL PROTEIN EF-H LIKE DOMAIN, WW DOMAIN
X (HMC	EGULAT SF1, HM RIPTIOI 3, DNA 2 EGULAT	X	A-GAMA	JCIN, TR	, SIGNA	ORYLA	DOXIN,	EX DUCER/		MAIN W	TRANS	MAIN W	NIV.	MAIN W	MAIN W	TRANS	TOTYP N DESIG	TOTO	N DESIG	TURAL J
COMPLI-	GENE RI HMG; LI TRANSC BINDING COMPLI GENE R	COMPLI	GT BET	PHOSDI	GAMMA	PHOSPE	THIORE	(TRANS		SH3 DO	SIGNAL	SH3 DO	ANIDIO POR	SHS DO	SH3 DO	SIGNAL	SH3 PR	SH3 PR	PROTE	STRUC LIKE D
	Ä: A;	Ġ,								EIN;		EĽ;		EIN;	EIN;		i: A;	ľ. A;		••
	ANCER- R; CHAI B; DNA (	HAIN: B	, ı ., ıı							G PROT		G PROT		G PROT	G PROT		; CHAIN	; CHAIN		HAIN: A
	ID ENHL FACTO CHAIN: ]	UCIN; C	CII, CII							BINDIN	<u>ئ</u> ز	NIONIA ,	ا ا انته	BINDIN 4:	BINDIN	.,	TOTYPE	TOTYPE		PHIN; C
	LYMPHO BINDING DNA (5'- ( CHAIN: C	TRANSD	rnospo							FORMIN	CHAIN: 7	FORMIN	CHAIN:	FORMIN CHAIN:	FORMIN	CHAIN:	WWPRO	WWPRO		DYSTROPHIN; CHAIN: A;
	0.71	-0.20						<u></u>		96.0		0.94		0.90	0.98		0.87	0.35		0.22
	0.27	0.10								09.0		0.72		0.17	0.09		0.03	0.64		0.27
		Se-09								.1e-07		.5e-09		60-a	.5e-08		.4e-09	.4e-12		3.4e-06
		+			·	<del></del>				1			7				159 3	1		117
																	129	+		82
									+									-		A
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CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: B, G; CHAIN: CHAIN: B, G; CHAIN: CHAIN: B, G; CHAIN: CHAIN: B, CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	21ef   A   45   116   6e-27   0.27   0.71   ENAPHOID ENHANCER-   DNA (5'- CHAIN: A; DNA (5'- D)   DNA (5'- CHAIN: B; DNA (5'- D)   DNA (5'- CHAIN: B; DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA (5'- D)   DNA	21ef   A   45   116   6e-27   0.27   0.71   BINDING FACTOR; CHAIN: A; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: B; DNA (3*-CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A;	21ef A   45   116   6e-27   0.27   0.71   DIVIDIO ENHANCER- BINDING FACTOR; CHAIN: 4; DIVA (5'- CHAIN: B; DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, DNA (5'- CHAIN: B, CHAIN: C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, CHAIN: B, C, C, C, C, C, C, C, C, C, C, C, C, C,	21ef   A   45   116   6e-27   0.27   0.71   I.YMPHOID ENHANCER- II. Se-09   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.10   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0.20   0	21ef   A   45   116   6e-27   0.27   0.71   BINDING FACTOR; CHAIN: A; DNA (5°- CHAIN: B; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; DNA (5°- CHAIN: C; 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CHAIN: A; DNA (5'-CHAIN: B; DNA (5'-CHAIN: B; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: B; DNA (5'-CHAIN: B; DNA (5'-CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; CHAIN: C; 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PDB annotation	ISOMERASE PINI; PEPTIDYL- PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING		SH3 DOMAIN WW DOMAIN, FBP28,	SH3 DOMAIN WW DOMAIN, FBP28,	SH3 PROTOTYPE WWPROTOTYPE,	SH3 PROTOTYPE WWPROTOTYPE,	PROTEIN DESIGN	ISOMERASE PİNI; PEPTIDYL. PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE	BIINDIING	TRANSFERASI; TRANSFERASE.	METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE	BIOSYNTHESIS	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE	TRANSFERASE PSAT	AMINOTRANSFERASE.	PYRIDOXAL-5".PHOSPHATE,	PHOSPHOSERINE, 2 ALKALIPHILIC	LYASE ALPHA/BETA FOLD	TRANSFERASE SHMT; HYDROXYME1HYL TRANSFERASE.
Coumpound	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;		FORMIN BINDING PROTEIN; CHAIN: A:	FORMIN BINDING PROTEIN; CHAIN: A:	WWPROTOTYPE; CHAIN: A;	WWPROTOTYPE; CHAIN: A;		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PITIDE; CHAIN: C.	CILLYIN, C,	SERINE	HYDROXYMETHYLTRANSFER ASE; CHAIN: A;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN:	A, B;	AMINOTRANSFERASE; CHAIN:	PHOSPHOSERINE	AMINOTRANSFERASE; CHAIN:	A;	The second second second	CSDB PROTEIN; CHAIN: A;	SERINE HYDROXYMETHYLTRANSFER
SEQFOL D score	·										<del></del>	355.62				•				·
PIMF score	0.01		0.82	0.94	66.0	0.99		0.01		0.78			100	3	1.00			5	2007	0.39
Verify	-0.06		-0.19	0.72	0.25	0.25		-0.06		0.20			0.71	*	0.84			90.0	07.0	0.07
Psi Blast	90 <del>-</del> 99		1e-07	1.5e-09	6.8e-05	6e-05		90-99		1.7e-67		1.7e-58	1.7e-58		5.1e-60	<del>-</del>		170-61	T	3.16-0/
END	185		125	124	121	121		148		387		389	389	}	389	•		389	207	) S
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PDB ID	1f8a		1e0i	1e01	1e0m	le0m	140	1104	-	1bj4		ngor .	1bjn		1bt4		-	1c0n	+	$\dashv$
SEQ ID NO:	1602		1603	1603	1603	1603	1603			1606	,	1606	1606		1606			1606	1606	

ind PDB annotation	Wat Ton Ample Monday 2.	1 CAKBON METABOLISM	LTRANSFER METHYLASE; ALPHA PLP C, D; ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD			TRANSFERASE TRANSFERASE, LTRANSFER METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE	ASE; CHAIN: AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS				FER	TTRANSFER METHYLASE; ALPHA PLP C, D; ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	TRANSFERASE SHMT; SERINE-
Coumpound	$\dashv$	ASE; CHAIN: A, B;	SERINE   HYDROXYMETHYLTRANSFER   ASE; CHAIN: A, B, C, D;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;		SERINE   HYDROXYMETHYLTRANSFER   ASE: CHAIN: A:	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A. B:	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	CSDB PROTEIN; CHAIN: A;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	SERINE
SEQFOL D score							282.66						
PMF			99.0	0.42		0.18		1.00	1.00	0.48	0.43	-0.02	0.07
Verify			0.11	-0.02		0.15		0.58	0.59	-0.01	-0.04	0.07	0.07
Psi Blast			1.7e-67	1.7e-66		3.4e-62	1.7e-49	1.7e-49	5.16-51	8.5e-56	6.8e-62	5.1e-66	5.1e-59
END	1		386	386	_	344	343	337	336	344	344	344	344
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PDB	a		1dfo	leji		1bj4	16jn	15jn	1bt4	100	1cj0	1dfo	leii
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PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER	COMPIET (TE ANISCENTE CONT.	FACTOR/DIA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION,	COMPLEX (IRANSCRIPTION   FACTOR/DNA)	CHAPERONE ARCHAEAL PROTEIN		CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CA		LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,		TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
ASE; CHAIN: A, B, C, D;	STAT3B: CHAIN: A: 18-MFB	DESOXYOLIGONUCLEOTIDE; CHAIN: B;	•	PREFOLDIN; CHAIN; A; PREFOLDIN; CHAIN; B; PREFOLDIN; CHAIN; C;		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) ICHC 3 (NMR, 1 STRUCTURE) ICHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C.	(Trans. C)	EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;
						70.36					
	0.04			0.11				0.01	0.22		0.04
	-0.48			-0.33				-0.23	0.31		0.02
	0.00051					7.5e-05		3.4e-11			6.8e-14
	20			82		345		603	611		885
	1			-		96		552	515		828
	4	=		€		<b>A</b>			∢		4
	lbgl		12.1.	IIXK		nnb _I		1chc			1b0x
	1608		1500	9001	30,7	1609		1612	1612	┪	1614
		ASE; CHAIN: A, B, C, D;   A   1   70   0.00051   -0.48   0.04   STAT3B: CHAIN: A-18 MED	1bg1         A         1         70         0.00051         -0.48         0.04         STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	1bg1         A         1         70         0.00051         -0.48         0.04         STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	1bg1         A         1         70         0.00051         -0.48         0.04         STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;           1fkk         A         1         82         1.2e-06         -0.33         0.11         PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: C	1bg1         A         1         70         0.00051         -0.48         0.04         STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;           1fkk         A         1         82         1.2e-06         -0.33         0.11         PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: C	1bg1         A         1         70         0.00051         -0.48         0.04         STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B; CHAIN: B;           1fkk         A         1         82         1.2e-06         -0.33         0.11         PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	1bg1	1bg1	1bg1	1bg1

SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	CALCIUM-BINDING PROTEIN CALB; CALCIUM++PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID
EPHB2; CHAIN: A, B, C, D, E, F, G, H;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
-0.09	1.00	1.00	0.37	1.00	0.59	0.89	0.00
0.21	0.08	0.32	0.33	-0.05	-0.02	0.85	-0.50
6.8e-15	1.5e-26	4.5e-16	1.5e-36	3e-28	1.2e-08	6.8e-22	1.5e-14
885	716	864	871	717	721	856	669
825	588	728	755	588	618	732	909
Ą	А	A	A	4	∀	4	4
1b4f	1a25	1a25	1a25	1byn	1byn	1byn	1djx
1614	1616	1616	1616	1616	1616	1616	1616
	1b4f A 825 885 6.8e-15 0.21 -0.09 EPHB2; CHAIN: A, B, C, D, E, F, G, H;	1b4f         A         825         885         6.8e-15         0.21         -0.09         EPHB2; CHAIN: A, B, C, D, E, F, G, H;           1a25         A         588         716         1.5e-26         0.08         1.00         PROTEIN KINASE C (BETA);           CHAIN: A, B;	1b4f         A         825         885         6.8e-15         0.21         -0.09         EPHB2; CHAIN: A, B, C, D, E, F, G, H;           1a25         A         588         716         1.5e-26         0.08         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;           1a25         A         728         864         4.5e-16         0.32         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;	1b4f         A         825         885         6.8e-15         0.21         -0.09         EPHB2; CHAIN: A, B, C, D, E, F, G, H;           1a25         A         588         716         1.5e-26         0.08         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;           1a25         A         728         864         4.5e-16         0.32         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;           1a25         A         755         871         1.5e-36         0.33         0.37         PROTEIN KINASE C (BETA); CHAIN: A, B;	1b4f         A         825         885         6.8e-15         0.21         -0.09         EPHB2; CHAIN: A, B, C, D, E, F, G, H;           1a25         A         588         716         1.5e-26         0.08         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;           1a25         A         728         864         4.5e-16         0.32         1.00         PROTEIN KINASE C (BETA); CHAIN: A, B;           1a25         A         755         871         1.5e-36         0.33         0.37         PROTEIN KINASE C (BETA); CHAIN: A, B;           1byn         A         588         717         3e-28         -0.05         1.00         SYNAPTOTAGMIN I; CHAIN: A;	1b4f         A         825         885         6.8e-15         0.21         -0.09         EPHB2; CHAIN: A, B, C, D, E, F, G, H;           1a25         A         588         716         1.5e-26         0.08         1.00         PROTEIN KINASE C (BETA);           1a25         A         728         864         4.5e-16         0.32         1.00         PROTEIN KINASE C (BETA);           1a25         A         755         871         1.5e-36         0.33         0.37         PROTEIN KINASE C (BETA);           1byn         A         588         717         3e-28         -0.05         1.00         SYNAPTOTAGMIN I; CHAIN: A;           1byn         A         618         721         1.2e-08         -0.02         0.59         SYNAPTOTAGMIN I; CHAIN: A;	1b4f   A   825   885   6.8e-15   0.21   0.09   EPHB2; CHAIN: A, B, C, D, E, F, G, H;     1a25   A   728   864   4.5e-16   0.32   1.00   CHAIN: A, B;     1a25   A   755   871   1.5e-36   0.33   0.37   CHAIN: A, B;     1byn   A   588   717   3e-28   -0.05   1.00   SYNAPTOTAGMIN I; CHAIN: A;     1byn   A   732   856   6.8e-22   0.85   0.89   SYNAPTOTAGMIN I; CHAIN: A;

PD B annotation	DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	TRANSFERASI: CALCIUM++, PHOSPHOLIPII) BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATID/J.SERINE, PROTEIN	TRANSFERASI: CALCIUM++, PHOSPHOLIPII) BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPII) BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			ENDOCYTOSIS/EXOCYTOSIS C2-
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALR) 1RSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN (CAIR) 1 PSY 3	RABPHILIN 3-A; CHAIN: A;
SEQFOL D score									
PMF score		1.00	1.00	0.99	0.17	0.58	1.00	0.59	0.36
Verify score		0.13	-0.11	0.20	0.12	-0.09	0.12	0.39	0.07
Psi Blast		8.5e-59	1.2e-27	4.5e-14	1.7e-39	9e-20	6e-30	6.8e-22	3.4e-46
END		875	716	845	872	726	717	856	874
STAR T AA		587	588	728	751	909	288	732	730
CHAI N ID		Ą	A	A	Ą				Ą
PDB ID		ldqv	1dsy	Idsy	1dsy	Irlw	Irsy	Irsy	3rpb
SEQ No d		1616	1616	1616	1616	1616	1616	1616	9191

PDB annotation	DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	CALCIUM-BINDING PROTEIN CALE; CALCIUM++/PHOSPHOL/PID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
Coumpound		PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;
SEQFOL D score				59.65				
PMF		0.34	1.00		0.21	1.00	1.00	-0.05
Verify		0.28	0.08		0.26	0.33	-0.05	0.13
Psi Blast		6.8e-27	1.5e-26	1.5e-26	6.8e-23	1.7e-27	3e-28	1.7e-16
END		351	197	208	343	196	198	333
STAR T AA		230	69	69	221	69	69	230
CHAI		V	4	A	A	¥	∢	V
PDB		1a25	1a25	1a25	1byn	1byn	1byn	Icjy
SEQ ID	NO:	1617	1617	1617	1617	1617	1617	1617

	PD:B annotation	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2	TRANSFERASI: CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN	KINASE C TRANSFERASI: CALCIUM++, PHOSPHOLIPII) BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE. PROTEIN	KINASE C TRANSFERASE CALCIUM++, PHOSPHOLIPII BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYI SERINE PROTEIN,	KINASE C HYDROLASE CALB DOMAIN; HYDROLASE, (22 DOMAIN, CALB	DOMAIN			
	Coumpound	SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	DOMAIN) (CALB) IRSY 3 CALCIUM/PHOSPHOLIPID
CEOPOI	D score			-				69.42		
PME	score	0.39	0.13	0.70	1.00	0.58	0.07		1.00	1.00
Verify	score	-0.26	0.24	-0.23	-0.11	-0.09	0.16		0.39	0.12
Psi Blast		3.4e-52	1.2e-28	3.4e-21	1.2e-27	9e-20	6.8e-23	6e-30	1.7e-27	6e-30
END	¥¥	356	351	203	197	207	343	200	196	198
STAR	TAA	71	232	89	69	87	221	29	69	69
CHAI	NID	Ą	Α .	∢	4					
PDB	OI	Idqv	1dsy	1dsy	Idsy	lrlw	Irsy	Irsy	lrsy	Irsy
SEQ	e ö	1617	1617	1617	1617	1617	1617	1617	1617	1617

PDB annotation		ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C		DOTTA CENTRA CHIANNET C	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X. RAY 2 STRUCTURE, APLYSIA KVI.1	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2
Coumpound	BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;	SVN A BTOTA GMIN I: CHAIN: A:	(C. C. C. C. C. C. C. C. C. C. C. C. C. C	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3		POTASSIUM CHANNEL KVI.I; CHAIN: NULL;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score										
PMF score		0.45	0.96		`. 	0.13	0.16		1.00	0.65
Verify		0.15	0.22		0.29	-0.00	0.14		0.38	0.65
Psi Blast		3.4e-27	8.5e-20	,	1.3e-06	0.0045	1.5e-05		5.16-26	6.8e-05
END		354	206	,	366	356	366		68	104
STAR T AA		236	71		264	264	264		င	5
CHAI N ID		A	A		<b>4</b>	A				4
PDB ID		3rpb	Згрь		1byn	ldsy	lrsy		1a68	1buo
SEQ U	O	1617	1617		1618	1618	1618		1620	1620

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEIKEMIA GENE REGIII ATTON	SIGNALING PROTEIN VOLTAGE. GATED POTASSUM CHANNEL, ASSEMBLY DOMAIN TETRAMED	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE,	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KVI.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOI.ECULAR 2 RECOGNITION, ZINC-BINDING	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2
Coumpound		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A. B. C. D. F. G. H.	KV BETA2 PROTEIN; CHAIN; A; POTASSIUM CHANNEL KVI.1; CHAIN: E;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KVI.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score								53.11
PMF score		0.99	0.99	0.82	0.95	1.00	0.01	
Verify score		0.28	0.31	-0.10	0.38	0.55	-0.18	
Psi Blast		3.4e-25	1.5e-26	1.7e-26	1.2e-26	8.5e-29	0.003	0.003
END		68	92	101	101	102	158	212
STAR T AA		3	2	en en	m	2	17	
CHAI N ID		Ą	យ	/ <b>4</b>	¥		۷.	4
PDB ID		1dsx	1exb	1qdv	ltid	3kvt	lcun	Icun
SEQ ID NO:		1620	1620	1620	1620	1620	1621	1621

PDB annotation	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN	COMPLEX (PROTEIN KINASE/CYCLIN) DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY- SUBUNIT, 2 BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
	TANDE	CELL CY CYCLE F HERPES' CYCLIN	CELL DIV (RECOMB CYCLE, C PROTEIN	COMPLEX KINASE/CY DEPENDEN PROTEIN K COMPLEX KINASE/CY PHOSPHOI	BINDI CYCLI SUBUI	COMPLEX COMPLEX ZINC FINC PROTEIN	COMPLEY COMPLEY ZINC FIN	COMP
Coumpound		CYCLIN HOMOLOG; CHAIN: A;	CYCLIN H; CHAIN: NULL;	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; G2/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	CYCLIN A; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLJGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
SEQFOL D score								
PMF score		0.37	0.30	0.76	0.77	0.84	0.89	0.70
Verify score		0.05	0.03	0.33	0.40	0.35	-0.10	-0.01
Psi Blast		1.4e-19	1.2e-12	8.5e-42	1.7e-40	1.2e-19	6.8e-22	1.4e-25
END		149	148	148	148	169	134	165
STAR T AA		52	78	41	47	110	33	70
CHAI		4		В		4	Ą	٧
PDB ID		1bu2	1jkw	1qmz	1vin	1a1h	1a1h	lalh
SEQ	Ö	1623	1623	1623	1623	1624	1624	1624

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PDB annotation	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	CO. M. P.Y. (22 10 E.S.)	COMPLEX (ZINC FINGER/DNA) ZINC	INTERACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTISIN-DNA	INTERACTION, PROTEIN DESIGN, 2
Coumpound	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FKOIEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA: CHARI. A D D E.	CONSENSUS ZINC FINGED	PROTEIN: CHAIN: C. F. G:			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN: CHAIN: C E G:	110 LDILY, CITATIV. C, 1, C,
SEQFOL D score									-			58.17																
PMF score		0.92			0.46			0.75								0.18					0.98				200	0.00		
Verify		0.35			-0.29			90.0				-	•			00.0-					80.0				77.0	#.0		
Psi Blast		3.4e-33			1.7e-41			3.4e-45				3.4e-45				6.8e-38				,	1.5e-13				†	11-50:1		-
END		169			134	-	;	165	•			991				93					134				165			
STAR T AA		109			33			80	•			89				7				100	<u> </u>				135	?		
CHAI N ID		υ			ر							۔ ن				C				,					٢	,		
PDB ID		Ітеу			ımey			ішеу				ımey				lmey				+	ımey		-	_	1mev			
SEQ ID NO:		1624		1604	1024		1604	1024				1024				1624				1631	+201 -				1624			

PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
Coumpound		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					51.82
PMF		0.12	0.25	-0.02	
Verify score		0.43	-0.23	0.21	
Psi Blast		16-14	3.46-17	1.7e-13	5.16-28
END		169	165	169	166
STAR T AA		110	69	117	30
CHAI		A	Ą	U	ပ
PDB ID		11f3	Etil Etil	lubd	lubd
SEQ		1624	1624	1624	1624

	<del></del>	7		<del></del>	<del></del>			
PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATION, INITIATOR, FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION ADRI ZINC FINGER NAR		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	EINDING PROTEINDNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN
Coumpound	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A;	HEPTAPEPTIDE; CHAIN: B; NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;
SEQFOL D score						54.14		52.53
PMF score	0.42	0.63	0.29	0.10	0.09		0.84	
Verify	-0.13	-0.20	0.14	0.03	0.01		0.83	
Psi Blast	5.1e-28	3.4e-15	1e-09	6.8e-25	8.5e-21	4.5e-19	4.5e-19 (	1.5e-14
END	165	167	165	164	169	186	181	170
STAR T AA	99.	110	105	13	76	56	9	48
CHAI N ID	၁		∢	ď.	∢	A	4	4
PDB ID	Iubd	2adr	Zdrp	2gli	2gli	1b8q	1b8q	1be9
SEQ ID NO:	1624	1624	1024	1624	1624	1627	1627	1627

SEQ	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
NO:										LOCALIZATION
1627	1be9	4	86	153	1.5e-14	0.12	0.24		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1627	1i16		35	161	3e-22			70.34	INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1116		19	157	3e-22	0.39	0.76		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1kwa	4		149	3e-19	0.55	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1627	1qau	A	19	176	1.2e-20	0.47	0.37		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1627	Iqav `	A	29	149	6e-20	1.02	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER
1627	1qfc	A	29	149	3e-22	0.75	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95, PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	1qlc	∢	85	143	1.5e-15	0.05	0.17		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	3pdz	A	56	143	1.7e-17	0.30	0.65		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS,

PDB annotation	SPECIFICITY 2 OF BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING		LIPID TRANSI ORT APO A-I;	CHOLESTEROL METABOLISM. 2	ATHEROSCLEROSIS, HDL, LCAT-	DESIGNED HELICAL BUNDLE	SNED HELICAL BUNDLE		RNA-BINDING PROTEIN/RNA TRA	PRE-MKNA; SPLICING	REGULATION, RNP DOMAIN, RNA	LEX	RNA-BINDING PROTEINRNA TRA PRE-MRNA : SPI ICING	REGULATION, RNP DOMAIN RNA	LEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SFLICING	REGULATION, RNP DOMAIN, RNA	LEX	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-KNA COMPLEX, GENE	LAIIONKNA		GENE REGULATION/RNA POLY(A)	BINDING PROJEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE
	SPEC	HYD PHOS SPEC		LIPIC	CHOI	ATHE	DESI	DESIG			PKE-		-		REGU	COMPLEX	RNA-1	PRE-N	REGU	COMPLEX	GENE	DNIA PORT	PROTE	2		GENE	BINDI	PROTI
Coumpound		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;		APOLIPOPROTEIN A-I; CHAIN: A. B. C. D:			DHPI; CHAIN: NULL;			SXL-LETHAL PROTEIN; CHAIN:	D/D*CD*I ID*I ID*CD*I ID*IID*	IN TO THE TIP TIP TO THE TOTAL OF THE TIP TIP TIP TIP TIP TIP TIP TIP TIP TIP	OF OF OF OP CHAIN: P, U;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-	R(P*GP*UP*UP*UP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; KNA (5-	K(F*GF*UF*GF*UP*UP*UP*	OF*UF*UF*UJ-CHAIN: P, Q;	POLYDENYLATE BINDING PROTFIN 1: CHAIN: A P C D	F F G H. DNA /51	E, t, C, tt, tC, C. R(*AP*AP*AP*AP*AP*AP*AP*	ΔP*ΔP*ΔP*Δ\.3"	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-
SEQFOL D score				63.32									27.00	/4.65	,											81.71		
PMF score		1.00					0.01		0.10	0.70							00.1			5	9.1							
Verify score		0.92					0.12		0.70	0	•			-			0.91			96 0	~~							
Psi Blast		4.5e-22		5.1e-07			0.0043		1 70-16	21-27:			1 50.36	00000		,	1.5e-36			3 46-20			•			1.7e-34		
END AA	97,	149		258			366		128	3			23.1			6	677			148	?					757		
STAR T AA	1	8		53			325		150				89	3		70	2			58			_		_			
CHAI N ID		ŧ.		∢					A	-			A			~	ς			A								
PDB ID	22007	zpdc	,	lavi			4hbi		1b7f				1b7f			11,76	_			lcvj				-	$\top$	icol	_	
SEQ ID NO:	1627	1021	300	1028			1628		1629				1629			1620	3			1629					1690			

PDB annotation	REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/KNA FOLT(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONARNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONRNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A)
Coumpound	R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP* AP*AP*AP-3); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING
SEQFOL D score			75.65		52.68		
PMF score		1.00		1.00		1.00	1.00
Verify		0.89		0.71	·	0.41	0.36
Psi Blast		1.7e-34	1e-30	1e-30	16-33	5.1e-27	1e-33
END		233	218	202	212	202	206
STAR T AA		71	70	71	07	71	73
CHAI N ID		A	В	æ	Ţ.	ĮT.	F
PDB ID		lcvj	1cvj	Icvj	lovj	1cvj	Icvj
SEQ ID	:0 ZO	1629	1629	1629	1629	1629	1629

<del></del>	<del></del>				
BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONANA	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN AII, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNP SINDING, 2	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	C, f, Q, h, S, 1; POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* O, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, C, P, P, P, P, P, P, P, P, P, P, P, P, P,	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3); CHAIN: M, N, O, P, O, R, S, T:	HNRNP AI; CHAIN: NULL;	HNRNP A1; CHAIN: NULL;
	53.52	-			
		1.00	66.0	1.00	1.00
		0.35	0.51	0.69	1.05
	1.4e-31	8.5e-27	1.4e-31	3.46-25	3.46-56
	209	202	209	144	229
	70	71	72	52	65
	н	н	Н		
	1cvj	lcvj		lha!	IhaI
	1629	1629	1629	1629	1629
	AIN: A, B, C, D, (5'- AP*AP*AP*AP* 3); CHAIN: M, N,	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-10')	The color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the	1evj   H   70   209   1.4e-31   53.52   PROTEIN I; CHAIN: A, B, C, D, R, AP+AP+AP+AP+AP+AP+AP+AP+AP+AP+AP+AP+AP+A

FMF SEQFOL  Score  D Score  D Score  D Score  RIBONUCLEOPROTEIN  NUCLEAR PROTEIN  HETEROGENEOUS NUCLEAR  RIBONUCLEOPROTEIN A1,  NUCLEAR PROTEIN, HRNP, RBD,  RRM, RNP, RNA BINDING, 2  RIBONUCLEOPROTEIN A1,  NUCLEAR PROTEIN, HRNP, RBD,  RRM, RNP, RNA BINDING, 2  RIBONUCLEOPROTEIN D0;  RIBONUCLEOPROTEIN D0;  RIBONUCLEOPROTEIN D0;  RIBONUCLEOPROTEIN D0;  RIBONUCLEOPROTEIN D0;  BINDING DOMAIN  CHAIN: A;  RIBONUCLEOPROTEIN D0;  BINDING PROTEIN RNA-  BINDING DOMAIN  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  CHAIN: A;  RIBONUCLEOPROTEIN RNA-  BINDING PROTEIN NON-SPECIFIC PORIN,  OSMOPORIN, OUTER MEMBRANE  CI19  PHOSPHOPORIN (PHOE) 1PHO 3  RIBONUCLEOPROTEIN PTB, PTB-  TRANSMEMBRANE  CI19  RIBONUCLEOPROTEIN PTB, PTB-  TRANSMEMBRANE  CI19  RIBONUCLEOPROTEIN PTB, PTB-  TRANSMEMBRANE  CI19  RIBONUCLEOPROTEIN PTB, PTB-  TRANSMEMBRANE  CI19  RIBONUCLEOPROTEIN PTB, PTB-  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANSMEMBRANE  TRANS			
1.00		0.60	0.60
Verlfy score 1.26 1.29 1.27 1.08 0.55		0.66	0.66
3.4e-56 3.4e-27 1.5e-11 1.5e-11 6e-17		6e-25	6e-25
END AA 230 144 144 329 329 145		150	150
71 71 241 241 22	·**	61	61
CHAI N ID A A			
10sm 1qm9		Isxl	Isxl
SEQ 1629 1629 1629 1629 1629		1629	1629

				Т		
PDB annotation		INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2	KIBONUCLEOPROTEIN A1 COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP I; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2	KIBONUCLEOFROTEIN A1 COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2	RIBONUCLEOPROTEIN A1 RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL, INHIBITOR, SFX 3
Соитроина	LETHAL PROTEIN (C. TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score				-	165.44	70.15
PMF score		-0.20	1.00	1.00		
Verify score		1.23	1.05	81.18		
Psi Blast		9e-13	1e-28	5.1e-57	5.1e-57	5.1c-36
END		328	144	233	239	229
STAR T AA		237	52	64	2	69
CHAI N ID			∢	¥	A	4
PDB ID		2omf	2up1	2up1	2up1	3sxl
SEQ NO: NO:		1629	1629	1629	1629	1629

PDB annotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	TA MOSS COLLECTION A STATE OF	COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B FACTOR IIA; COAGULATION/CRYSTAL STRUCTURE/HEPARIN-BINDING SITE/ 2 HIRUDIN/THROMBIN INHIBITOR	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
Coumpound		SEX-LETHAL; CHAIN: A, B, C;		THROMBIN; CHAIN: A,B,C; THROMBIN; CHAIN: D,E,F; HAEMADIN; CHAIN: I,J,K;	HORSE PLASMA GELSOLIN; CHAIN: A, B	HORSE PLASMA GELSOLIN; CHAIN: A, B	MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;
SEQFOL D score						876.96	
PMF score		1.00		0.98	1.00		0.95
Verify score		0.88		0.77	0.81		0.54
Psi Blast		5.16-36		9:006	0	0	90-99
END		229		84	715	715	130
STAR T AA		70		47	S	w	06
CHAI N ID		4		<b>}</b>	A	A	4
PDB		3sxl		1e0f	1d0n	140n	1akh
SEQ	Ö	1629		1635	1637	1637	1641

SKO         PDB         CHAI         STAR         RAD         F91 Bisst         Verify verify score         PMB         SEQPED         Commpound         PDB sunotation           1641         In         7 AA         AA         AA         134         7.5e-66         0.22         0.53         PTI-1; CHAIN: A. B. DNA;         PROTESTONA, OHF-1; COMPLEX (DIAL-BINDING PROTESTONAL), PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, BINDING PROTESTONAL, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C. B. DNA, C							,																				
Pub   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL   Score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D score   D sc	PDB annotation	•	COMPLEX (DIVA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA),	PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING	PROTEIN, PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD	HOMEODOMAIN TIM DOMAIN	COMPLEX (DNA-BINDING	PROTEIN/DNA) DNA-BINDING	PROTEIN, DNA, PAIRED BOX,	COLUMN TENSION 2 REGULATION	COMPLEX (DIVA-BINDING	PROTEIN DNA, PAIRED BOX,	TRANSCRIPTION 2 REGULATION				DNA-BINDING PROTEIN								
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score	Coumpound		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B;	DNA CHAIN: D; DNA CHAIN: E;	INSULIN GENE ENHANCER PROTEIN ISI - 1: CHAIN: NIII 1:	, cramin nout,	PAIRED PROTEIN; CHAIN: A, B,	C; DNA; CHAIN: D, E, F		PAIDED DEOTERN: CHARL A B	C. DAIA. CITABLE D. P. P.	C, DIVA, CITAIN: D, E, F		DNA-BINDING PROTEIN OCT-2	AVERAGE STRUCTURE) 1HDP	3	OCT-3; 10CP 5 CHAIN: NULL;	10CP 6	DNA BINDING PROTEIN OCT-1	PINDING PROTERNAVI TAXET	WITH 1806 2 ABG GIV SEE	HIS MET INSERTED AT THE N.	TERMINUS AND ASP ILE 1POG	4 INSERTED AT THE C-	TERMINUS (INS(RGSHM R6).INS(166-DI) 1POG 5 (NMR
PDB CHAI STAR END   Psi Blast   Verity score	SEQFOL D score																										
PDB CHAI   STAR   END   Psi Blast   TAA   AA   TAB   TAA   AA   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB   TAB	PMF score		0.55		0.33		0.49		86.0			0.08			3	0.69			0.62		0.78						
PDB   CHAI   STAR   END   FSI Blast	Verify score		0.22		-0.02	1,	0.17	-	0.89			0.71			000	0.33			99.0		0.46						
PDB   CHAI   STAR	Psi Blast	i t	00-957		1.5e-05	1 2 0 0	1.3e-06		1.2e-05			96-06			T							-,		_			
PDB CHAI	END	:	1.34		136	137	134		134			134			134	134			134		134			<u>.</u>			
PDB	STAR T AA	5	7.		25	50	7,		92			92			82	3			72		<u>~~</u>				-		
	CHAI N ID		<u> </u>		Д				∢			В															
2	PDB ID	72			1672	115,005	CWOI	1	Ē			1fj1			1641	d			Тоср		god						
	SEQ ID	NO:			1641	1641		:,;;	1041			1641			H				1641	†							

PDB annotation																													
Coumpound		13 STRUCTURES) 1POG 6	HYDROLASE(CARBOXYLIC FSTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIPASE	AND INHIBITED 1LPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIPASE	AND INHIBITED ILPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (1 WO	Or Wooda' O'GO TO GENERAL	HYDROLASE(CARBOATLIC FETTER ASE) I IPASE (F.C.3.1.13)	COMPLEXED WITH COLIPASE	AND INHIBITED 1LPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO	CONFORMATIONS) 1LPB 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	AMINATORD AVER AGE	STRUCTURE) IPCN 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	PROCOLIPASE B 1PCN 3 (NMR,	MINIMIZED A VERAGE STRUCTURE) IPCN 4	LIPASE PROTEIN COFACTOR
SEQFOL	D score			,											50.95														26.60
PMF	score		0.81				٠	0.88													1.00				1.00				
Verify	score		-0.36					-0.35													-0.36				-0.36				
Psi Blast			8e-19				•	3e-20							3e-20						3.2e-20				6e-22				6e-22
END	AA		64		-		_	65							99						69				69	:			69
STAR	TAA		29					29	1												29				29	1			2
CHAI	NB		A					A			_				¥								-						
PDR	e		11pb					1lph	2.						11pb						1pcn				Inch	::			1pcn
SEO	ja ģ		1653					1653							1653						1653				1653	}			1653

	1	Т	T	<u> </u>	_	_			1	:						<del></del>
PDB annotation			COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION	DOMAIN, PP60 2 SRC SH2 DOMAIN	PHOSPHORYL ATION SIGNAL TRANSDUCTION, TYROSINE	KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE,	PHOSPHORYLATION	SIGNALING PROTEINTRANSFERASE NAK; COMPLEX, SIGNAL	TRANSDUCTION, PHOSPHOTYROSINE BINDING?	DOMAIN (PTB), ASYMMETRIC CELL DIVISION	PHOSPHOTRANSFERASE C-SRC,	POU-SKU; SKC, TYROSINE KINASE,	PHOSPHOTYROSINE, PROTO-	ONCOGENE, PHOSPHOTE ANISEED ASE	
Coumpound	PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED A VERAGE STRUCTURE) IPCN 4		C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C,	PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;			NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;			TYROSINE-PROTEIN KINASE	Sic, Circin: NOLL;		,	PHOSPHOTRANSFERASE V. SRC TYROSINE KINASE
SEQFOL D score		,														
PMF score			0.03	0.06		0.11			0.95	•		0.01				0.04
Verify score			-0.10	-0.06	1	-0.37			80.0	-		-0.32			_	-0.17
Psi Blast			3.2e-28	3.2e-29	200	3.26-27			3e-17	_		3.2e-44				9.6e-29
END AA			66	102	6	3			<del></del>							66
STAR T AA				-	]-			†	071	<del>_</del>	<del>-  </del>	<del>-</del> -				
CHAI N ID			∢					\ \ \	€	-						<b>∀</b>
PDB ID			1a09	1bkl	121		- ·	1992			1.01		_		$\dashv$	Isha
SEQ NO:			1654	1654	1654			1654	† 0		1554					1654

PDB annotation	4		CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3
Coumpound	TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SHC; CHAIN: A; TRKA RECEPTOR PHOSPHOPEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;
SEQFOL	D score			51.48	
PMF	score	0.10	0.93		86:0
Verify	score	0.17	0.21		0.34
Psi Blast		0.00075	9e-24	9e-24	0.00032
END	<b>A</b> A	247	247	248	260
STAR	TAA	110	108	108	110
CHAI	e a	∢	4	Ą	< −
PDB	А	Ishc	Znmb	2nmb	2nmb
SEQ	A Ö	1654	1654	1654	1654

PD/8 annotation	REGULATION	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR	SUI; TRANSLATION INITIATION FACTOR FACTOR		HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATDARE TO ANISDONE	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTECT VSTS	OTO LACOTTONIA TOTAL	PHOSPHOTRANSFERASE C-SRC,	P60-SRC; SRC, LYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-	ONCOGENE, PHOSPHOTE ANSEED A SE	COMPLEX (SIGNAL	IKANSDUCTION/PEPTIDE) COMPLEX (SIGNAL	TRANSDUCTION/PEPTIDE), SH3 DOMAIN					
Coumpound		EIF1; CHAIN: NULL;	EIF1; CHAIN: NULL;		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A:	HEAT SHOCK PROTEIN HSLU; CHAIN: A:		TYROSINE-PROTEIN KINASE	SRC; CHAIN: NULL;		GRB2; CHAIN: A; SOS-1;	CILAIN; B;		SIGNAL TRANSDUCTION	PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2	(GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN COMPI EXED	WITH SOS-A PEPTIDE 1GBR 4	S SINOCIONES) IGBK
SEQFOL D score		141.21																
PMF score			1.00		0.36	0.13		0.45			0.17			0.59				
Verify score			0.42		-0.15	-0.14	,	-0.13			60.0			60.0				
Psi Blast		1.6e-44	1.6e-44		1.6e-11	1.3e-17		4.8e-22			9.6e-15			1.6e-15				
END AA		149	149		257	260		426			386			392				
STAR T AA		29	42		186	140		334			335			335				
CHAI N ID					Ą	A					∢			∢				
PDB ID		2if1	2ifi	5	1020	1g41		Ifmk	·		Igbq		_	1gbr				
SEQ ID NO:		1658	1658	1666	1000	1660		1663			1663			1003	-			

PDB annotation		SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GR1 14	COMPLEX (KINASE/PEPTIDE)	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR · PROTEIN; ARM REPEAT	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-
Coumpound	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	ABL TYROSINE KINASE; CHAIN: NULL;	KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN: C, D, E, F;	BETA-CATENIN; CHAIN: NULL;
SEQFOL D score								
PMF score	0.83	0.35	0.28	0.09	0.96	-0.06	0.41	0.10
Verify score	0.40	-0.64	0.30	0.20	0.43	0.03	0.09	0.02
Psi Blast	6.4e-15	6.4e-16	1.4e-18	1.6e-21	1.66-16	4.8e-16	3e-05	7.5e-10
END	389	389	425	426	389	426	416	530
STAR T AA	333	304	334	333	330	327	36	107
CHAI N ID		٧	A	A	A		٧	
PDB ID	1gfc	1gri	11ck	lącf	lsem	2abi	1ec4	2bct
SEQ ID	1663	1663	1663	1663	1663	1663	1669	1669

	7		<del></del>	T	-γ	<del> </del>		<del></del>
PDB annotation	CATENIN, STRUCTURAL PROTEIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (IL-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 PEPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	STAND STANDARD COLEGO FRO LEIN COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP PIRONI IT FORDOTTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNB PROMITTE FORDOTERN	COMPLEX (NUCLEAR) PROTEIN(RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SUBMB PROMINGS ENDROGERS)	COMPLEX (NUCLEOR TO LEIN PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONI/CLEOPROTEIN
Coumpound		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score								
PMF score		0.27	1.00	0.40	0.74	0.37	0.34	0.82
Verify score		0.16	0.54	0.10	0.36	0.41	-0.03	0.28
Psi Blast		6.4e-12	1.5e-37	1.5e-19	9.6e-07	1e-23	1.5e-22	9e-20
END AA		362	314	301	131	171	230	301
STAR T AA		27	29	126	27	30	53	126
CHAI N ID		<	¥	Ą	Ą	Ą	V	, ,
PDB ID		1a4y	la4y	la9n	1a9n	1a9n	1a9n	1a9n
SEQ ID NO:		1671	1671	1291	1671	1671	1671	1671

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PDB annotation	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH
Coumpound	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;
SEQFOL D score										
PMF score	0.60	0.00	56.0	0.84	0.01	0.57	0.94	0.93	1.00	-0.19
Verify score	0.50	0.13	0.24	0.40	0.44	0.16	0.70	0.18	0.31	0.04
Psi Blast	4.5e-24	0.00064	9e-18	9.6e-07	9e-24	6e-23	1.6e-23	1.6e-21	6e-14	8e-21
END AA	299	342	334	131	174	240	290	381	106	521
STAR T AA	171	216	220	27	30	53	138	173	53	360
CEAI N ID	ပ	ပ	ပ	ပ	ပ	O	4	V	Ą	А
PDB ID	1a9n	la9n	1a9n	1a9n	1a9n	1a9n	1d0b	1d0b	1d0b	1d0b
SEQ EQ	1671	1671	1671	1671	1671	1671	1671	1671	1671	1671

SEQ El	PDB EDB	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PD)3 annotation
100										REPEAT, CALCIUM BINDING, CELL
1671	1d0b	Ą	43	961	1.3e-27	0.74	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCITUM BINDING, CELL APPESION
1671	140b	Ą	70	242	8e-28	0.61	1.00		INTERNALIN B; CHAIN: A;	REPEAT, CALCIUM BINDING, CELL ADHESION
1671	1dce	∢	145	250	4.8e-14	0.49	1.00		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT;	TRANSFERASI; CRYSTAL STRUCTURE, FAB GERANYLGERANYLTRANSFFRASF
								74-1	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D:	2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	14ce	٧	-	107	3.2e-06	0.18	0.36		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B. D:	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	1dce	¥	27	130	4.8e-10	0.66	1.00		RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE AASE BETA SUBUNIT; CHAIN:	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1671	ldce	∢	48	154	4.8e-12	0.68	0.89		CASTON TO THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE AND THE	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINF, AI PHA

-	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
	<u>e</u>	O N	TAA	Ψ¥		score	score	D score		
									RASE BETA SUBUNIT; CHAIN: B, D;	SUBUNIT, BETA SUBUNIT
<del>                                     </del>	lds9	A	154	289	1.6e-13	-0.03	0.11		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1ds9	∢	165	299	1.4e-21	-0.14	69.0	•	OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1ds9	A	201	380	6.4e-10	-0.32	0.01		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1ds9	4	27	148	1.6e-12	0.03	0.64		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1ds9	4	59	195	3.2e-16	0.09	0.52		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1f88	В	403	702	1.5e-14	-0.04	0.05		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1671	1fo1	4	27	83	8e-05	0.27	0.72		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1671	1fo1	Ą	45	107	1.1e-05	-0.08	0.22		NUCLEAR RNÁ EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-

REPEAT 2 (LRIV)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH-	TRANSCRIPTION RNA IP; RANGAP; GTPA SE-ACTIVATING DEOTERN	FOR SPII, GTPASE-ACTIVATING	PROTEIN, GAP, RNAIP, RANGAP, LRK, LEUCINE: 2 RICH REPFAT	PROTEIN, TWINNING,	HEMIHEDRAL TWINNING, 3 MEROHEDRAI TWINNING	MEROHEDRY	ACETYLATION RNASE INHIBITOR, RIBONICLEASE/ANGIOGENIN	INHIBITOR ACETYLATION,	LEUCINE-KICH REPEATS	ACELITATION KNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN	INHIBITOR ACETYLATION,	ACETYLATION RNASE INHIBITOR,	RIBONUCLEASE/ANGIOGENIN	INHIBITOR ACETYLATION, I RIICHNE PICH BEBEATS	EE CHAPTONI NETEALS	LIGASE SKP2 F. BOX; SKP1; SKP1,	SKP2, F-BOX, L'RR, LEUCINE-RICH	REPEAT, SCF, UBIQUITIN, 2 E3,	UBIQUITIN PROTEIN LIGASE	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, SKP2 F-BOX 1 PP 1 FILCHE PICE	REPEAT SCF THROUTHN 2 F3
	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1 SCHPO	CHAIN: A, B;					RIBONUCLEASE INHIBITOR; CHAIN: NULL;		RIBONITO EASE INITIBITOR.	CHAIN: NULL;		RIBONUCLEASE INHIBITOR;	CHAIN: NULL;			CYCLIN A/CDK2-ASSOCIATED	PI9; CHAIN: A, C; CYCLIN	AVCUKZ-ASSUCIATED P45;	CIRCIN: D, D;	CICLIN A/CDK2-ASSOCIATED   P19; CHAIN: A. C. CYCLIN	A/CDK2-ASSOCIATED P45:
					-	**							,									
-	06'0	0.25	•					0.68		0.21			1.00				0.34			0 5 0	60.0	
	0.32	-0.01					.,	0.41		0.19			0.33				-0.85			T		
	1.1e-05	1.5e-16					0.5	06-20		1.4e-16			3e-31							$\dagger$		
	107	154	,				21.4	410		424			334				129			129		
	45	29					20	3		30			66				8			92		
	<b>n</b>	⋖			_															A		
	1101	lyrg					2hnh			2bnh			2bnh			7				1fs1	<del></del>	
	1/0/	1671					1671			1671			1671				16/3			1673		
		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	1fol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           FACTOR 1; CHAIN: A, B;           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING           PROTEIN RNA 1 SCHPO.	Ifol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           FACTOR 1; CHAIN: A, B;           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B; CHAIN: A, B;	1fol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           FACTOR 1; CHAIN: A, B;           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	Ifol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           FACTOR 1; CHAIN: A, B;           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	Ifol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	Ifol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;           2hrh         20         214         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         6.60         <	Ifol         B         45         107         1.1e-05         0.32         0.90         NUCLEAR RNA EXPORT           Iyrg         A         29         154         1.5e-16         -0.01         0.25         GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;           2bnh         29         314         6e-50         0.41         0.68         RIBONUCLEASE INHIBITOR; ACHAIN: NULL;	1f01 B	1fo	1fol B   45   107   1.1e-05   0.30   NUCLEAR RNA EXPORT     1yrg   A   29   154   1.5e-16   -0.01   0.25   GTPASE-ACTIVATING     2bnh   29   314   6e-50   0.41   0.68   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16	1fol B	1fol B   45   107   1.16-05   0.32   0.90   NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;     1yrg   A   29   154   1.56-16   -0.01   0.25   GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;     2bnh   29   314   66-50   0.41   0.68   RIBONUCLEASE INHIBITOR;   1.25     2bnh   30   424   1.46-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   30-31   1.00   RIBONUCLEASE INHIBITOR;   1.25     2bnh   99   334   36-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-31   30-3	1fol B   45   107   1.1e-05   0.32   0.90   NUCLEAR RNA EXPORT     Iyrg   A   29   154   1.5e-16   -0.01   0.25   GTPASE-ACTIVATING     PROTEIN RNA1_SCHPO; CHAIN: A, B; CHAIN: A, B; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; 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  CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;   CHAIN: A, B;	1fol B   45   107   1.1e-05   0.32   0.90   NUCLEAR RNA EXPORT	1   161   B   45   107   1.1e-05   0.32   0.90   NUCLEAR RNA EXPORT     1yrg   A   29   154   1.5e-16   -0.01   0.25   GTPASE-ACTIVATING     2bnh   29   314   6e-50   0.41   0.68   CHAIN: NULL;     2bnh   30   424   1.4e-16   0.19   0.21   CHAIN: NULL;     2bnh   99   334   3e-31   0.33   1.00   CHAIN: NULL;     1   161   A   90   129   1.6e-08   0.34   CYCLIN ACDK2-ASSOCIATED   1	1foi	1fol B   45   107   1.1e-05   0.32   0.90   NUCLEAR RNA EXPORT	1fol B   45   107   1.1e-05   0.32   0.90   NUCLEAR RNA EXPORT	1f01 B   45   107   1.1e-05   0.32   0.90   NUCLEAR RIVA EXPORT     1yrg   A   29   154   1.5e-16   -0.01   0.25   GTPASE-ACTIVATING     2bnh   29   314   6e-50   0.41   0.68   RIBONUCLEASE INHIBITOR;   1.2bnh   30   424   1.4e-16   0.19   0.21   RIBONUCLEASE INHIBITOR;   1.2bnh   99   334   3e-31   0.33   1.00   RIBONUCLEASE INHIBITOR;   1.1e-08   -0.85   0.34   CYCLIN ACDK2-ASSOCIATED   1.1e-08   -0.85   0.59   CYCLIN ACDK2-ASSOCIATED   1.1e-08   -0.62   0.59   CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. CYCLIN B. 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PDB annotation	UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	ANTIFUNGAL PROTEIN OSMOTIN- LIKE PROTEIN; ANTIFUNGAL PROTEIN, PATHOGENESIS- RELATED PROTEIN, PR-5D, 2 OSMOTIN, THAUMATIN-LIKE PROTEIN	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE
Coumpound	CHAIN: B, D;	SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	GLYCEROL KINASE; CHAIN: O, Y, Z, X;	GLYCEROL KINASE; CHAIN: 0, Y, Z, X;	PR-5D; CHAIN: NULL;	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A
SEQFOL D score				310.87	52.19				
PMF score		0.28	1.00			0.09	0.00	-0.14	-0.18
Verify score		-0.51	0.56			-0.16	1.29	1.60	0.79
Psi Blast		6.4e-09	0	0	0.009	4.5e-17	6e-16	6e-15	3e-19
END AA		162	491	492	191	201	162	118	197
STAR T AA		06	18	18	-	134	42	4	84
CHAI N ID		A	0			4	4	4	Ą
PDB		1fs2.	1bu6	1bu6	laun	1c2a	1c2a	1c2a	1c2a
SEQ ID	Ö	1673	1675	1675	1676	1676	1676	1676	1676

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INHIBITOR	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE	PLANT PROTEIN TWO POMOLOGOUS HEVEIN-LIKE	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE	SUGAR BINDING PROTEIN UDA; LECTIN, HEVELN DOMAIN, UDA,	SUCERANTIOEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,	SUPERANTIGEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,	SUPERANTIGEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,	SUPERANTIGEN SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE	BINDING SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE	BINDING SUGAR BINDING PROTEIN UDA:
	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;	AGGLUTININ ISOLECTIN VIAGGLUTININ ISOLECTIN V;	AGGLUTININ ISOLECTIN VIVAGGLUTININ ISOLECTIN V;	AGGLUTININ ISOLECTIN VIVAGGLUTININ ISOLECTIN V;	CHAIN: A; AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A	IN ISOLECTIN ININ ISOLECTIN V/	AGGLUTININ ISOLECTIN IAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN
	0.01	-0.14	-0.12	-0.18	-0.12	0.15	-0.14	-0.17	-0.14	-0.12	0.15
	0.87	1.43	1.28	1.17	0.05	1.32	1.70	1.37	0.98	1.34	1.29
	1.2e-17	1.2e-19	3e-18	1.5e-18	1.3e-14	7.5e-18	1.5e-19	3e-18	le-18	3e-17	1.1e-16
	192	100	172	116	192	86	142	172	192	106	98
	104	10	84	10	124	٣	64	77	104	10	3
	∢	¥	Ą	¥	Ą	A	4	A	¥	4	A
	Iehd	1ehd	1ehd	leis	Ieis	leis	leis	leis	len2	1en2	len2
	1676	1676	1676	1676	1676	1676	1676	1676	1676	1676	1676
		0.01 AGGLUTININ ISOLECTIN VI; CHAIN: A	lehd         A         104         192         1.2e-17         0.87         0.01         AGGLUTININ ISOLECTIN VI;           lehd         A         10         1.2e-19         1.43         -0.14         AGGLUTININ ISOLECTIN VI;	lehd         A         104         192         1.2e-17         0.87         0.01         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         10         1.0e-19         1.43         -0.14         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         84         172         3e-18         1.28         -0.12         AGGLUTININ ISOLECTIN VI; CHAIN: A	lehd         A         104         192         1.2e-17         0.87         0.01         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         10         1.0e-19         1.43         -0.14         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         84         172         3e-18         1.28         -0.12         AGGLUTININ ISOLECTIN VI; CHAIN: A           leis         A         10         116         1.5e-18         1.17         -0.18         AGGLUTININ ISOLECTIN VI; CHAIN: A	lehd         A         104         192         1.2e-17         0.87         0.01         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         10         1.0e-19         1.43         -0.14         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         10         1.2e-19         1.43         -0.12         AGGLUTININ ISOLECTIN VI; CHAIN: A           leis         A         10         116         1.5e-18         1.17         -0.18         AGGLUTININ ISOLECTIN V; CHAIN: A           leis         A         124         192         1.3e-14         0.05         -0.12         AGGLUTININ ISOLECTIN V; CHAIN: A	lehd         A         104         192         1.2e-17         0.87         0.01         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         10         100         1.2e-19         1.43         -0.14         AGGLUTININ ISOLECTIN VI; CHAIN: A           lehd         A         84         172         3e-18         1.28         -0.12         AGGLUTININ ISOLECTIN VI; CHAIN: A           leis         A         10         116         1.5e-18         1.17         -0.18         AGGLUTININ ISOLECTIN V; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; 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CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   AGGLUTININ ISOLECTIN V; CHAIN: A   A   A   A   A   A   A   A   A   A	1ehd   A   104   192   1.2e-17   0.87   0.01   AGGLUTININ ISOLECTIN VI;	Iehd   A   104   192   1.2e-17   0.87   0.01   AGGLUTIMIN ISOLECTIN VI;	1ehd   A   104   192   1.2e-17   0.87   0.01   AGGLUTININ ISOLECTIN VI;

PDB annotation					SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN		GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	1	R SIGNALLING PROTEIN TYPE I : A, RECEPTOR, STNFRI; INCF 8 BINDING PROTEIN. CYTOKINE	1NCF 19	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	; D- COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-
Coumpound		VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,	D, 11101 J	OMPK36; CHAIN: A, B, C;	FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: I;
SEQFOL	D score			59.75					84.67	50.00			
PMF	score		0.01		-0.19	-0.20	0.05	-0.15				-0.20	-0.20
Verify	score		1.54		0.74	0.85	1.09	1.39				1.57	0.33
Psi Blast			3e-18	3e-15	3e-15	6e-25	3e-25	6e-24	3e-25	1e-11		4.5e-14	4.5e-19
END	Ψ¥	,	172	199	197	200	199	159	160	200		138	201
STAR	T AA		74	47	49	10	35	3	4	46		<b>5</b>	42
CHAI	A I		A	Ą	A	∀				<b>V</b>	,	Ą	1
PDB	8		len2	lext	lext	ligr	1klo	1klo	1klo	lncf		losm	1pfx
SEQ	ВŞ		1676	1676	1676	1676	1676	1676	1676	1676		1676	1676

PDIs annotation	BINDING, HYDROLASE, 3 GLYCOPROTEIN	MEMBRANE A DHESION SHORT	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN	2 N-GLYCOSYLATION, MULTI-	SERINE PROTEINS INHIBITOR	FACTOR XA INHIBITOR:	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	SERINE DROTE A SE INITIDIO	FACTOR XA INHIBITOR:	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	SIKUCIUKE, FACIUK XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS		
Coumpound		HUMAN BETA2-	OF I COPROTEIN I; CHAIN: A;		ANTISTASIN: CHAIN: NI II I					ANTISTASIN: CHAIN: NI II 1						ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;						MEMBRANE PROTEIN	VITELLINE MEMBRANE OUTER LAYER PROTEIN I
SEQFOL D score																						66.99							
PMF score		-0.20			-0.15					0.29						-0.12							·				300	-0.20	
Verify score		0.83			0.92					1.27					,	0.53									,		1,20	1.30	
Psi Blast		1.4e-30			6e-15	-		_		1.le-15	,				;	6e-21				-	10.5	17-20			•		1, 2, 3, 1	1.36-14	
END		200			168					175						861					500	707					102	<u> </u>	
STAR T AA		εn_			13					74					1	33					8	2					-		
CHAI N ID		٧																									_	ς	
PDB ID		1qub			1skz					Iskz		-			10/2/2	ISKZ					1 ckr	7					1 time		
SEQ ID NO:		1676			1676					1676					1676	10/0					1676	2					1676	2	

SEQ	PDB ID	CHAI	STAR T AA	END	Psi Blast	Verify score	PIMF score	SEQFOL D score	Coumpound	PDB annotation
S									1VMO 3	
1676	9wga	V	∞	189	4.5e-23			101.83	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1680	1c0p	A	=	39	0.00048	-0.46	0.19	·	D-AMINO ACID OXIDASE; CHAIN: A;	OXIDOREDUCTASE ALPHA-BETA- ALPHA MOTIF, FLAVIN CONTAINING PROTEIN, OXIDASE
1680	1chu	¥	7	46	0.00014	-0.05	0.13		L-ASPARTATE OXIDASE; CHAIN: A;	FLAVOENZYME FLAVOENZYME, NAD BIOSYNTHESIS, FAD, OXIDOREDUCTASE
1680	lcic	A	10	457	3.2e-37			62.05	ADRENODOXIN REDUCTASE;	OXIDOREDUCTASE ADR, NADPH:
	•	_							CHAIN: A;	ADRENODOXIN OXIDOREDI ICTASE:
							• *		•	FLAVOENZYME, MAD ANALYSIS,
						•				ELECTRON I KAINSFERASE
1680	1d4d	Ą	142	318	3.2e-09	-0.03	0.36		FLAVOCYTOCHROME C FUMARATE REDUCTASE:	OXIDOREDUCTASE TETRAHEME FLAVOCYTOCHROME C
							47		CHAIN: A;	FUMARATE REDUCTASE, 2
										UAIDUKEDUCIASE
1680	1djn	4	2	182	1.6e-12	-0.09	0.12		TRIMETHYLAMINE DEHYDROGENASE; CHAIN: A,	OXIDOREDUCTASE IRON-SULFUR FLAVOPROTEIN, ELECTRON
									B;	TRANSFER, OXIDOREDUCTASE
1680	1djn	A	5	359	9e-13	-0.08	0.70		TRIMETHYLAMINE	OXIDOREDUCTASE IRON-SULFUR
									DEHYDROGENANE; CHAIN: A, B;	FLAVOFROIEIN, ELECTRON TRANSFER, OXIDOREDUCTASE
1680	1dxl	A	2	118	0.003	-0.41	0.00		DIHYDROLIPOAMIDE	OXIDOREDUCTASE LIPOAMIDE
							_		DEHYDROGENASE; CHAIN: A, B, C, D;	DEHYDROGENASE, L'ROTEIN, E3, DLDH, DIHYDROLIPOAMIDE
										DEHYDROGENASE, MULTIENZYME
										COMPLEX 2 PROTEIN, PYRUVATE
										DEHYDROGENASE COMPLEX,
										COMPLEX, FLAVOPROTEIN

		T						
Phi	TOTA ATTRICTURE	OXIDOREDUC TASE LIPOAMIDE DEHYDROGENASE, L PROTEIN, E3, DLDH, DIHYDROLIPOAMIDE DEHYDROGENASE, MULTIENZYME COMPLEX 2 PROTEIN, PYRUVATE DEHYDROGENASE COMPLEX, GLYCINE 3 DECARBOXYLASE	COMPLEX, FLAVOPROTEIN COMPLEX (OXIDOREDUCTASE/TRANSFERASE ) E3BD; REDOX: ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE	OXIDOREDUCIASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, O- 2 AMINOBENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD- 3	NIDING DOMAIN		OXIDOREDUCI ASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE,	OXIDOREDUCTASE REDOX-ACTIVE CENTER. OXIDOREDITASE
Соптроинд		DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B, C, D;	DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B; DIHYDROLIPOAMIDE ACETYLTRANSFERASE; CHAIN: C.	CHAIN: A, B, C, D, E, F, G, H;	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCSD) 1FCD 3	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;
SEOFOL	D score	,				83.15		
PMIF	score	0.39	0.69	0.04	0.22		0.51	-0.01
Verify	score	-0.07	-0.04	-0.50	0.10		0.11	0.00
Psi Blast	·	3.26-94	1.6e-95	1.6e-07	1.6e-19	1.6e-19	7.5e-05	1.6e-74
匚		462	462	49	407	394	118	459
STAR		∞	14	9	10	σ.	2	8
CHAI	e z	<b>∢</b>	¥	∢	¥	<	Ą	A
PDB	e	Idxi	lebd	1f8s	1fcd	D D	1fec	] Lec
SEQ	a ö	1080	1680	1680	1680	1680		1680
								. 1

PDB annotation	FLAVOPROTEIN, FAD, NADP	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2	RESPIRATION, OXIDOREDUCTASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE							
Coumpound		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N;	FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE	REDUCTÁSE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD	HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE PERICTA SE 13 VM	HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE DIHYDROLIPOAMIDE	DEHYDROGENASE (E.C.1.8.1.4)   COMPLEX WITH 1LPF 3	FLAVIN-ADENINE- DINUCLEOTIDE (FAD) 1LPF 4	OXIDOREDUCTASE
SEQFOL D score												
PMF score		0.05	0.37		0.05	•			0.15			0.04
Verify score		-0.79	-0.74		-0.56				-0.25			-0.14
Psi Blast		0.00032	3.2e-06		0.00032				3,2e-95			3.2e-75
END		43	43		391				462			462
STAR T AA		12	12		310				<b>∞</b>			13
CHAI N ID		<b>V</b>	V		A				4			
PDB ID		1foh	1fum		1fum				11pf			11vl
SEQ ID		1680	1680		1680				1680			1680

Γ			T	T.,	T		<del></del>	Т	т—	т—	<del></del>
DIN Secretary	f D.5 annotation			OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2	CLAVOTROTEIN, FAD, P64K OXIDOREDUCIASE OXIDOREDUCIASE,	OXIDOREDUCIASE, NAD OXIDOREDUCIASE OXIDOREDUCIASE			TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT:
Commonned		DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1L/VL 3 NICOTINAMIDE-ADENINE. DINICI FOTTIPE (AADENINE)	OXIDOREDUCTASE (NPX) NADH PEROXIDASE (NPX) (E.C.I.11.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY	SURFACE PROTEIN; CHAIN: NULL;	L-ALANINE DEHYDROGENASE; CHAIN: A;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3		TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A,	TEPRESSOR TUP1; CHAIN: A,	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;
SEOFOL	D score	·	76.88			-					
PMF	score			0.22	0.11	90.0	0.35		0.01	0.99	-0.14
Verify	score			-0.06	0.02	-0.43	-0.06		0.25	0.56	0.43
Psi Blast			1.6e-57	6.4c-88	0.0048	6.4e-05	3.2e-91		I.6e-61	3.2e-72	1.4e-55
END	AA		418	463	177	49	462	إ	479	624	476
STAR			12	9	145	4	8		173	304	155
CHAI	e z				∢	A	Ą		€	Ą	В
PDB	e		lnhp	lojt	1pjc	~	3lad	+	iei)	lerj	lgot
SEQ	A Ö		1680	1680	1680		1680	1691	1001		1681

PDB annotation	GAMMAI, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION		COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	<del>                                     </del>
Coumpound	CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	OMPK36; CHAIN: A, B, C;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN
SEQFOL D score		74.60				
PMF score	·		0.71	-0.20	-0.18	-0.20
Verify score			0.76	0.86	1.11	0.90
Psi Blast		1.4e-55	3.26-74	4.5e-10	1.5e-12	1.2e-11
END		524	621	79	18	08
STAR T AA		179	302	in	∞	4
CHAI N ID		В	В	A .	ď	
PDB ID		1got	1got	Iosm	losm	1pho
SEQ ID	2	1681.	1681	1685	1685	1685

PDB annotation	INTEGRAL MIMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 12 PROTEIN 20MF 12	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS,	SIRUCTURAL PROTEIN	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2	PROTEIN FOLIJING, ATPASE CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2	CHAPERONIN HSP60 CLASS, ATP,	TRANSFERASE PYRUVATE KINASE, GLYNOTETE AND STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET S	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, IDNA-BINDING
Coumpound	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	ALPHA SPECTRIN; CHAIN: A, B, C;	HYDROLASE CYTIDINE DEAMINASE (CDA) (E.C.3.5.4.5) COMPLEXED WITH 1CTT 3 3,4- DIHYDROZEBULARINE (DHZ) 1CTT 4	THERMOSOME; CHAIN: A, B;	THERMOSOME; CHAIN: A, B;	GROEL; CHAIN: A, B, C, D, E, F, G, H, T, K, M, N:	PYRUVATE KINASE; CHAIN: A, B, C, D, E, F, H, G;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
SEQFOL D score								
PMF score	-0.19	0.04	0.22	1.00	1.00	0.72	0.23	-0.19
Verify score	1.14	-0.05	-0.02	-0.12	-0.29	-0.14	-0.18	0.06
Psi Blast	1.3e-10	0.00015	9.6e-27	8e-55	6.4e-51	1.6e-68	0.0008	1.4e-09
END	08	210	124	186	186	186	106	114
STAR T AA	∞	86	14	15	20	12	5	33
CHAI N ID		A		₹	В	4	∢	4
PDB UD	2omf	Icun	, left	1a6d	1a6d		1 pkd	Ialh
SEQ NO EI	1685	1688	1690	1692	1692	1692	1692	1696

und PDB annotation				DNIQ	, D, E; COMPLEX (ZINC FINGER/DNA) ZINC				C. F. G:   FINGER, PROTEIN-DNA   INTERACTION, PROTEIN DESIGN, 2		D F: COMPLEX (ZINC FINGER/DNA) ZINC			CRYSTAL STRUCTURE, COMPLEX	Ⅎ	_		GENE, NMK, TFIIIA, PROTEIN, DNA,	INAINOCAL TION FACTOR, 33 MAR 2	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	(REGULATION/DNA)		(US P5 REGULATION/DNA) YING-YANG 1;		
OL Coumpound	ą.	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN: CHAIN: C. F. G:		DNA. CHAIN: A B D E	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		-	TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;	-				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	CHAIN: A R.	(
F SEQFOL	e D score									-																_
PMF	score	-	-0.14		-0.18			-0.17	·	<u></u>	0.10	7.0.				-0.19							-0.14			
Verify	score		0.07		0.07		<u> </u>	0.10			0.16	2				90.0							0.04			
Psi Blast			6.4e-27		3.2e-19			8e-35			1 12 00	1.15-02				1.4e-13							3.2e-28			
END	ΑA		168		114			142	.,		1.7	<u>+</u>				138							168			
STAR	TAA		96		31			61				6				69	·						63			
CHAI	OI N		А		၁			U				ל				A							U			
PDB	A		lalh		lmey			1mey				і шеу				143							lubd			
SEO	ΑŞ	5	9691		9691			1696				1090				1696							1696	•		_

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(TRANSCRIPTION REGIL ATTONONA)	COMPLEX (DIA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		COMPLEX (NI JCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA.	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NICLEAR	(NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NI ICLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	CELL ADHESION LEUCINE RICH	REPEAT, CALCIUM BINDING, CELL	ADHESION	TRANSFERASI: CRYSTAL	STRUCTURE, IVAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETFIIONINE, ALPHA	SUBUNIT, BETA SUBUNIT		TRANSFERASI; CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N- FORMATI METHIONINE AT MILE
	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q, R. 112 A'' CHAIN: A C. 112 B".	CHAIN: B, D;		U2 RNA HAIRPIN IV; CHAIN: Q,	K; U2 A; CHAIN: A, C; U2 B";	CHAIN: B, D;	INTERNALIN B; CHAIN: A;		47	KAB	GERANYLGERANYLTRANSFE	KASE ALPHA SUBUNIT;	CHAIN: A, C; KAB	GEKANYLGEKANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	B, D;	KAB	GERANYLGERANYLTRANSFE	KASE ALPHA SUBUNIT;	GERANYI, GERANYI, TRANSEF
	-0.11		0.94		0.00		0	0.96			1.00		90	7.00							5.6			
	0.03	5	0.03		-0.34		000	67.0			0.51		890	0.00						55.0	77.0			
	4.8e-17	6.42.10	0.46-13	,	(ee-1)		6.41.13	0.4e-13.			1.4e-28		3 20-15	7:57:5						3 70 17	71-27-6			
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000	1090	1698		1609	1070		1698	2		303.	1698		1698							1698	!			
		ZINC FINGER PROTEIN GL/1; CHAIN: A; DNA; CHAIN: C, D;	2gli A 7 144 4.8e-17 0.03 -0.11 ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLJI;           CHAIN: A; DNA; CHAIN: C, D;         CHAIN: A; DNA; CHAIN: C, D;         CHAIN: A; DNA; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: A, C; UZ B"; CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII;           CHAIN: A; DNA; CHAIN: C, D;         CHAIN: A; DNA; CHAIN: C, D;         CHAIN: A; DNA; CHAIN: Q, R; U2 A; CHAIN: Q, R; U2 A; CHAIN: Q, CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, R; IJ 2 B"; CHAIN: A, C; IJ 2 B";	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         U2 RNA HAIRPIN IV; CHAIN: Q, CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B;           1a9n         A         43         140         6e-11         -0.34         0.00         R; UZ A; CHAIN: A, C; UZ B;           1a9n         C         10         R; UZ A; CHAIN: A, C; UZ B;         CHAIN: B, D;         CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: Q, CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: Q, CHAIN: B, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, Q, Q, CHAIN: Q, Q, Q, CHAIN: Q, Q, Q, CHAIN: Q, Q, Q, CHAIN: Q, Q, Q, CHAIN: Q, Q, Q, Q, CHAIN: Q, Q, Q, Q, Q, Q, Q, Q, Q, Q, Q, Q, Q,	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; D; R; UZ A; CHAIN: A, C; UZ B"; D; R; UZ A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; A; CHAIN: A, C; UZ B"; D; D; D; D; D; D; D; D; D; D; D; D; D;	2gii         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A; CHAIN: A, C; UZ B"; CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: B, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: A, C; UZ B"; CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;           1a9n         A         43         140         6e-11         -0.34         0.00         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         U2 RNA HAIRPIN IV; CHAIN: Q, CHAIN: Q, CHAIN: Q, CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: B, CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: B, D; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C; U2 B"; CHAIN: A, C;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLJI; CHAIN: C, D;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: C, UZ B"; CHAIN: B, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: B, D;           1a0b         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: B, D;           1a0b         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, UZ B"; CHAIN: A, C; UZ B"; CHAIN: B, D;           1d0b         A         18         140         1.4e-28         0.51         1.00         R; UZ A; CHAIN: A, C; UZ B"; CHAIN: A, C; UZ B"; CHAIN: B, D;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII; CHAIN: C, D;           Ia9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ B"; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; 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CHAIN: Q, D;           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, D;           1d0b         A         18         140         1.4e-28         0.51         1.00         NTERNALIN B; CHAIN: A, C; UZ B";           1doe         A         14         3.2e-15         0.68         1.00         RAB	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLJI;           1a9n         A         18         115         6.4e-13         0.03         0.94         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: Q, CHAIN: A, C; UZ B";           1a9n         A         43         140         6e-11         -0.34         0.00         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: A, C; UZ B";           1a9n         C         18         115         6.4e-13         0.29         0.96         UZ RNA HAIRPIN IV; CHAIN: Q, CHAIN: A, C; UZ B";           1d0b         A         18         140         1.4e-28         0.51         1.00         IRRIPRIALIN B, CHAIN: A, C; UZ B";           1doe         A         18         140         1.4e-28         0.51         1.00         RAB	18   15   6.4e-13   0.03   -0.11   CHAIN: A; DNA; CHAIN: C, D; CHAIN: B, D; CHAIN: C, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, U2 B°; CHAIN: B, D; CHAIN: C, U2 B°; CHAIN: B, D; CHAIN: C, CHAIN: B, D; CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, C	2gli         A         7         144         4.86-17         0.03         -0.11         CHAIN: A; DNA; CHAIN: C, D;           189n         A         18         115         6.46-13         0.03         0.94         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B";           189n         A         43         140         66-11         -0.34         0.00         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B";           140h         A         115         6.46-13         0.029         0.96         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 B";           140b         A         115         6.46-13         0.029         0.96         U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 B";           140b         A         18         140         1.46-28         0.51         1.00         NTERNALIN B; CHAIN: A, C; U2 B";           14ce         A         18         140         1.46-28         0.51         1.00         RAB           14ce         A         18         140         1.46-28         0.51         1.00         RAB           14ce         A         14         3.26-15         0.68         1.00         RAB           14ce         A         14         114         3.26-15         0.68         1.00	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GLII;           1a9n         A         18         115         6.4e-13         0.03         0.94         U2 RNA HAIRPIN IV; CHAIN: Q, DB";           1a9n         A         43         140         6e-11         -0.34         0.00         U2 RNA HAIRPIN IV; CHAIN: Q, RB";           1a9n         C         18         115         6.4e-13         0.29         0.96         U2 RNA HAIRPIN IV; CHAIN: Q, RB, D;           1d0b         A         43         140         6e-11         -0.34         0.00         U2 RNA HAIRPIN IV; CHAIN: Q, RB, DB;           1dob         A         18         115         6.4e-13         0.29         0.96         U2 RNA HAIRPIN IV; CHAIN: Q, RB, DB;           1dob         A         18         140         1.4e-28         0.51         1.00         RAB           1dce         A         14         114         3.2e-15         0.68         1.00         RAB           GERANYLIRANSEE         RASE ALPHA SUBUNIT;         CHAIN: A, C, RB ALPHA SUBUNIT;         CHAIN: A, C, RB ALPHA SUBUNIT;         CHAIN: A, C, RB ALPHA SUBUNIT;	2gli         A         7         144         4.8e-17         0.03         -0.11         ZINC FINGER PROTEIN GL11; CHAIN: 4, DNA; CHAIN: C, D; CHAIN: A, DNA; CHAIN: C, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C, CAB CHAIN: C,	185   A   7   144   4.86-17   0.03   -0.11   CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D; CHAIN: B; DIA; CHAIN: C, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; UZ B°; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; UZ B°; CHAIN: B, D; CHAIN: B, D; CHAIN: A, C; UZ B°; CHAIN: B, D; CHAIN: A, C; UZ B°; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, UZ B°; CHAIN: B, D; CHAIN: C, UZ B°; CHAIN: B, D; CHAIN: C, UZ B°; CHAIN: B, D; CHAIN: C, UZ B°; CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN: C, C, CHAIN:	12gi	189n   A   7   144   4.8e-17   0.03   -0.11   CHAIN: A; DNA; CHAIN: C, D; CHAIN: A; DNA; CHAIN: C, D; CHAIN: B, DNA; CHAIN: C, D; CHAIN: B, D; CHAIN: C, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, C, C, C, C, C, C, C, C, C, C, C, C,	189   A   7   144   4.8e-17   0.03   -0.11   CHAIN: 4; DNA; CHAIN: C, D; CHAIN: 4; DNA; CHAIN: C, D; CHAIN: 4; DNA; CHAIN: C, D; CHAIN: 4; DNA; CHAIN: C, D; CHAIN: 4; DNA; CHAIN: C, D; CHAIN: 4; DNA; CHAIN: C, D; CHAIN: A; C; U2 B°; CHAIN: B, D; CHAIN: A; C; U2 B°; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: B, D; CHAIN: C, C, U2 B°; CHAIN: B, D; CHAIN: C, C, U2 B°; CHAIN: B, D; CHAIN: C, C, U2 B°; CHAIN: C, C, C, DB°; CHAIN: C, C, C, DB°; CHAIN: C, C, C, C, C, C, C, C, C, C, C, C, C,

SEO	PDR	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	PDB annotation
βBŞ	a	NID	TAA	AA		score	score	D score		
:									RASE BETA SUBUNIT; CHAIN: B, D;	SUBUNIT, BETA SUBUNIT
1698	1ds9	A	25	142	8e-23	-0.55	0.24		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1698	lyrg	∢	73	133	3e-09	-0.36	0.21		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, MEROHEDRAL
1698	2bnh			139	9.6e-10	90.0	0.49		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1699	lelk	4	2	141	1.4e-44	0.84	1.00		TARGET OF MYB1; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES
1699	1elk	4	2	143	1.2e-56	0.78	1.00		TARGET OF MYB1; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES
1700	1b7f	<b>A</b>	126	268	1.46-22	0.09 -	-0.06		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*UP. CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1700	167£	Ą	328	481	6.4e-30	0.96	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	RNA-BINDING PROTBIN/KNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1700	1cvj	Ą	128	307.	3.2e-31	0.05	-0.15		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)

	<del></del>	T	<del></del>		- ₁	
PDB annotation	BINDING PRO TEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA, COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3); CHAIN: M, N, O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP* O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN 1; CHAM: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3); CHAIN: M, N, O, P, O, R, S, T.	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, D, D, D, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, C, P, P, C, P, P, P, P, P, P, P, P, P, P, P, P, P,	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C; D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*
SEQFOL D score						
PMF score		0.93	1.00	1.00	1.00	1.00
Verify score		0.69	1.28	0.99	. 86.0	1.29
Psi Blast		4.8e-19	4.5e-28	4.8e-25	4.5e-24	4.8e-24
END	;	411	485	487	468	473
STAR T AA		310	331	331	331	331
CHAI N ID		Ą	A	A	В	Ф
PDB U		levj	levj	lcvj	levj	lcvj
SEQ EQ		1700	1700	1700	1700	1700

PDB annotation		GENE REGULATION/RNA POLY(A)  D. BINDING PROTEIN 1, PABP 1; RRM,		P* REGULATION/RNA		GENE REGULATION/RNA POLY(A)			P* REGULATION/RNA	Ź	GENE REGULATION/RNA POLY(A)	D,   BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	P* REGULATION/RNA	Ź		RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RIBONUCLEOPROTEIN UIA117;	RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME		C23; RNP, RBD, RRM, RNA BINDING	DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1.
Coumpound	O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN; A. B. C. D.	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E. F. G. H: RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;		HU ANTIGEN C; CHAIN: A;		HU ANTIGEN C; CHAIN: A;		UI SMALL NUCLEAR	RIBONUCLEOPROTEIN A;	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;			HNRNP A1; CHAIN: NULL;
SEQFOL D score																													
PMF score		0.64				0.07					1.00					_	0.71	_	0.83		0.00		0.58			0.37			-0.17
Verify score		0.46				0.27	į				0.72						0.30		0.93		0.55		0.71			0.82			0.26
Psi Blast		4.8e-25				6.4e-26	)   				3e-21						3.2e-22		1.6e-17		3.2e-16		3e-17			1.5e-16			4.8e-31
END AA		216				233	}				461						208		409		209		417			412			301
STAR T AA		128				128	3				331	:					126		327		127		323			321			126
CHAI N ID		F				П	:				I	1					Ą		Ą		A					<b>∀</b>			
PDB ID		lcvj				1cvi	2				1cvi						1d8z		148z		1d9a		1tht			1fic	,		1ha1
SEQ	2	1700				1700	3				1700	3				_	1700		1700		1700		1700		_	.1700			1700

1			<b>γ</b> —																_										
	PD/8 annotation	NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	NUCLEAR PROTEIN HURNE RED	RRM, RNP, RNA BINDING, 2	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEO!/ROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA-	BINDING DOMAIN		,							i				
	Coumpound		HNRNP A1; CHAIN: NULL;				HNRNP A1; CHAIN: NULL:					HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN DO:	CHAIN: A;	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN D0; CHAIN: A:	RIBONUCLEOPROTEIN	PROTEIN FROM UI SMALL	NUCLEAR	RIBONUCLEOPROTEIN (SNRNP	UI) INKC 3 (N-TERMINAL	FRAGMENT, RESIDUES 1 - 95)	MUIANI WITH GLN 85 INRC 4	REPLACED BY CYS (Q85C)	INRCS	RIBONUCLEOPROTEIN	PROTEIN FROM UI SMALL	NUCLEAR	KIBONUCLEOPROTEIN (SNRNP
10000	D score																												
27/20	score		-0.19				0.99					0.77			0.98		0.49									0.43			
W.	score		0.17				0.78					0.82			0.86		-0.09									-0.19	-		
Dei Diest	1 Si Didsi		1.6e-20				1.4e-34		·			4.8e-23			1.3e-20		1.6e-12								†	1.3e-12	•		
END	AA		405			~	481					206		,	399		509						-		100	/07			
DATA	TAA		226				325					127			351		127								127	/71			
CHAI	NED											A		1	<		∢								0	۹			
PDR	B		IhaI				1ha1					1hd1			ושפו		lnrc	•							t	3			
SEO	ΑÖ		1700				1700					1700		002,	2007		1700				_				1700	3			
													_							_	_	_	_						

PDB annotation		RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION		COMPLEX (RIBONUCLEOPROTEIN/RNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN,
Coumpound	UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POLYPYRIMIDINE TRACT. BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 15XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL 5	U1A SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 21MER HAIRPIN (5'- (AP*AP*UP*CP*CP*AP*UP*UP* 1URN 11 CHAIN: P, Q, R 1URN	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A;
SEQFOL D score								
PMF		-0.14	0.33	0.99	0.10	0.11	0.84	0.96
Verify score		0.25	0.06	0.71	0.59	0.47	0.82	0.60
Psi Blast		4.8e-09	1.4e-15	6e-16	3.2e-18	1.3e-20	1.1e-17	4.5e-16
END		217	211	406	206	210	411	406
STAR T AA		128	126	323	127	126	328	322
CHAI N ID		A		⋖	∢			
PDB ID		1qm9	Isxl	lum	2mss	2sxl	2sxl	2ula
SEQ NO.		1700	1700	1700	1700	1700	1700	1700

_		_					_		_			_	_				_	_										
NUCLEAR PROTEIN	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HNRNP A1, UP1; COMPLEX	HETER OGENEOUS NITCLEAR 2	RIBONUCLEOPROTEIN A1	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HNRNP A1, UP1; COMPLEX	(RIBONUCLEOPROTEIN/DNA).	HETEROGENEOUS NUCLEAR 2	RIBONUCLEOPROTEIN A1	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HNRNP A1, UP1; COMPLEX	(RIBONUCLEOPROTEIN/DNA),	HETEROGENEOUS NUCLEAR 2	RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION		ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK	COMPLEX (TRANSCRIPTION
CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN AI;	CHAIN: A; 12-NUCLEOTIDE	TELOMETRIC DNA: CHAIN: B:		HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1;	CHAIN: A; 12-NUCLEOTIDE	SINGLE-STRANDED	TELOMETRIC DNA; CHAIN: B;		HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1;	CHAIN: A; 12-NUCLEOTIDE	SINGLE-STRANDED	TELOMETRIC DNA; CHAIN: B;		SEX-LETHAL; CHAIN: A, B, C;								TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA:
																				-						1000	0/./0	-
	0.05	-0.19			,		-0.14						0.87			•		5	3									1.00
	0.53	0.01			•		0.35						0.49					101	1.01									0.92
	9.6e-13	1.1e-34					4.8e-22						1.36-33					3 24.20	7.22-63						1	150 20	2000	3e-45
200	706	311				,	410					707	484					VLP	† †							101		298
122	171	126				700	077		_			300	223		-			320	3							3.5	;	145
	A	∢					₹					<	ζ	-				\ \ \	:								•	В
2000	1707	Zup1				2	1ďn7					$\dagger$	_								<u>-</u>					185e		lawc
1700	3077	1700				1700	7700					1700	3					1700	?							1701		1701
	CHAIN: NULL;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           SUBUNIT; CHAIN: A;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A1; 12-NUCLEOTIDE           SPLICING FACTOR U2AF 65 KD           SUBUNIT; CHAIN: A;           CHAIN: A1; 12-NUCLEOTIDE           SPLICING PROTEIN A1;           CHAIN: A2; 12-NUCLEOTIDE	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2upl         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; L2-NUCLEOTIDE SINGLE-STRANDED           2upl         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; L2-NUCLEOTIDE SINGLE-STRANDED	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED           2up1         A         0.01         -0.19         TELOMETRIC DNA; CHAIN: B; TELOMETRIC DNA; CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2upl         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED           2upl         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR RIBONUCLEAR RIBONUCLEOR OUT B	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEAR         RIBONUCLEOPROTEIN A1;           CHAIN: A; 12-NUCLEOTIDE         CHAIN: A; 12-NUCLEOTIDE	2u2f         A         127         206         9.6e-13         0.63         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOTIDE         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN; B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN; A; 12-NUCLEAR         RIBONUCLEOPROTEIN A1;         CHAIN; A; 12-NUCLEAR           SINGLE-STRANDED         SINGLE-STRANDED         SINGLE-STRANDED	2u2f         A         127         206         9.6e-13         0.63         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEAR         RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEAR           SINGLE-STRANDED         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;         TELOMETRIC DNA; CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A;         CHAIN: A;         CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         SINGLE-STRANDED         CHAIN: B;           A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEOTIDE           SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;         TELOMETRIC DNA; CHAIN: B;         TELOMETRIC DNA; CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B;           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD SUBUNT; CHAIN: A;           2upl         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1;           2upl         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1;           2upl         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEARR           RBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;           2upl         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEARR           RBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOPROTEIN A1;         CHAIN: B; CHAIN: B;         CHAIN: CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           2up1         A         326         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           RBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         CHAIN: B;         CHAIN: B;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR           RIBONUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOTIDE         SINGLE-STRANDED         TELOMETRIC DNA; CHAIN: B;           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR           CHAIN: A; 12-NUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOPROTEIN A1;         CHAIN: A; 12-NUCLEOPROTEIN A1;	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 68 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOROTEIN A1; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: A1; CHAIN: A1; CHAIN: B; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; CHAIN: A1; C	2u2f         A         127         206         9.6e-13         0.63         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHA	2u2f         A         127         206         9.6e-13         0.53         0.05         SPLICING FACTOR U2AF 65 KD           2up1         A         126         311         1.1e-34         0.01         -0.19         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED           2up1         A         226         410         4.8e-22         0.35         -0.14         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B; 12-NUCLEOTIDE SINGLE-STRANDED           2up1         A         325         484         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B; 12-NUCLEOTIDE SINGLE-STRANDED           3sxl         A         325         474         1.3e-35         0.49         0.87         HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: B; 12-NUCLEOTIDE SINGLE-STRANDED           3sxl         A         325         474         3.2e-29         1.01         1.00         SEX-LETHAL; CHAIN: A; B, C; 1	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR UZAF 65 KD	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR UZAF 65 KD	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR UZAF 6S KD	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR UZAF 63 KD	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR U2AF 65 KD	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR U2AF 65 KD	2up  A   127   206   9.6e-13   0.53   0.05   SPLICING FACTOR U2AF 65 KD SUBJECT CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAI	2u2f   A   127   206   9.6e-13   0.53   0.05   SPLICING PACTOR U2AF 65 KD

<u> </u>	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
	<u>e</u>	OI N	TAA	ΨΨ		score	score	D score		
<del> </del>									CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX
									DNA; CHAIN: D, E;	(TRANSCRIPTION REGIT ATTON/DNA), DNA-BINDING,
										2 NUCLEAR PROTEIN, ETS DOMAIN,
	,									ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
╀	lawc	В	150	298	1.1e-40	0.94	1.00		GA BINDING PROTEIN ALPHA;	COMPLEX (TRANSCRIPTION
									CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:	REGULATION/DNA) GABPALPHA; GABPBETA1: COMPLEX
									DNA; CHAIN; D, E;	(TRANSCRIPTION
										REGULATION/DNA), DNA-BINDING,
										2 NUCLEAR PROTEIN, ETS DOMAIN,
										ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
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	14WC	a		3	3	2	) :		CHAIN: A; GA BINDING	REGULATION/DNA) GABPALPHA;
			.,—…						PROTEIN BETA 1; CHAIN: B;	GABPBETA1; COMPLEX
									DNA; CHAIN: D, E;	(TRANSCRIPTION
										REGULATION/DNA), DNA-BINDING,
										2 NUCLEAR PROTEIN, ETS DOMAIN,
										ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
+	103170	ď	17	165	1 60-37	111	9		GA BINDING PROTEIN ALPHA:	COMPLEX (TRANSCRIPTION
	Jawe	1	·	3	7.00.1	:	3		CHAIN: A; GA BINDING	REGULATION/DNA) GABPALPHA;
									PROTEIN BETA 1; CHAIN: B;	GABPBETA1; COMPLEX
									DNA; CHAIN: D, E;	(TRANSCRIPTION
										REGULATION/DNA), DNA-BINDING,
										2 NUCLEAR PROTEIN, ETS DUMAIN,
				-						ANKYRIN REPEATS,
1									ATTACA TATABAN CAR CAR CAR CAR CAR CAR CAR CAR CAR CAR	CONTRIBUTION STREET
1701	lawc	<u>m</u>	212	363	3e-45			90.41	GA BINDING FROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCERFITOR) REGULATION/DNA) GABPALPHA;
									PROTEIN BETA 1; CHAIN: B;	GABPBETAI; COMPLEX

<del></del>				
(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	IKANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REIFEATS,	IKANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	IKANSCKIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGIL ATTON/DNA) DNA BENDENC
DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;
	,			
	1.00	1.00	1.00	1.00
	0.64	0.25	1.07	0.46
	1.2e-41	3.2e-32	16-32	66-39
	395	427	405	199
	212	250	278	45
	В	В	В	æ
	lawc	lawc	lawc	lawc
	1701	1701	1701	1701
		lawc         B         212         395         1.2e-41         0.64         1.00         GA BINDING PROTEIN ALPHA; CHAIN: B; DNA; CHAIN: D, B;	lawc         B         212         395         1.2e-41         0.64         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING PROTEIN ALPHA;         CHAIN: A; GA BINDING PROTEIN B;         DNA; CHAIN: B;           lawc         B         250         427         3.2e-32         0.25         1.00         GA BINDING PROTEIN ALPHA;           CHAIN: A; GA BINDING         CHAIN: A; GA BINDING         PROTEIN BETA 1; CHAIN: B;         DNA; CHAIN: B;	Iawc   B   212   395   1.2e-41   0.64   1.00   GA BINDING PROTEIN ALPHA; GA BINDING PROTEIN ALPHA; GA BINDING PROTEIN B; DNA; CHAIN: B; DNA; CHAIN: B; GA BINDING PROTEIN ALPHA; GA BINDING PROTEIN ALPHA; GA BINDING PROTEIN ALPHA; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN

PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	PIJINKAD CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INFIIBITOR; CHAIN: NULL;
SEQFOL D score				87.58						
PMF		1.00	1.00		1.00	1.00	0.77	1.00	1.00	1.00
Verify		0.72	0.42		0.85	0.81	0.39	0.67	0.44	0.80
Psi Blast		4.8e-37	3e-37	1.4e-38	7.5e-38	1.5e-37	1.4e-38	4.5e-30	1.4e-36	1.4e-38
END		199	299	301	168	333	397	405	201	234
STAR		50	113	145	17	183	215	279	46	82
CHAI		В								
PDB		lawc	1bd8	1bd8	1bd8	1bd8	1bd8	1648	1bd8	1bd8
SEQ	NO	1701	1701	1701	1701	1701	1701	1701	1701	1701

Q. P.BB         CHAI         STAR         END         Psi Blast         Verify         PNF         SEOPOL         Coumpound           11         1bix         B         114         271         9e-38         0.72         1.00         CYCLIN-DEPENDENT KINASE           1         1bix         B         12         170         1.5e-39         0.92         1.00         CYCLIN-DEPENDENT KINASE           1         1bix         B         13         170         1.5e-39         0.92         1.00         CYCLIN-DEPENDENT KINASE           1         1bix         B         183         338         1.4e-38         0.48         1.00         CYCLIN-DEPENDENT KINASE           1         1bix         B         183         338         1.4e-38         0.48         1.00         CYCLIN-DEPENDENT KINASE           1bix         B         183         338         1.4e-38         0.48         1.00         CYCLIN-DEPENDENT KINASE           1bix         B         215         401         3e-39         0.43         1.00         CYCLIN-DEPENDENT KINASE           1bix         B         46         205         9e-38         0.32         1.00         CYCLIN-DEPENDENT KINASE           1bix <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>																								
Q         PDB         CHAI         STAR         END         Psi Blast         Verify score         PMF         SEQFOL           0.         ID         N ID         T AA         AA         Psi Blast         Verify score         B Score         D Score           11         1bbx         B         114         271         9c-38         0.72         1.00           1         1bbx         B         12         170         1.5c-39         0.92         1.00         0           1         1bbx         B         183         338         1.4c-38         0.48         1.00         0           1bbx         B         215         401         3c-39         0.43         1.00         0           6         6         6         6         6         6         6         6           1bbx         B         46         205         9c-38         0.32         1.00         0	PI)B annotation	ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	ACCIENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O	ALPHA/BETA, COMPLEX	COMPLEX (INHIBITOR	PROTEIN/KINASE) INFIBITOR	KINASE, CELI, CYCLE 2 CONTROL.	ALPHA/BETA, COMPLEX	(INTIBITOR PIKOTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALFRADE 1A, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	KINASE, CELL CYCLE 2 CONTROL.	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INITIBITOR PROTEIN/KINASE) INHIBITOR	rkulein, CYCLIN-DEPENDENT
XQ         PDB         CHAI         STAR         END         Psi Blast         Verify         PMF         SEOFCOL           11         1bix         B         114         271         9e-38         0.72         1.00         B.0.38           1         1bix         B         12         170         1.5e-39         0.92         1.00         80.38           1         1bix         B         13         170         1.5e-39         0.92         1.00         1.00           1         1bix         B         183         338         1.4e-38         0.43         1.00         1.00           1bix         B         215         401         3e-39         0.43         1.00         1.00           1bix         B         46         205         9e-38         0.32         1.00         1.00	Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	o C		CYCLIN-DEPENDENT KINASE 6: CHAIN: A: P19TNK4D: CHAIN:	B;		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B;			CVCI IN DEPENDENT VINIAGE	6; CHAIN: A; P19INK4D; CHAIN:	<b>B</b> ;			CYCLIN-DEPENDENT KINASE	o, Chalin: A; Figink4D; CHAIN:   B:			OVCI BI PEREN IN IN IN IN IN IN IN IN IN IN IN IN IN	6; CHAIN: A; P19INK4D; CHAIN: R:	
CHAI         STAR         END         Psi Blast         Verify           D         ID         N ID         TAA         AA         Score           11         1blx         B         114         271         9e-38         0.72         1           1         1blx         B         12         170         1.5e-39         0.92         1.           1         1blx         B         183         338         1.4e-38         0.48         1.           1blx         B         215         401         3e-39         0.43         1.0           1blx         B         46         205         9e-38         0.32         1.0	SEQFOL D score					80.38		,																
1   1bix   B   115   170   1.5e-39   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e   1.5e	PMF score		00.1	-					1.00				1.00				90	3				90		
PDB         CHAI         STAR         END         Psi Blast           1         1blx         B         114         271         9e-38           1         1blx         B         12         170         1.5e-39           1         1blx         B         13         170         1.5e-39           1         1blx         B         183         338         1.4e-38           1blx         B         215         401         3e-39         0           1blx         B         46         205         9e-38         0	Verify score		7/.0						0.92				0.48				2	.45				.32		
2Q         PDB         CHAI         STAR         END           D         ID         N ID         T AA         AA           D         ID         T ID         AA         AA           D         ID         B         114         271           D         ID         B         12         170           D         ID         B         ID         ID           D         ID         B         IB         IB           D         ID         B         ID         A01           D         ID         B         46         205	Psi Blast	00.00	06-50		00 9 6	1.56-39	<del> </del>						$\vdash$				1				-			
1 1bix B 113 1 1bix B 12 1 1bix B 13 1 1bix B 13 1 1bix B 13 1 1bix B 183	END	271	7/7		120	2			170				338				104	 }	·	<del></del>		t		
20 PDB CHAI D	STAR T AA	114	<b>.</b>		12	71			13			-	183				$\top$		_					
20 PDB	CHAI N ID	æ	)		a	٦			В	3			<u>—</u>		-		+							
8 9 6 1	PDB ID	1blx			-							7	_				$\top$					$\vdash$		
1701 1701 1701	SEQ NO:	1701			1701				1701			$\dashv$					1701					1701		

ound PDB annotation		KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	$\dagger$		 CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR			P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR			DENT KINASE SIGNALING PROTEIN HELIX-TURN-				INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	F		 ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR		_	N: C; I-KAPPA-   IKB/NFKB COMPLEX	$\neg$	SUBUNIT; TRANSCRIPTION FACTOR P65;
Coumpound			CVC! IN-DEPENDENT KINASE	6 INHIBITOR: CHAIN: A:			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;
SEOFOL	D score						92.05														89.22		 						
PMF	score		0.05	7.7								1.00		1.00		0.93							 		0.35				1.00
Verify	score		700	47.0								0.60	)	0.80	) } 	0.43	!								0.19	}			0.71
Psi Blast			3.75.20	3.25-30			1.3e-35		-			30-37	)	1 50-36	2	1.4e-29					9e-38				1.2e-53	}			1.5e-39
END	ΑA		430	437			177					237	}	401		431	<u>:</u>				236				371	:			173
STAR	TAA		22.0	CC7			0	·				104	÷	960	) 	253	3				250	:	 		145	}			17
CHAI	NB		\ <	₹			A	;				V	ζ	V	ζ	A					A				<u> </u>	,			Ω
pnR (	А		=	anar			11,10	3				1,400	1073	1,40°	507	1:14	<u> </u>				1ihb	}	 		15	1			1 ikn
CEC	Αġ		, 200	10/1	 		1701	10/1				1701	1,701	1701	70.	1701					1701	:	 		1701	-			1701

PDIS annotation		TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR,	INB/INFINE CONFLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX		ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEY
Coumpound	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A, NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	DF-ALPHA; CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	DF-ALF RA, CHAIN: D, NF-KAPPA-B P65 SUBUNIT; CHAIN: A, NF-KAPPA-B P50D SUBUNIT; CHAIN: C, I-KAPPA-	B-ALFHA, CHAIN: D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D STRINIT: CHAIN: C. 1 VADA	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	D-ALTHA; CHAIN; D; NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B. D:
SEQFOL D score							81,35						
PMF		0.92	0.99	1.00	1.00			0.99	i	0.71	1.00		0.99
verity score		0.05	0.49	0.11	0.13			0.28		0.25	0.58		0.10
Fsi Blast		1.1e-38	3e-50	4.8e-43	4.5e-52	,	4.5e-52	4.5e-52	+	2	9e-51		3e-49
END AA		427	403	232	240	0	253	276	301	160	311		401
TAA		212	215	45	45		ç	82	247	1	113	*****	143
NID		<u> </u>	Ω	О	Д		ລ	Ω			n)		E
a a		<u> </u>	likn	likn	likn		uy U	1 ikn	Im vo	,	1111		Infi
ge ö		10/1	1701	1701	1701	1701	10/1	1701	1701		10/1		1701

SEO	PDR	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	PDB annotation
ΑŞ	e.	NID	TAA			score	score	D score		
									I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	lnfi	E	17	170	4.5e-39	0.94	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX
1701	1nfi	E	210	427	1.1e-38	0.42	0.70		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX
				•					I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT),
,		t	Ş	C	1 60 61			27.55	NE.KABBA-B B65: CHAIN: A C.	COMPLEX (TRANSCRIPTION
1701		<u> 1</u>	7+	747	1.35.1			77.10	NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									· .	ANKYRIN 2 REPEAT HELIX
1701	lnfi	3	43	238	1.5e-51	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									F;	REGULATION/ANK REPEAT),
1201	1,1,1	Ĺī	44	232	6 4e-43	0.59	8		NF-KAPPA-B P65: CHAIN: A. C:	COMPLEX (TRANSCRIPTION
<u> </u>		1	<u> </u>	1	2	<u>}</u>			NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAFFA-B-ALFHA; CHAIN: E, F;	(IKANSCKIF 110N REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1701	1sw6	A	19	287	4.5e-36	-0.06	0.28		REGULATORY PROTEIN SWI6;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION,
									6-6	ANKYRIN REPEATS, CELL-CYCLE
1701	1sw6	∢	9/	320	4.5e-36			70.20	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
				1						

		1					
D. C. C.	r Dr. annotation	COMPLEX (AN IT- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-	COMPLEX (ANTI- COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	(STATION VICTORIANS)	KINASE KINASE, SIGNAL TRANSDUCTION, CALCITIM/CALMODITIN		PROTEIN KINASE CDK2: PROTEIN
Commonard		P53; CHAIN: A; <b>53BP2; CHAIN:</b> B;	P53; CHAIN: A; 53BP2; CHAIN: B;		CALCTUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL:	TRANSFERASE(PHOSPHOTRA NSTERASE) \$C-/AMP\$- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	z
SECTOR	D score	70.78					
PMR	score		0.55		0.65	0.86	0.11
Verify	score		-0.07		0.08	0.30	0.22
Psi Blast		7.5e-35	4.56-37		1.6e-70	6.46-98	1.1e-46
END	AA	396	283		303	312	266
STAR	TAA	214	. 81		31	29	29
CHAI	N ID	m	В			ш	
PDB	А	lycs	1 yes		1a06	lapm	laq1
SEO	ВÖ	1021	1701		1702	1702	1702

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
A Š	A	A II	TAA	AA		score	score	D score		
									KINASE 2; CHAIN: NULL;	KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1702	1b3u	Ą	231	416	0.0003	0.22	1.00		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1702	1b3u	A	278	560	1.4e-33	0.29	1.00		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1702	1cmk	ъ	29	312.	3.2e-99	0.10	0.75		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1702	1ctp	ш	29	303	8e-94	0.01	0.86		TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1702	1f3m	o ·	29	264	3.2e-49	0.35	0.98		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1702	Ihel		53	266	4.8e-49	0.26	0.60		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1702	Iial	Υ	328	551	6e-05	0.26	0.24		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2

PD B annotation	ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGIII ATION	KINASE KINASE, TWITCHIN, NITO A STEPLING PECTINAL A TROOP	KINASE KINASE, TWITCHIN,	TRANSFERASIS MITOGEN ACTIVATED PROTEIN KINASE, TRANSFERASIS, MAP KINASE, SERINE/THREONINE-PROTEIN	KINASE, 2 P38 KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASI; SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-13INDING,	CALMODULIN-BINDING CALMODULIN, CALCIUM BINDING, HELIX-LOOP-FIELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA- CATENIN, STRUCTURAL PROTEIN	CALCTUM-BINDING PROTEIN CALCTUM-MYIUSTOYL SWITCH, CALCUIM-BINDING PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRIIS SAIMIRI VIRAI
Coumpound		TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	PHOSPHORYLASE KINASE; CHAIN: NULL;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	BETA-CATENIN; CHAIN: NULL;	RECOVERIN; CHAIN: NULL;	CYCLIN HOMOLOG; CHAIN: A;
SEQFOL D score				81.88					
PMF score		0.75	96'0		66.0	0.09	0.52	0.07	0.30
Verify		0.30	0.51		0.48	-0.18	-0.31	-0.04	-0.26
Psi Blast		1.3e-58	8e-57	3.2e-42	6.4e-71	1.le-19	0.0001	0.0003	3.2e-26
END		304	265	334	264	453	260	440	352
STAR T AA		29	29	m	16	301	438	308	157
CHAI N ID			Ą			4			4
PDB ID		1koa	1kob	1p38	1phk	<del> </del>	2bct	1iku	1bu2
SEQ ID NO:		1702	1702	1702	1702	1702	1702	1704	1705

PDB annotation	CYCLIN		FACTOR, TATA SEQUENCE- BINDING PROTEIN, PROTEIN-DNA COMPLEX, CYCLIN-LIKE FOLD,	•	.,	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN-		KINASE/CYCLIN), CYCLIN, CDK, 2	PHOSPHORYLATION, SUBSTRATE COMPLEX	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA 1 TRANSDICIN GAMMA	SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), GPROTEIN HETEROTRIMER 2
Coumpound		GENERAL TRANSCRIPTION FACTOR IIB; CHAIN: A, E, I, M, Q; TATA BOX BINDING	PROTEIN; CHAIN: B, F, J, N, R; ADMLP TATA-BOX DNA CONTAINING IIB	RECOGNITION CHAIN: C, G, K, O, S; ADMLP TATA-BOX DNA CONTAINING IIB	RECOGNITION CHAIN: D, H, L, P, T;	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C;	A; CHAIN: B, D; SUBSTRATE	FEFTIDE; CRAIN: E, F;		CYCLIN A; CHAIN: NULL;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B. C.	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G:	5
SEQFOL D score		-											
PMF		0.17				0.01				0.04	1.00	0.93	
Verify score		-0.02				-0.21				-0.11	0.65	0.35	
Psi Blast		1.3e-23				4.8e-49				4.8e-48	8e-67	1.46-59	
END		350				345				345	571	529	
STAR T AA		183				136				142	277	230	
CHAI		Ą				В					Ą	В	
PDB ID		1c9b				1qmz				lvin	1erj	1got	
SEQ US		1705				1705				1705	1708	1708	

PDI annotation  SIGNAL TRANSDUCTION COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETIROTRIMER 2 SIGNAL TRANSDUCTION COMPLEX (GTI)- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCIN) GAMMA COMPLEX (TRANSFERASI/PEPTIDE) COMPLEX (TRANSFERASI/PEPTIDE) COMPLEX (TRANSFERASI/PEPTIDE)	COMPLEX (PROTO- ONCOGENE/EARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN SIGNAL TRANSITICATION
	5 5 5
Coumpound  GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: B; GT-GAMMA; CHAIN: G; GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHIMERA; CHAIN: B; GT-GAMMA; CHAIN: G; BETA; CHAIN: B; GT-GAMMA; CHAIN: G; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE); CHAIN: C, D; TRANSFERASE(PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (AREI SON SH2 AND 1 AB2 3	(NMR, 20 STRUCTURES) 1AB2 5 FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P
SEQFOL D score	
1.00 0.09 0.12	0.06
0.55 0.38 0.38	0.47
Psi Blast 1.6e-69 1.6e-69 8e-25 1.6e-22	4.8e-21
569 569 380 382	378
242 242 280 282 282	282
CHAI N ID B	ţr.
1got 1got 1a09 1ab2	laot
SEQ ID NO: 1708 1709	1709

1	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
	e Z	TAA	ΥΥ		score	score	D score		
<del> </del>									PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
+		284	385	1.6e-24	0.29	0.01		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN
		275	379	1.6e-22	0.31	0.07		P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION
1	∢	281	379	1.1e-17	0.44	-0.01		SYK PROTEIN TYROSINE KINASE; CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PROTEIN-TYROSINE KINASE SH2 DOMAIN, COMPLEX 2 (PHOSPHOTRANSFERASE/PEPTIDE)
Icwd	H	286	375	1.4e-19	0.13	0.07		P56LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P;	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE) PHOSPHOTRANSFERASE, COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
		281	377	1.1e-17	0.18	0.16		GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	SH2 DOMAIN GRB2; GRB2, SH2 DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
	4	242	379	6.4e-26	0.08	0.01		P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	COMPLEX (KINASE/PEPTIDE)
	∢	282	379	3.2e-21	0.49	0.15		HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU- ILE; ILKK 11 CHAIN: B; ILKK	COMPLEX (TYROSINE KINASE/PEPTIDE)

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PDI3 annotation				TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, BISTI BY STONIA THE STONIA THE STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONIA STONI	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSFERASE, TRANSFERASE TRANSDUCTION, TRANSFERASE	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE, HALOPEROXIDASE,	HALOPEROXIDASE HALOPEROXIDASE HALOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE L;
Coumpound	12	PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SIGNALLING PROTEIN PHOSPHATIDYLINOSITOL 3- KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTI IRFS) 2PNA 4	SHP-2; CHAIN: A, B;	HCK SH2; CHAIN: NULL;	CHLOROPEROXIDASE L; CHAIN: A, B, C;	CHLOROPEROXIDASE L; CHAIN: A, B, C;
SEQFOL D score						85.13	
PMR score		0.07	0.78	0.04	0.25		1.00
Verify score		0.51	0.33	-0.31	0.19		0.36
Psi Blast		1.6e-24	6.4e-18	3.2e-27	1.6e-22	3e-41	3e-41
END AA		380	383	439	379	357	356
STAR T AA		284	286	257	281	92	84
CEAI		∢		Ą		Ą	4
PDB ID		Isha	2pna		3hck	1a88	1a88
SEQ ID NO:		6027	1709	1709	1709	1710	1710

PDB annotation	OXIDOREDUCTASE		HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX				HALOPEROXIDASE HALOPEROXIDASE A2, CHLOROPEROXIDASE A2; HALOPEROXIDASE, OXIDOREDUCTASE, PEROXIDASE, ALPHA/BETA 2 HYDROLASE FOLD,
Coumpound		BROMOPEROXIDASE A1; CHAIN: NULL;	CHLOROPEROXIDASE F; CHAIN: NULL;	CHLOROPEROXIDASE F; CHAIN: NULL;	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HAĽOALKANE DEHALOGENASE; CHAIN: NULL;	BROMOPEROXIDASE A2; CHAIN: NULL;
SEQFOL D score		95.47	83.84		67.83	94.11		89.86
PMF score				1.00			1.00	
Verify				0.61			0.45	
Psi Blast		8e-31	9e-41	96-41	1.5e-36	3e-43	3e-43	8e-32
END		360	357	356	355	357	.356	357
STAR T AA		78	78	84	63	44	83	76
CHAI N ID					A			
PDB ID		1a8q	1a8s	1a8s	1azw	1b6g	1b6g	1brt
SEQ TO	2	1710	1710	1710	1710	1710	1710	1710

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PDB annotation	HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXAIDIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA- HYDROI ASF	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE,	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYDRON, CIS-PEPTIDE,	HYDROLLASE HYDROLASE, HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPICHI OR OHYDRING	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTION IREA 2 NAMEROLOGY
Coumpound	2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A:	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A:	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A:	HALOALKANE DEHALOGENASE; CHAIN: A;	TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	EPOXIDE HYDROLASE; CHAIN: A, B;
SEQFOL D score	77.34	122.01					119.90	
PMF score			1.00	1.00	0.63	0.07		1.00
Verify			0.58	0.60	0.11	0.25		0.52
Psi Blast	3.2e-36	9e-47	9e-47	36-44	3e-13	4.8e-09	9.6e-37	8e-43
END	357	360	358	358	199	212	356	356
STAR T AA	72	<i>L</i> 9	74	73	101	97	99	79
CHAI N ID	A	A	Ā	K			<b>V</b>	∢
PDB ID	Ic4x	lcqw	lcqw	10v2	lcvl	lcvl	lehy	lek1
SEQ ID	NO: 1710	1710	1710	1710	1710	1710	1710	1710

SEO	PINR	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	PDB annotation
i A E	8	NID	TAA	AA		score	score	D score	•	
1710	lek1	⋖	70	356	1.2e-54	0.56	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1710	1ek1	В	62	356	8e-43	0.58	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1710	1ek1	В	69	356	3e-56	69.0	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1710	1hlg	A	86	226	1.5e-06	0.13	0.07		LIPASE, GASTRIC; CHAIN: A, B;	HYDROLASE LIPASE
1710	1qe3	A	85	215	4.5e-05	0.76	0.27		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION
1710	Iqge	Q	92	238	6e-25	0.38	0.81		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1710	1qge	Q	97	212	4.8e-09	0.37	0.28		TRIACYLGLYCEROL HYDROLASE, CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1710	1407	∢	74	358	1.5e-45	0.46	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE EH; EPOXIDE HYDROLASE, ALPHA/BETA HYDROLASE
1710	1qtr	∢	29	360	6.4e-29			80.11	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1710	4lip	Q	97	215	4.8e-10	0.10	0.11		TRIACYL-GLYCEROL- HYDROLASE; CHAIN: D, E;	LIPASE LIPASE, LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE

PDI: annotation	ANALOGUE, ENANTIOSELECTIVITY			METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	PROTEIN (CST) DNA-BINDING PROTEIN V(D)J ECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CIJUSTER, ZINC FINGER, DNA-JINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CIJUSTER, ZINC FINGER, DNA-HINDING PROTEIN	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/RFTA FOILD	TRANSCRIPTION INHIBITOR BETA- PROPELLER
Coumpound		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A:	RAGI; CHAIN: NULL;	RAGI; CHAIN: NÜLL;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;
SEQFOL D score								,
PMF score		 0.84	0.71	0.00	0.74	0.64	0.12	0.88
Verify		-0.31	-0.18	-0.64	-0.02	-0.00	0.16	0.52
Psi Blast		6e-17	3.2e-14	4.5e-14	3e-11	1.3e-07	0.009	1.4e-28
END		328	332	321	328	331	297	307
STAR T AA		275	278	276	272	280	194	171
CHAI				Ą	·		A	∢ .
PDB ID		1chc	1chc	1g25	Irmd	1rmd	lorz	Ierj
SEQ NO:		1711	1711	1711	1711	1711	1712	1712

PDB annotation	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE,
Coumpound	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/Gi-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	MJ0882; CHAIN: A;	CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;
SEQFOL D score			63.92			
PMF score	0.96	1.00		1.00	0.43	0.30
Verify score	0.33	0.43		0.54	-0.10	-0.07
Psi Blast	1.3e-44	6.4e-39	1.6e-48	1.6e-48	6.4e-10	7.5e-11
END	289	290	307	305	446	455
STAR T AA	37	14	-	28	338	334
CHAI N ID	A	В	В		∢	
PDB ID	lerj	1got	lgot	lgot	1dus	1vid
SEQ NO.	1712	1712	1712	1712	1713	1713

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PDJ3 annotation	METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION		REPLICATION DNA NUCLEOTIDE	HELICASE, 2	HYPERTHERMOSTABLE PROTEIN	REPLICATION DNA NUCLEOTIDE	EACISION KEPAIK, UVRABC,   HELICASE, 2	HYPERTHERMOSTABLE PROTEIN	HYDROLASE HEPATITIS C VIRUS,	BIFUNCTIONAL, PROTEASE-	HELICASE	PROTECTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	INDIENT ASSESSED TO THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND	PROTEIN	GENE REGULATION APO PROTEIN		GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION	FACTOR 4A, E1F4A: HELICASE.	INITIATION FACTOR 4A, DEAD-BOX	PROTEIN	TRANSLATION EUKARYOTIC	INITIATION FACTOR 4A; IF4A,	HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC	INITIATION FACTOR 4A; IF4A,	TRANSI ATION FITE ARVOTTE
Coumpound	,		DNA NUCLEOTIDE EXCISION PEDA ID ENZYME TIMBE.	CHAIN: A;		DNA NUCLEOTIDE EXCISION BEDAID ENIXME HERBE	CHAIN: A;		PROTEASE/HELICASE NS3;	CHAIN: A, B;	EVORUTOI EASE ABO SIERIE	B. CHAIN. A.	EVORITOTEASE ABO STRIPTED	B; CHAIN: A;	EXCINUCLEASE UVRABC	COMPONENT UVRB; CHAIN: A;	EXCINUCLEASE UVRABC	EUKARYOTIC INITIATION	FACTOR 4A; CHAIN: A;			YEAST INITIATION FACTOR	4A; CHAIN: A, B;	VE A ST Print A Trick I TO A TV	YEAST INITIATION FACTOR	4A; CHAIN: A, B;	YEAST INITIATION FACTOR
SEQFOL D score																											
PMF			0.53			96.0			0.77		0.62	70.0	98.0	0.00	0.99		0.43	0.18			200	0.35		70.0	9		0.21
Verify score			0.14			0.50			0.42		000	<u>}</u>	-0 11		0.35		0.20	0.07			8	0.02		200	4.0		90.0
Psi Blast			3.2e-13		,	4.5e-16			90000		3 20-13	) )	1 50-16		3e-20		3.2e-18	1.1e-39			1 6- 06	1.6e-25		0	<b>-</b>		1.6e-25
END			497			494			170		497		513		525		208	508			150	601		508	2	-,-	169
STAR T AA			345			3/1		Į,	70		345		370		346		354	338			,	٧.	-	119	}		2
CHAI			⋖			∢			∢		4		\ \		<		<b>-</b>	Ą				<		B	<b>)</b>		В
PDB ID			1040	-	1-4-	5			Icui		1d2m		1d2m		1d9x	of t	XADI	1fuk	_		14,11			1fuu	_		1fuu
SEQ ID NO:			1719		1710	1/13		0,2,5	61/1		1719		1719		1719	21.0	1/19	1719			1710			1719	<u> </u>		1719

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PDB annotation	INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE	GENE REGULATION EIF4A; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY	HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	COLLAGEN-BINDING COLLAGEN- BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN
Coumpound	4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	HELICASE PCRA; CHAIN: A, F; HELICASE PCRA; CHAIN: B, G; DNA (5'-D(*TP*TP*TP*T)-3'); CHAIN: C, D; DNA (5'-D(*GP*C)- 3'); CHAIN: H; DNA (5'- D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	VON WILLEBRAND FACTOR; CHAIN: A, B;	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;
SEQFOL D score			1			75.90	89.44	65.12			
PMF		0.22	0.39	0.33	1.00				0.99	-0.01	0.41
Verify score		0.29	0.10	0.22	0.62				0.79	0.22	0.65
Psi Blast		0.0014	3.2e-23	0.0006	1.1e-21	1.1e-21	4.8e-17	1.6e-26	1.6e-26	3.2e-11	9e-12
END		170	169	82	170	220	213	221	220	305	427
STAR T AA		13	2	2	28	28	31	23	30	211	329
CHAI N ID		A	Ą	Y	Ą	¥	Ą				
PDB ID		Ihei	1qde	2pjr	laox	1аох	latz	lauq	lauq	1bpv	1bpv
SEQ ID NO:		1719	1719	1719	1721	1721	1721	1721	1721	1721	1721

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PDI) annotation	TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	SIGNATING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BEIA SUBUNIT, SIGNAL INC. PROTEIN	NIGIOU DAIRGES												STRUCTURAL PROTEIN L-DOMAIN	METAL BINDING, COLLAGEN,	STRUCTURAL PROTEIN L-DOMAIN	METAL BINDING, COLLAGEN,	ADRESION
Coumpound		TITIN; CHAIN: NULL;	GP130; CHAIN: A, B;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGI 14N	(CHYMOTRYPTIC FRAGMENT	CONTAINING THE 1CFB 3 TWO AMINO PROXIMAI	FIBRONECTIN TYPE III	REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFR 5	NEURAL ADHESION	MOLECULE DROSOPHILA	NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT	AMINO PROXIMAL	FIBRONECTIN TYPE III	REPEATS ICFB 4 (RESIDUES	INTEGRIN ALPHA-1: CHAIN: A.	B;	INTEGRIN ALPHA-1; CHAIN: A.	B;	CELL ADHESION PROTFIN
SEQFOL D score				52.60									-							
PMF score		60:0	0.48						-0.07							00.1		00.1		0.72
Verify score		0.47	0.45			•			0.09					•		0.46		96.0		0.49
Psi Blast		3.2e-13	3.2e-12	1.4e-11					1.4e-11							9.6e-21		6e-38		1.1e-13
END AA		418	419	427					412							170		209		415
STAR T AA		342	337	208					209							33		34		338
CHAI N ID			Ą													A		A		
PDB ID		1bpv	1bqu	1cfb					lcfb	<del></del> -	<del>.</del>					1ck4		1ck4		1fna
SEQ ID NO:		1721	1721	1721					1721							1721		1721		1721

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PDB annotation		CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	IMMUNE SYSTEM VON	GLYCOPROTEIN IBA (A:ALPHA)	BINDING, 2 COMPLEX	(WILLEBRAND/IMMUNOGLOBULIN	VON WILLEBRAND DISEASE	CELL ADHESION PROTEIN A-	DOMAIN INTEGRIN, CELL ADHESION PROTEIN	GLYCOPROTEIN, EXTRACELLULAR	2 MATRIX, CYTOSKELETON	CELL ADHESION PROTEIN A-	ADHESION PROTEIN.	GLYCOPROTEIN, EXTRACELLULAR	2 MATRIX, CYTOSKELETON	CELL ADHESION LFA-1, ALPHA- LBETA-2 INTEGRIN, A-DOMAIN;
Coumpound	FIBRONECTIN CELL- ADHESION MODULE TYPE III- 10 IFNA 3	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	IMMUNOGLOBULIN NMC-4	IMMUNOGLOBULIN NMC-4	IGG1; CHAIN: H; VON	WILLEBRAND FACTOR;	CHAIN: A;	INTEGRIN; CHAIN: NULL;				INTEGRIN; CHAIN: NULL;				CD11A; 1LFA 5 CHAIN: A, B; 1LFA 6
SEQFOL D score				91.50		73.33							91.05								78.17
PMF score		0.13	-0.06		-0.09		0.49	1.00									1.00				
Verify score		-0.05	-0.00		0.16		-0.04	0.97						-			0.65		-		
Psi Blast		1.4e-26	1.6e-31	1.6e-31	1.6e-24	1.1e-26	1.1e-26	1.6e-25					7.5e-37				7.5e-37				1.5e-36
END		444	415	425	421	421	445	217					208				206	<del></del>			213
STAR T AA		106	27	28	107	133	213	30					32				34				33
CHAI N ID					Ą	A	A	A													A
PDB UD		1fnf	1fnf	1fnf	1fnh	1fnh	1fnh	Ifns					lido				lido				11fa
SEQ NO.		1721	1721	1721	1721	1721	1721	1721					1721				1721			_	1721

PDB annotation	1LFA 8	CELL ADHESION LFA-1, ALPHA- L\BETA-2 INTEGRIN, A-DOMAIN;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEVARIN-BINDING,	CELL ADHESION INTEGRIN, CELL ADHESION	CELL ADHESION INTEGRIN, CELL ADHESION	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXHROCELLULAR 2 MATRIX, EXHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
Coumpound		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B:	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;
SEQFOL D score			75.51						
PMF score		1.00		0.58	0.37	1.00	1.00	-0.07	0.72
Verify score		0.68		0.08	0.42	0.55	0.99	0.05	0.04
Psi Blast		1.5e-36	6.4e-24	6.46-24	8e-17	8e-21	7.5e-28	1.6e-18	1.6e-22
END		209	425	415	445	170	209	419	421
STAR T AA		34	211	215	342	30	34	214	214
CHAI N ID		⋖				¥	∢ .	∢ .	4
PDB ID		llfa 	lmfn	lmfn	1mfn			Iqg3	1qr4
SEQ ID NO:		1721	1721	1721	1721	1721	1721	1721	1721

PDB annotation	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN				PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	COAGULATION FACTOR	-
Coumpound	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS
SEQFOL D score	77.31								
PMF score		0.34	0.99	0.81	0.70	0.84	0.86	-0.17	-0.19
Verify		0.55	0.06	0.92	0.27	0.55	0.71	90.0	0.08
Psi Blast	1.6e-22	1.4e-13	3e-12	1.2e-13	3.2e-14	1.3e-06	3.2e-11	1.1e-12	1.5e-16
END	421	445	301	421	415	281	421	416	422
STAR T AA	214	337	210	33.5	337	215	337	215	215
CHAI N ID	A	A				4	4		В
PDB	1qr4	1qr4	Iten .	1ten	1ttf	2fnb	2fnb	2hft	3hhr
SEQ E	1721	1721	1721	1721	1721	1721	1721	1721	1721

PDE annotation		TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	KINASE KINASE, SIGNAL TRANSDUCTION,		COMPLEX (KINASE/INHIBITOR)
Coumpound	RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	CALCIUM/CALMODULIN. DEPENDENT PROTEIN KINASE; CHAIN: NIIIT:	. Bed MH is med MH is	CYCLIN-DEPENDENT KINASE (
SEQFOL D score				59.46	52.92
PMF score		0.58	0.27	0.88	
Verify score		0.19	-0.31	-0.22	
Psi Blast		4.5e-06	4.8e-39	3.2e-47 3.2e-47	8e-24
END		236	355	413	33
STAR T AA		146	147	77	104
CHAI N ID		В		ш ш	4
PDB ID		1fuu	1a06	lapm lapm l	1
SEQ ID NO:		1723	1724	1724	┨

PMF SEQFOL score D score
6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;
0.70 PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT PROTEIN CAMP 3 (P. C. 7, 7, 1, 37) 1 CMK 4
59.27 PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4
0.77 TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4
58.35 TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4
0.54 SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; C.D. CHAIN: C. D.
56.49 P38 MAP KINASE; CHAIN:

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PDI annotation	KINASE KINASE, TWITCHIN,	KINASE KINASE, TWITCHIN, INTRACTEDIC BEGILFATION	TRANSFERASE MITOGEN ACTIVATED BY OTEN VENASE.	TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN	KINASE, 2 P38	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE;	GLYCOGEN MITABOLISM,	SERINE/THRECININE DROTTEN 2	KINASE, ATP-BINDING,	TRANSEED ASE MAD VINIAGE	SERINE/THREONINE PROTEIN	KINASE, TRANSFERASE	TRANSFERASE MAP KINASE,	SERINE/THREONINE PROTEIN	SERINE KINASI SERINE KINASE	TITIN, MUSCLE, AUTOINHIBITION		AMINE/CARBOXYLATE LIGASE AMINE/CARBOXYLATE LIGASE		COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEX	(NUCLEAR PROTEIN/RNA), RNA,	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA: SPI ICING
Coumpound	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL:			PHOSPHORYLASE KINASE; CHAIN: NULL;				ERK2: CHAIN: NITI 1			ERK2; CHAIN: NULL;		TITIN; CHAIN: A. B.			GLUTATHIONE SYNTHETASE; CHAIN: A;	•	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-
SEQFOL D score			60.82			-							58.82	<del></del>									3 7
PMF score	0.11	0.55				0.81	.•			0.13					0.54		3	0.32		0.52	-		0.95
Verify score	-0.27	-0.31		-	200	0.03				-0.10					-0.27		223	-0.23		0.40		· · · · · · · · · · · · · · · · · · ·	0.26
Psi Blast	1.1e-33	6.4e-34	1.6e-24		3 75 47	3.26-43				1.1e-24			1.1e-24		3.2e-27		00000		1	7.5e-07			) Se-05
END	356	356	403		356	000				414		200	276		362		,	3		555			919
STAR T AA	148	150	42		127	771				162		0,0	ç		150		3	,	200	989			542
CHAI N ID		Ą							-						Ą		A	•		 q			∢
PDB ID	Ikoa	1kob	1p38		1nhk					Ipme		Inme	)		1#: 		2hos	-	+	layn -			167f /
SEQ ID NO:	1724	1724	1724		1724					1724		1724	17/1		.1724		1726	$\dashv$	1730			$\dashv$	1728

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Conmpound	PDB annotation
A Š	a	OI N	TAA	ΑA		score	score	D score		
									R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	REGULATION, RNP DOMAIN, RNA COMPLEX
1728	167f	Ą	688	958	3e-07	0.08	0.43		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1728	Icun	∢	720	835	0.003	-0.04	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1728	1cvj	∢	544	612	4.5e-05	-0.10	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1728	lcvj	⋖	688	956	7.5e-07	0.47	0.57		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1728	1cvj	[I4	887	950	7.5e-07	0.54	0.43		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1728	1cx0	⋖	540	614	6e-05	-0.15	0.53		U1A PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	RNA BINDING PROTEINRNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE
1728	1d8z	4	540	614	1.5e-05	0.64	0.53		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN

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RNA BINDING PROTEIN RNA-	BINDING DOMAIN ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT RIBONUCLEOFROTEIN UIA117; RIBONUCLEOFROTEIN, RNP	DOMAIN, SPLICEOSOME STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN MICTEDI IIS	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN RNA BINDING PROTEIN RNA- BINDING DOMAIN		RIBONUCLEOPROTEIN PTB, PTB. C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN RNP, RNA, SPICING, 2 TRANSI A TROM
HU ANTIGEN C; CHAIN: A;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A;	CHAIN: B; UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: MITTER	NUCLEOLIN RBD1; CHAIN: A;	HNRNP AI; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A:	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POLYPYRIMIDINE TRACT. BINDING PROTEIN; CHAIN: A;
0.80	0.37	0.68	0.21	0.99	0.71	0.99	0.22
0.48	-0.23	0.65	0.48	0.42		0.13	-0.14
3e-05	3e-06	1.5e-05	6e-07	1.5e-05	6e-07	1e-08	7.5e-05
598	835	614	947	612	614	946	614
542	709	540	887	541	560	98 88 98	493
Ą	В		Ą	-	A	В	∢
1d9a	1dn1	1fht	1fj7	lha1			Iqm9
NO: 1728	1728	1728	1728	1728	1728	1728	1728
	1d9a         A         542         598         3e-05         0.48         0.80         HU ANTIGEN C; CHAIN: A;	1d9a         A         542         598         3e-05         0.48         0.80         HU ANTIGEN C; CHAIN: A;           1dn1         B         709         835         3e-06         -0.23         0.37         SYNTAXIN BINDING PROTEIN           1, CHAIN: A; SYNTAXIN 1A;         1, CHAIN: A; SYNTAXIN 1A;	1d9a         A         542         598         3e-05         0.48         0.80         HU ANTIGEN C; CHAIN: A;           1dn1         B         709         835         3e-06         -0.23         0.37         SYNTAXIN BINDING PROTEIN           1; CHAIN: A; SYNTAXIN 1A;         CHAIN: B;         CHAIN: B;           1fht         540         614         1.5e-05         0.65         0.68         UI SMALL NUCLEAR           RIBONUCLEOPROTEIN A;         RIBONUCLEOPROTEIN A;         CHAIN: MILL NUCLEAR         CHAIN: MILL NUCLEAR	1d9a         A         542         598         3e-05         0.48         0.80         HU ANTIGEN C; CHAIN: A;           1dn1         B         709         835         3e-06         -0.23         0.37         SYNTAXIN BINDING PROTEIN           1fht         540         614         1.5e-05         0.65         0.68         UI SMALL NUCLEAR           1fj7         A         887         947         6e-07         0.48         0.21         NUCLEOLIN RBD1; CHAIN: A;	1d9a         A         542         598         3e-05         0.48         0.80         HU ANTIGEN C; CHAIN: A;           1dn1         B         709         835         3e-06         -0.23         0.37         SYNTAXIN BINDING PROTEIN           1fht         540         614         1.5e-05         0.65         0.68         UI SMALL NUCLEAR           1fj7         A         887         947         6e-07         0.48         0.21         NUCLEOLIN RBD1; CHAIN: A;           1ha1         541         612         1.5e-05         0.42         0.99         HNRNP AI; CHAIN: NULL;	1d9a   A   542   598   3e-05   0.48   0.80   HU ANTIGEN C; CHAIN: A;   1dn1   B   709   835   3e-06   -0.23   0.37   SYNTAXIN BINDING PROTEIN II; CHAIN: B;   1.5e-05   0.65   0.68   U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A;   1fj7   A   887   947   6e-07   0.48   0.21   NUCLEOLIN RBD1; CHAIN: A;   1fh1   A   560   614   6e-07   0.32   0.71   HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0;   CHAIN: A. CHAIN: NULL;   1fh1   A   560   614   6e-07   0.32   0.71   RIBONUCLEOPROTEIN D0;   CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. CHAIN: A. 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CHAI	149a   A   542   598   3e-05   0.48   0.80   HU ANTIGEN C; CHAIN: A;   140   B   709   835   3e-06   -0.23   0.37   SYNTAXIN BINDING PROTEIN   1; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: B; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN

PDB annotation	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION		COMPLEX (RIBONUCLEOPROTEIN/RNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA),
Coumpound	POL YPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	UIA SPLICEOSOMAL PROTEIN; 1URN 5 CHAIN: A, B, C; 1URN 6 RNA 21MER HAIRPIN (5:- (AP*AP*UP*CP*CP*AP*UP*UP* 1URN 11 CHAIN: P, Q, R 1URN	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED
SEQFOL D score								
PIMF score	0.10	0.82	0.40	0.03	0.75	0.39	0.43	0.75
Verify score	0.10	0.51	-0.03	-0.03	0.18	0.42	0.05	0,51
Psi Blast	1.5e-07	0.0001	0.0001	1e-06	4.5e-06	3e-05	6e-07	7.5e-07
END	947	610	619	614	614	616	946	612
STAR T AA	828	540	540	999	542	542	887	525
CHAI N ID	4		A	A				A
PDB ID	Iqm9	1sxl	lurn	2mss	2sxl	2u1a	2u1a	2up1
SEQ ID	1728	1728	1728	1728	1728	1728	1728	1728

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PDB annotation	HETEROGENEOUS NUCLEAR 2	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HNRNP A1, UP1; COMPLEX	(RIBONUCLEOPROTEIN/DNA),	HETEROGENEOUS NUCLEAR 2	RIBONUCLEOFROTEIN A1	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMIPENSATION	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION		PLASMA PROTEIN PLASMA	PROTEIN, METAL-BINDING, LIPID-	Distriction						
Соитроинд	TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1;	CHAIN: A; 12-NUCLEOTIDE	SINGLE-STRANDED	TELOMETRIC DNA; CHAIN: B;		SEX-LETHAL; CHAIN: A, B, C;							SEX-LEIHAL; CHAIN: A, B, C;							orning training	SEKUM ALBUMIN; CHAIN: A;			DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 1AHD 3	REPLACED BY SER (C39S)	COMPLEX WITH DNA (NMR,
SEQFOL D score									-									•						_						_	
PMF		0.95					00	00.1						0,10	0.40							0.17				0.18					
Verify		0.32					050	0.0						0.20	00.0	-	-			_		20.02	1			-0.46					
Psi Blast		7.5e-07					10.05	CO-21:						38-07								0.0015				1.1e-28		,	<del></del>		
END		947				-	619	710						958	2							336				347	_		-		
STAR T AA		688					542	1						889	<u>}</u>				•			199	-			267					
CHAI N ID		4					<b> </b>	:						   	1					_		4				<u>Д</u> ,					
PDB ID		2up1					3sxl							3sxl								le7f				lahd			-		
SEQ ID NO:		1728					1728		_	_				1728								1730			ᅥ	1733					

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PDB annotation		PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION				
Coumpound	5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) 1LFB 3	GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA- BINDING 1PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) 1PRA 4	GENE REGULATING PROTEIN REPRESSOR (AMINO- TERMINAL DOMAIN) (R1-69) 1R69 4	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT
SEQFOL D score		·				,			
PMF score		0.07	0.46	0.92	1.00	0.99	0.51	0.78	0.19
Verify score		-0.02	-0.12	-0.04	0.38	0.61	0.08	0.15	0.09
Psi Blast		6.4e-24	6.4e-24	3.2e-23	9.6e-22	6e-24	0.00015	0.0003	1.6e-26
END		343	340	341	339	336	205	205	347
STAR T AA		271	270	266	267	271	173	173	273
CHAI N ID		A	A	<	Д		÷		
PDB ID		1672	168i	141	lţjı	11fb	lpra	1r69	1san
SEQ NO:		1733	1733	1733	1733	1733	1733	1733	1733

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	TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION BEGIN A TION	NOTION TO THE PROPERTY.	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)			PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN PROTEIN/DNA	TRANSCRIPTION/DIA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PR()TEINS, DEVELOPMENT; 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEINMA) DNA BRIDBIG
WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C398,DEL 1-6) ISAN 4 (NMR, 20 STRITCTI IBES) ISAN 4	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D: DNA CHAIN: E:	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'-	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D. E. F
	0.17	0.29	0.04		0.18	0.07	0.28	0.92
	-0.16	-0.59	-0.27		-0.46	-0.02	-0.31	-0.04
	0.0003	0.0003	3.2e-26		1.6e-28	1.6e-24	8e-24	1.6e-23
	205	205	341		347	343	340	341
	173	173	271		267	271	271	266
			A		Ω,	٠ ۲	∢	A
	1zug	2cro	9ant		lahd	1672	1 <b>b</b> 8i	161
	1733	1733	1733		1734	1734	1734	1734
	WITH CYS 39 ISAN 3  REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRICTT BES) ISAN 4	WITH CYS 39 1SAN 3   REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 5   STRUCTURES) 1SAN 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PDB annotation	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION													TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD;
Coumpound		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) ILFB 3	GENE REGULATING PROTEIN PEPPESSOR PROTEIN FROM	BACTERIOPHAGE 434 (DNA- BINDING 1PRA 3 DOMAIN,	RESIDUES 1-69) (NMR, 20 STRUCTURES) 1PRA 4	GENE REGULATING PROTEIN	TERMINAL DOMAIN) (RI-69)	INUS 4	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 ISAN 3	RESIDUES 1-6 DELETED	(C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRIPTIBES) 1SAN 5	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C,
SEQFOL D score																	
PMF score		1.00	66.0	0.51			0.78			0.19					0.17	0.29	0.04
Verify score		0.38	0.61	80.0			0.15			0:00					-0.16	-0.59	-0.27
Psi Blast		8e-22	6e-24	0.00015			0.0003			6.4e-26					0.0003	0.0003	8e-26
END		339	336	205			205			347					205	205	341
STAR T AA		267	271	173			173			273					173	173	271
CHAI N ID		В															A
PDB ID		141	11fb	1pra			1169			Isan					1zug	2cro	9ant
SEQ ED		1734	1734	1734			1734			1734					1734	1734	1734

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HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)		MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY,	CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY,	CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY,	CALCIUM BINDING	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC-	DOMAIN, RESIDUES 1 - 75; CERIUM-	LOADED, CALCIUM-BINDING	rnotein	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION,	TROPONIN C, CARDIAC MUSCLE 2	HVDROI ASE CAI CRIETERI.	HYDROLASE CALCINEOMIN;	IMMUNOSUPPIXESSION	MUSCLE CONTRACTION MUSCLE	CONTRACTION, CALCIUM-	ACTIVATED, TROPONIN, E-F HAND	2 CALCIUM-BINDING PROTEIN	CALCIUM-BINIDING PROTEIN	SNTNC; CALCIUM-BINDING,	REGULATION, TROPONIN C,	SKELETAL MUSCLE, 2	MISCIE PROTEIN ME: MISCIE
D, E, F;	TDODOMINI O CITATAL MERI	INOPONIN C; CHAIN; NULL;	TP ODOMINI C. CITA BIL 3H H.	IKUPONIN C; CHAIN: NULL;		IROPONIN C; CHAIN: NULL;		CALMODULIN; CHAIN: NULL;		•	CAN TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O	CAKDIAC N-TROPONIN C; CHAIN: NULL;		SERINE/THREONINE	PHOSPHATASE 2B; CHAIN: A.	B;	TROPONIN C; CHAIN: A, B;				N-TROPONIN C; CHAIN: NULL;				MYOSIN; CHAIN: A. B. C. D. E.
			82 97	16:70				75.36			61 26	01.30					<del>*** .</del> .								57.30
	900	2			0.0	0.70								-0.01											
	-0.11				0.17	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \								-				1.77			-				
	4.8e-30		1.4e-38		1 10.39	00.54:1	1 1 200	1.16-29			6 40-73	7-2-27		3.2e-20			3.2e-26			20, 27	/7-20				4.8e-34
	101		170	2	160	}	101	<u> </u>			109			101		,	9			†	-				170
	1		23		25	}	30	3			22	}				1	07			200	2	-			33
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	laj4		laj4	1	laid		1948				lap4					+				Thin	-		_		1br1 1
	1738		1738		1738		1738				1738			1738		1730	200			1738	<del></del>	_			1738
		1ai4 1 101 4.8e-30 -0.11 0.06 Thompstring contractions	1aj4     1     101     4.8e-30     -0.11     0.06     TROPONIN C; CHAIN; NULL;	laj4     l     101     4.8e-30     -0.11     0.06     TROPONIN C; CHAIN; NULL;       laj4     23     170     1.4e-38     62.07     TROPOSITIO GIVER 1.2	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN: NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN: NULL;	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN; NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN; NULL;           laj4         25         160         1.45.30         0.17         0.20	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN: NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN: NULL;           laj4         25         169         1.4e-38         0.17         0.70         TROPONIN C; CHAIN: NULL;	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN: NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN: NULL;           laj4         25         169         1.4e-38         0.17         0.70         TROPONIN C; CHAIN: NULL;           lak8         30         104         1.1c.20         Troponin C; CHAIN: NULL;	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN; NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN; NULL;           laj4         25         169         1.4e-38         0.17         0.70         TROPONIN C; CHAIN; NULL;           lak8         30         104         1.1e-29         75.36         CALMODULIN; CHAIN; NULL;	1aj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN; NULL;         1aj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN; NULL;         1aj4       25       169       1.4e-38       0.17       0.70       TROPONIN C; CHAIN; NULL;         1ak8       30       104       1.1e-29       75.36       CALMODULIN; CHAIN; NULL;	laj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN: NULL;         laj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN: NULL;         laj4       25       169       1.4e-38       0.17       0.70       TROPONIN C; CHAIN: NULL;         lak8       30       104       1.1e-29       75.36       CALMODULIN; CHAIN: NULL;	1aj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN; NULL;         1aj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN; NULL;         1aj4       25       169       1.4e-38       0.17       0.70       TROPONIN C; CHAIN; NULL;         1ak8       30       104       1.1e-29       75.36       CALMODULIN; CHAIN; NULL;         1ab4       72       100       6.4e-23       100       6.4e-23	laj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN; NULL;           laj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN; NULL;           laj4         25         169         1.4e-38         0.17         0.70         TROPONIN C; CHAIN; NULL;           lak8         30         104         1.1e-29         75.36         CALMODULIN; CHAIN; NULL;           lap4         22         109         6.4e-23         61.36         CARDIAC N-TROPONIN C;	1aj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN: NULL;         1aj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN: NULL;         1aj4       25       169       1.4e-38       0.17       0.70       TROPONIN C; CHAIN: NULL;         1ak8       30       104       1.1e-29       75.36       CALMODULIN; CHAIN: NULL;         1ap4       22       109       6.4e-23       61.36       CARDIAC N-TROPONIN C;	1aj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN; NULL;         1aj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN; NULL;         1aj4       25       169       1.4e-38       0.17       0.70       TROPONIN C; CHAIN; NULL;         1ak8       30       104       1.1e-29       75.36       CALMODULIN; CHAIN; NULL;         1ap4       22       109       6.4e-23       61.36       CARDIAC N-TROPONIN C;         1aui       B       1       101       3.2e-20       0.08       -0.01       SERINE/THREONINE	Iaj4       1       101       4.8e-30       -0.11       0.06       TROPONIN C; CHAIN; NULL;         Iaj4       23       170       1.4e-38       82.97       TROPONIN C; CHAIN; NULL;         Iak8       30       1.04       1.1e-29       75.36       CALMODULIN; CHAIN; NULL;         Iap4       22       109       6.4e-23       61.36       CARDIAC N-TROPONIN C; CHAIN; NULL;         Iaui       B       1       101       3.2e-20       0.08       -0.01       PHOSPHATASE 2B; CHAIN; A. 1	Iaj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN; NULL;           Iaj4         23         170         1.4e-38         0.17         0.70         TROPONIN C; CHAIN; NULL;           Iak8         30         104         1.1e-29         75.36         CALMODULIN; CHAIN; NULL;           Iaui         B         1         101         3.2e-20         0.08         -0.01         SERINE/ITREONINE           Iaui         B         1         101         3.2e-20         0.08         -0.01         SERINE/ITREONINE           Iaui         B         B;         B;         B;         B;         B;	Iaj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN; NULL;           Iaj4         23         170         1.4e-38         82.97         TROPONIN C; CHAIN; NULL;           Iaj4         25         169         1.4e-38         0.17         0.70         TROPONIN C; CHAIN; NULL;           Iap4         25         169         1.1e-29         75.36         CALMODULIN; CHAIN; NULL;           Iap4         22         109         6.4e-23         61.36         CARDIAC N-TROPONIN C;           Iaui         B         1         101         3.2e-20         0.08         -0.01           Iav5         A         26         106         3.2e-26         70.90         TROPONIN C; CHAIN; A, B;	Iaj4         1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN: NULL;           Iaj4         23         170         1.4e-38         0.17         0.70         TROPONIN C; CHAIN: NULL;           Iak8         30         104         1.1e-29         75.36         CALMODULIN; CHAIN: NULL;           Iawi         B         1         101         3.2e-20         0.08         -0.01         SERINETHREONINE         1           Iavs         A         26         106         3.2e-26         0.08         70.90         TROPONIN C; CHAIN: A, B;         1	Iaj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN; NULL;   1aj4   23   170   1.4e-38   0.17   0.70   TROPONIN C; CHAIN; NULL;   1aj4   22   169   1.4e-38   0.17   0.70   TROPONIN C; CHAIN; NULL;   1ap4   22   109   6.4e-23   61.36   CARDIAC N-TROPONIN C; CHAIN; NULL;   1au1   B   1   101   3.2e-20   0.08   -0.01   B;   B;   B;   B;   B;   B;   B;   B	Iaj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN: NULL;   1aj4   23   170   1.4e-38   0.17   0.70   TROPONIN C; CHAIN: NULL;   1aj4   22   109   6.4e-23   61.36   CALMODULIN; CHAIN: NULL;   1awi	Laj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN; NULL;   14e-38   0.17   0.70   TROPONIN C; CHAIN; NULL;   18p4   22   109   6.4e-23   0.18   0.01   0.01   0.00   TROPONIN C; CHAIN; NULL;   1ap4   22   109   6.4e-23   0.08   -0.01   0.01   0.00   TROPONIN C; CHAIN; NULL;   1au   101   3.2e-20   0.08   -0.01   0.00   TROPONIN C; CHAIN; A, B;   1   101   3.2e-26   0.08   -0.01   B;   1   101   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   3.2e-26   0.08   -0.01   TROPONIN C; CHAIN; A, B;   1   104   105   4e-27   11.63   N-TROPONIN C; CHAIN; NULL;   104   105   4e-27   11.63   N-TROPONIN C; CHAIN; NULL;   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105   105	Iaj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN: NULL;   1aj4   23   170   1.4e-38   0.17   0.70   TROPONIN C; CHAIN: NULL;   1aj4   25   169   1.4e-38   0.17   0.70   TROPONIN C; CHAIN: NULL;   1ap4   22   109   6.4e-23   61.36   CARDIAC N-TROPONIN C; CHAIN: NULL;   1aw   A   26   106   3.2e-26   0.08   -0.01   B.   B.   CARDIAC N-TROPONIN C; CHAIN: A, B;   1bb4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   20   20   20   20   20   20   20   2	Haj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN: NULL;   14   17   1.4e-38   0.17   0.70   TROPONIN C; CHAIN: NULL;   18   1   101   3.2e-20   0.08   -0.01   1.63   TROPONIN C; CHAIN: NULL;   18   1   101   3.2e-20   0.08   -0.01   1.63   TROPONIN C; CHAIN: NULL;   18   1   101   3.2e-20   0.08   -0.01   18   19   106   3.2e-20   0.08   -0.01   18   19   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   3.2e-20   106   106   3.2e-20   106   106   3.2e-20   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106   106	1aj4   1   101   4.8e-30   -0.11   0.06   TROPONIN C; CHAIN: NULL;   1aj4   23   170   1.4e-38   0.17   0.70   TROPONIN C; CHAIN: NULL;   1ap4   22   109   6.4e-23   61.36   CALMODULIN; CHAIN: NULL;   1av8   A   26   106   3.2e-26   0.08   -0.01   SERINE/THREONINE   B   B;   CHAIN: NULL;   1bl4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   1bl4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   1bl4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   1bl4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   1bl4   20   109   8e-27   71.63   N-TROPONIN C; CHAIN: NULL;   20   20   20   20   20   20   20   2

PDB annotation		PROTEIN	CALCIUM BINDING CALCIUM BINDING																											<u> </u>	CALMODULIN APO 1R2C-DOMAIN; 1CMF 9	STRUCTURAL PROTEIN HELIX-
Coumpound		F, G, H;	CALCTUM-BINDING PROTEIN; CHAIN: NULL;	CALCITIM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN (VEKTEBKATE)	ICLL 3	CALCIUM-BINDING PROTEIN	Characteristics   Characteristics   1 CLL 3	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	ICLL 3	CALMODULIN (VERTEBRATE);	1CMF 6 CHAIN: NULL; 1CMF 7	CARDIAC TROPONIN C;
SEOFOL	D score		50.72							85.63	•																89.87	}		68.52		
PMF	score			0.80	3000											0.92						0.40			0.81							0.28
Verify	score			0.01	10.0											0.08						- 60'0-			-0.02							0.00
Dei Riact	T St Diagr		3.2e-11	00.35	06-30					1.4e-47						1.4e-47	:					3.2e-35			9.6e-53		0 60-53	2220.		7.5e-23		4.8e-29
END	¥¥		103	100	102					158						169	}					102			169		170	?		104		101
CTAD	TAA		2	-	-4					33						33	}					-			33		33	3		33		-
CHAI	N IB			\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	∢					4						d	1															A
aua	<u>a</u>		1bu3	-	lcam					1cdm						lodin						Icli			Icll		101	13		lcmf		1dtl
Caro	ZA Š	120	1738	0 (1)	1/38					1738	2					1738	0071					1738			1738		1770	1/30		1738		1738

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TURN-HELIX	STRUCTURAL PROTEIN HELIX-	METAL TRANSPORT CALMODULIN,	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION DISCEPTED	THE THEORY TO A PROPERTY						,		CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN CALCIUM.	REGULATED 3 MUSCUE	CONTRACTION	CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	CONTRACTION, CALCIUM.	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM.	REGULATED 3 MUSCLE	CALCHIA PECIT ATTENDED	CONTRACTION MISCIE
CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	CALCIUM BINDING	PARVALBUMIN (PIKE, PI 5.0.	ALPHA COMPONENT)	COMPLEXED WITH IPVAA I	TWO CALCIUM IONS	(SYNCHROTRON X-RAY DIFFRACTION) IPVAA	CALCIUM-BINDING PROTEIN	ALPHA-PARVALBUMIN 1RTP 3	TROPONIN C; CHAIN: NULL;								TROPONIN C; CHAIN: NULL;							TROPONIN C. CHAIN: NIII I .	inci citin c, citain; incie,
				55.26						55.44	,											-						, 
	0.72	0.80	0.89									0.35											-				96.0	
	0.26	-0.11	0.03									-0.10					-											
	9.6e-36	3.2e-34	4.8e-51	1.6e-15						3.2e-16	1								;	1.06-41	•				-		1.6e-41	
,	169	101	169	104						104		101								5							169	
	10	-	31	_						7	-	_		-					1,00	±7		·					33	
_	₹	А	¥	A				-		_																		
1241	ını .	lexr	lexr	Ipva						Irtp	1406	1							1406							•	Itcf	
1739	1/30	1/38	1738	1738						1738	1730	000							1738	2							1738	
	14tl A 3: CHAIN: A;	1dtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C;           CHAIN: A:         CHAIN: A:         CHAIN: A:         CHAIN: A:	1dtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C; CHAIN: A;           1exr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;	Idtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;	ldtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING	Idtl         A         31         169         9.6e-36         0.26         0.72         CHADIAC TROPONIN C; CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           PARVALBUMIN (PIKE, PI 5.0.         PARVALBUMIN (PIKE, PI 5.0.	Idtl         A         31         169         9.6e-36         0.26         0.72         CHADIAC TROPONIN C; CHAIN: A;           lext         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lext         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           PARVALBUMIN (PIKE, PI 5.0,         ALPHA COMPONENT)	Idtl         A         31         169         9.6e-36         0.26         0.72         CHADIAC TROPONIN C; CHAIN: A;           lext         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lext         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           PARVALBUMIN (PIKE, PI 5.0, ALPHA COMPONENT)         ALPHA COMPONENT)         COMPLEXED WITH IPVAA I	Idtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C; CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           PARVALBUMIN (PIKE, PI 5.0, ALPHA COMPONENT)         ALPHA COMPONENT)         COMPLEXED WITH IPVAA I           TWO CALCIUM IONS         TWO CALCIUM IONS	1dtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C; CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           PARVALBUMIN (PKE, PI 5.0, ALPHA COMPONENT)         COMPLEXED WITH IPVAA I         TWO CALCIUM IONS           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS         (SYNCHROTRON Y-RAY           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS           COMPLEXED WITH IPVAA I         TWO CALCIUM IONS	Idtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C; CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALCIUM BINDING           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           lrpa         A         7         104         1.6e-15         ALPHA COMPONENT)           COMPLEXED WITH IPVAA I         1         1         1         1           Irtp         1         7         104         3.2e-16         55.44         CALCIUM-BINDING PROTEIN	1dtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           1exr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           1exr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           1pva         A         7         104         1.6e-15         S5.26         CALCIUM BINDING           1rpva         A         7         104         1.6e-15         S5.26         CALCIUM BINDING           1rpva         A         7         104         1.6e-15         S5.26         CALCIUM BINDING           1rpva         A         7         104         1.6e-15         S5.26         CALCIUM BINDING           1rpva         A         7         104         1.6e-15         S5.26         CALCIUM BINDING           1rpva         7         104         3.2e-16         S5.44         CALCIUM-BINDING PROTEIN           1rpva         7         104         3.2e-16         S5.44         CALCIUM-BINDING PROTEIN	Idtl         A         31         169         9.6e-36         0.26         0.72         CARDIAC TROPONIN C; CHAIN: A; CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALCIUM BINDING PARVALBUMIN (PIKE, PI 5.0, ALPHA COMPONENT)           lpva         A         7         104         1.6e-15         ALPHA COMPONENT)         COMPLEXED WITH IPVAA I TWO CALCIUM IONS           lrtp         I         7         104         3.2e-16         55.44         CALCIUM-BINDING PROTEIN ALPHA-PARVALBUMIN IRTP 3           ltcf         1         101         1.1e-30         -0.10         0.35         TROPONIN C; CHAIN: NULL;	1dtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           1exr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           1exr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           1pva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           1pva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           1pva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           1pva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           1pva         A         7         104         1.6e-15         1.70         1.70           1pva         A         7         104         3.2e-16         55.44         CALCIUM-BINDING PROTEIN           1pva         3         10         3.2e-16         25.44         CALCIUM-BINDING CHAIN: NULL;           1pva         1         101         1.1e-30         -0.10         0.35         TROPONIN C; CHAIN: N	1dt  A   31   169   9.6e-36   0.26   0.72   CARDIAC TROPONIN C; CARDIAC TROPONIN C; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CALCHUM BINDING PROPERTY COMPLEXED WITH IPVAA I Intp   1	ldtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           lrtp         I         1         104         3.2e-16         25.4         COMPLEXED WITH IPVAA I           lrtp         I         104         3.2e-16         55.4         CALCIUM-BINDING PROTEIN           licf         I         101         1.1e-30         -0.10         0.35         TROPOMIN C; CHAIN: NULL;	ldtl         A         31         169         9.6e-36         0.26         0.72         CHAIN: A;           lexr         A         1         101         3.2e-34         -0.11         0.80         CALMODULIN; CHAIN: A;           lexr         A         31         169         4.8e-51         0.03         0.89         CALMODULIN; CHAIN: A;           lpva         A         7         104         1.6e-15         0.03         0.89         CALCIUM BINDING           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           lpva         A         7         104         1.6e-15         55.26         CALCIUM BINDING           lpva         A         7         104         3.2e-16         55.44         CALCIUM BINDING PROTEIN           ltcf         1         101         1.1e-30         -0.10         0.35         TROPONIN C; CHAIN: NULL;	ldtl         A         31         169         9.6e-36         0.26         0.72         CAADIAC TROPONIN C; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; 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CHAIN: A; CARDIAC TROPONIN C; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: CHAIN: A; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN	14th   A   31   169   9.6e-36   0.26   0.72   CARDIAC TROPONIN C; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: CHAIN: A; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAI	16th   A   31   169   9.6e-36   0.26   0.72   CHAINI, A; 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CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALMODULIN; CHAIN: A; CALCIUM BINDING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING PROPRING P	14th   A   31   169   9.6e-36   0.26   0.72   CHAINI: A;     1ext   A   1   101   3.2e-34   -0.11   0.80   CALMODULIN; CHAINI: A;     1ext   A   31   169   4.8e-51   0.03   0.89   CALMODULIN; CHAINI: A;     1pxa   A   7   104   1.6e-15   55.26   CALCIUM BINDING PROPENT)     1rt   1   7   104   3.2e-16   55.44   COMPLEXED WITH IPVAA I I I I I I I I I I I I I I I I I I	1dt  A   31   169   9.6e-36   0.26   0.72   CGADIAC TROPONIN C; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CHAIN: A; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; CALMODULN; 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CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; 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PDB annotation	CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14				Ŋ		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2
Coumpound		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score			84.53			96.98		62.97			90.09
PMF score		0.41		0.94	0.30	,	1.00			0.36	
Verify score		-0.26		0.17	-0.20		0.13			-0.06	
Psi Blast		9.6e-34	1.6e-38	1.6e-38	3.2e-32	4.8e-42	4.8e-42	8e-22	3.2e-26	9.6e-36	1.1e-51
END		101	169	169	101	691	169	103	106	104	170
STAR T AA			24	33	1-1	20	33	36	31	-	31
CHAI								4		4	¥
PDB		ltnx	Itnx	Itmx	1top	1top	Itop	ltrc	1trf	1vrk	1vrk
SEQ	.; ON	1738	1738	1738	1738	1738	1738	1738	1738	1738	1738

	<del></del>											
PDE annotation	COMPLEX(CALCIUM-BINDING	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING	PROTEIN/PEPTIDE) MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN,	MUSCLE PROTEIN MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN,	MUSCLE PROTITING CALCIUM-BINI DING PROTEIN CTING; CARDIAC, MUSCLE, REGULATORY, CALCILIA BINI DING PROTEIN CTING	CAECIOM-BINLING PROTEIN			TRANSFERASE ATP: AMP- PHOSPHOTRANSFERASE,	IKANSFEKASE		
Coumpound		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULL;	CALCIUM BINDING CALCIUM- BINDING PARVALBUMIN (\$P*1=4.25) 4CPV 3	THE LATER AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A STREET AND A ST	IKANSFEKASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 1117.7.3	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KNASE (F. C.) 74.33.34 pt. 4	- XXXXX (C	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP LUKZ 3
SEQFOL D score			64.97	54.16	52.43	51.70						
PMF score		0.95					20.0	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	0.13	0.16		0.07
Verify score		0.15					20.0		-0.17	-0.25		-0.05
Psi Blast		1.1e-51	7.5e-26	1.1e-25	8e-10	1.3e-11	9000		0.0001	0.0075		0.0006
END		169	170	171	104	103	463	}	587	495		463
STAR T AA			33	33	31	9	362		362	362		362
CHAI N ID		Ą	В	ပ					Ą			
PDB ID		lvrk	1wdc	Iwdc	3ctn	4cpv	1ukz			3adk	1	Inkz
SEQ ID NO:		1738	1738	1738	1738	1738	1745			1745	•	

PDB annotation		TRANSFERASE ATP:AMP- PHOSPHOTRANSFERASE, TRANSFERASE		TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK	MOTIF, ZINC BINDING, A-LINKED Z AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-	PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN SIGNALING PROTEIN 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN SIGNALING PROTEIN 3- PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN ADAPTOR PROTEIN SIGNALING PROTEIN SIGNALING PROTEIN FACTOR AND PH DOMAIN
Coumpound			TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	BRUTON'S TYROSINE KINASE; CHAIN: A, B;		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-	CHAIN: A;	CHAIN: A; DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	CHAIN: A;  DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;  GRP1; CHAIN: A;
SEOFOL	D score								
PMF	score	0.13	0.16	0.04		0.83		0.99	0.99
Verify	score	-0.17	-0.25	-0.50		0.14	<del>-</del>	0.25	0.25
Psi Blast		0.0001	0.0075	90-99		3e-15		3e-16	3e-16 7.5e-12
END	¥¥	587	495	142		142		142	142
STAR	TAA	362	362	53		55		48	48
CHAI	OI N	Α		Ą		A		Y	A A
pnR	A	1zak	3adk	16tk		1fao		1fb8	1fb8 Ifgy
CEO	A S	1746	1746	1749		1749		1749	1749

PD)3 annotation		HYDROLASE ITYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME		OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II)	COMPLEX, CA'TECHOL	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN BECTY	COMPLEX, CATECHOL	HYDROLASE PHOSPHOLIPASE C;	GANGRENE DETERMINANT, C2	DOMAIN, CA 2 AND MEMBRANE	DINDING, HYDROLASE	COMPLEX (HYDROLASE/COFACTOR)	IKIACYLGLYCEROL LIPASE; COMPLEX	(HYDROLASE/COFACTOR), LIPID DEGRADATION	OXIDOREDUCTASE 15LOX;	OXIDOREDUCITASE, 15LO DEPOT2	OXIDOREDUCTASE, 151.0 DEPOT?	DIOXYGENASE L-1; DIOXYGENASE,	METALLOPROTEIN FATTY ACIDS	DIOXYGENASE L-1; DIOXYGENASE,	METALLOPROTEIN FATTY ACIDS	1011011 4 111111 1 111110
Coumpound		METALLO BETA-LACTAMASE II; CHAIN: A, B;		LIPOXYGENASE-3; CHAIN: NULL;	TYPO CHANGE CONTRACTOR	LIFOX YGENASE-3; CHAIN: NULL;		ALPHA-TOXIN; CHAIN: NULL;			TOTA CITY OF TAXON AND A LOTT	HYDROLASE; CHAIN: A, C;	COLIFASE, CHAIN: B, D		15-LIPOXYGENASE; CHAIN:	15-1.IPOXYGENASE: CHAIN:	NULL;	LIPOXYGENASE-1; CHAIN:		LIPOXYGENASE-1; CHAIN:		
SEQFOL	D score	-		253.58												482.93		231.83				
PMF	score	-0.05		i	90	99.		0.04			27.0	7			1.00					1.00		
Verify	score	0.18			0.36	27.0		-0.01			0.46	2			0.41					0.18		
Psi Blast		1.6e-14		0			1	1.6e-20			0.0045				0	0		0		0		
END	AA	170		711	711	4		111			66				711	711	1	111	7	===		
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PDB	OT .	2bc2	]	16%	1byt			ıcaı			1eth				llox	110x	1	 agk r		1 ygc		1
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PDB annotation	C. R. C. C. C.	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G-PROTEIN, SIGNALING PROTEIN	CELL CYCLE CDC42; KHO GDI 1; GTP-BINDING PROTEIN, CDC42, KHOGDI, X-RAY	CELL CYCLE CDC42; KHO GD1 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY			PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
Coumpound		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: B;
SEQFOL	D score					70.63		
PMF	score	1.00	1.00	1.00	1.00		0.90	0.98
Verify	score	0.50	0.33	0.48	0.48		-0.12	-0.15
Psi Blast		4.5e-66	9.6e-70	6e-76	1.6e-78	6,4e-36	6.4e-36	3e-31
END	¥Ψ	162	177	162	180	98	58	81
STAR	T AA	24	24	5	5	. 19	20	21
CHAI	NID	ம	ш	g	В	ď	<u>р</u> .	A
PDB	E .	1cc0	1000	1doa	1doa	lahd	lahd	1672
SEO	e ë	1753	1753	1753	1753	1757	1757	1757

|           | 7                                                     |                                                                                   | 1                                                                                                                                         |                                                                                                                                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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|           | HOMEOBOX PROTEIN HOX-B1;<br>CHAIN: A; PBX1; CHAIN: B; | UNA CHAIN: D' DNA CHAIN: E;                                                       | HOMEOBOX PROTEIN HOX-B1;                                                                                                                  | CHAIN: A; PBX1; CHAIN: B;                                                                                                                                                                   | LINA CHAIN: D; DNA CHAIN: E;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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CHAIN: A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | HOMEOROX PROTEIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | EXTRADENTICI F. CHAIN: B.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
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DIA CHAIN: B.     1572   A   9   81   3e-31   64.24   HOMEOBOX PROTEIN HOX-B1;     1581   A   20   77   6.4e-31   6.434   ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: B;     1581   A   20   77   6.4e-31   6.434   ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: B;     1581   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: B;     1582   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: A;     1683   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: A;     1694   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: A;     1695   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: A;     1696   A   2   78   6.4e-31   -0.14   0.82   CHAIN: CHAIN: B;     1697   DIVA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (AMR, 20 STRUCTURES) IFTZ 3     1694   C   1   79   3e-31   -0.70   0.23   DIVA-BINDING PROTEIN OCT-1 | 1572   A   24   81   3.2e-28   0.19   0.99   CHARIN: B; ENTI; CHARIN: B; DNA CHARIN: D.; DNA CHARIN: B; DNA CHARIN: B; DNA CHARIN: B; DNA CHARIN: B; DNA CHARIN: B; DNA CHARIN: B; DNA CHARIN: B; 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PDB annotation			COMPLEX (DNA-BINDING PROTEIN/DNA) FID; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)	LIPOCALIN LIPOCALIN, OLFACTION	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN	ALLERGEN LIPOCALIN, BETA BARREL		<i>i</i> .	ODORANT-BINDING PROTEIN OBP OLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2
Coumpound		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 5	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ODORANT BINDING PROTEIN; CHAIN: A, B;	HUMAN NEUTROPHIL GELATINASE; CHAIN: A, B;	ALLERGEN EQU C 1; CHAIN: A;	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) 1MUP 3 THIAZOLINE 1MUP 4	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	ODORANT-BINDING PROTEIN; CHAIN: A, B;
SEQFOL	D score			68.97					64.35	
PMF	score	0.98	1.00	,	0.86	1.00	0.95	1.00		-0.02
Verify	score	-0.17	-0.13		0.63	99.0	0.90	0.78		0.19
Psi Blast		1.6e-33	1.6e-33	1.6e-33	3e-35	4.5e-47	1.4e-38	6e-37	6e-37	9e-36
END	Ψ¥	85	79	79	169	169	169	168	168	172
STAR	T AA	26	24	24	38	20	30	25	25	30
CHAI	NID		4	4	A	A	4			4
PDB	A	Isan	9ant	9ant	la3y	1dfv	lew3	Imup	Imup	10bp
SEO	e ë	1757	1757	1757	1758	1758	1758	1758	1758	1758

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PROTEIN	NEUTROPHIL LIPOCALIN, SIGNAL	FROIEIN, GLYCOPROIEIN	LIPID BINDING PROTEIN A2U. GLOBULIN, LIPID BINDING	LIPID BINDING PROTEIN AZU. GLOBULIN, LIPID BINDING	PROTEIN LIPID BINDING PROTEIN A2U. GLOBULIN, LIPID BINDING PROTEIN	TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, i'AB HEAVY CHAIN COMPLEX (VIRAL	CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHARL OF ASSISTED	CELL RECEPTOR, VIRAL PEPTIDE, 2	PEPTIDE/RECEPTOR	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTTE PROCES ANAMA
	NEUTROPHIL GELATINASE; CHAIN: A;	RETINOL TRANSPORT RETINOL BINDING PROTEIN 1RRP 3	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIOF: CHAIN: C: T	CELL RECEPTOR ALPHA; CHAIN: D: T CELL RECEPTOR	BETA; CHAIN: E;	FAB B7-15A2; CHAIN: L, H;
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	1758	1758	1758	1758	1758	7.7.0	66/1	1750			+	
		1qqs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE;           CHAIN: A;         CHAIN: A;	1qqs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE;           1rbp         26         168         1e-35         0.14         -0.09         RETINOL TRANSPORT           1rbp         1rbp         1e-35         0.14         -0.09         RETINOL BINDING PROTEIN	Iqqs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE;           Irbp         26         168         1e-35         0.14         -0.09         RETINOL TRANSPORT           RETINOL BINDING PROTEIN         1RBP 3         1RBP 3           2a2u         A         25         169         1.3e-36         0.69         0.99         ALPHA-2U-GLOBULIN; CHAIN:           A, B, C, D         A, B, C, D	1qqs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE; CHAIN: A;           1rbp         26         168         1e-35         0.14         -0.09         RETINOL BRIDING PROTEIN IRBP 3           2a2u         A         25         169         1.3e-36         0.69         0.99         ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D           2a2u         A         25         169         1.5e-37         0.91         1.00         ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	1qqs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE; CHAIN: A;           1rbp         26         168         1e-35         0.14         -0.09         RETINOL BRIDING PROTEIN IRBP 3           2a2u         A         25         169         1.3e-36         0.69         0.99         ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D           2a2u         A         25         169         1.5e-37         0.91         1.00         ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D           2a2u         A         25         169         1.5e-37         0.91         1.00         ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	1qgs         A         17         169         4.5e-40         0.83         1.00         NEUTROPHIL GELATINASE;           1rbp         26         168         1e-35         0.14         -0.09         RETINOL BINDING PROTEIN           2a2u         A         25         169         1.3e-36         0.69         0.99         ALPHA-2U-GLOBULIN; CHAIN:           2a2u         A         25         169         1.5e-37         0.91         1.00         ALPHA-2U-GLOBULIN; CHAIN:           2a2u         A         25         169         1.5e-37         78.30         ALPHA-2U-GLOBULIN; CHAIN:	19qs   A   17   169   4.5e-40   0.83   1.00   NEUTROPHIL GELATINASE; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: BINDING PROTEIN IRBP 3   1.3e-36   0.69   0.99   ALPHA-2U-GLOBULIN; CHAIN: A   2.5   169   1.5e-37   0.91   1.00   ALPHA-2U-GLOBULIN; CHAIN: A   B. C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A, B, C, D   A,	19qs	19qs   A   17   169   4.5e.40   0.83   1.00   NEUTROPHIL GELATINASE; CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: A;   CHAIN: Binding PROTEIN IRBP 3   1.3e.36   0.69   0.99   ALPHA-2U-GLOBULIN; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAI	19qs   A   17   169   4.5e-40   0.83   1.00   CHAIN: A; 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CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: A; CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN:

PDB annotation		PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN	COMPLEX (MHC/VIRAL	HEAVY CHAIN; COMPLEX	(MHC/VIRAL PEPTIDE/RECEPTOR)		COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) H].A A2	HEAVY CHAIN: COMPLEX	(MHC/VIRAL PEPTIDE/RECEPTOR)	,						CATALYTIC ANTIBODY	CATALYTIC ANTIBODY 6D9	CATALYTIC ANTIBODY, ESTER	2 IMMUNOGLOBULIN								IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C
Coumpound			HLA-A 0201; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B; TAX PEPTIDE: CHAIN: C: T	CELL RECEPTOR ALPHA;	CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	HLA-A 0201; CHAIN: A; BETA-2	TAY DEPTITE: CHANGE. C. T.	CELL RECEPTOR ALPHA:	CHAIN: D; T CELL RECEPTOR	BETA; CHAIN: E;	IMMUNOGLOBULIN 3D6 FAB	TACAMATOCI ODIH IN EAD	FRAGMENT OF HUMANIZED	ANTIBODY 4D5, VERSION 4	IMMUNOGLOBULIN 6D9:	CHAIN: L, H;			COMPLEX	(ANTIBODY/BINDING	PROTEIN) IGGI FAB	FRAGMENT COMPLEXED	WITH PROTEIN G (DOMAIN III)	IIGC 5 PROTEIN G,	STREPTOCOCCUS 11GC 15	IGGZA INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D
SEQFOL	D score				,		386.70														. ,						
PMF	score		1.00									1.00	5	S: 		100	2			1.00							66.0
Verify	score		0.74									0.30		0.41		0.47				0.21							0.42
Psi Blast			1.2e-98			-	1.2e-98			,		9.6e-94		6.4e-96		180.05	7.00.1			1.6e-95							8e-99
END	AA		263				263					252		252		250	707			252							263
STAR	TAA		22				22					21		21		21	7			22							21
CHAI	N ID		Э				ш		_			H		В		1.	<b>G</b>			Н	ļ						В
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			_,																				•						
PDB annotation	REGION IMMI NOGI OBIII IN	IMMUNOGLOBULIN IMMINOGLOBULIN	ANTINOROGEODIN,	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)	IMMUNOGLOBULIN, IGG1; FAB	FRAGMENI, CROSS-REACTIVITY, HIVI PROTEASE ENZYME?	INHIBITION, COMPLEX.	(TEATH OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST	BI OOD COAGI II ATION SEDIME	PROTEASE COMPLEY OF EACTOR	2 RECEPTOR ENZYME INHIBITOR	GIA EGE 2 COMMITTED CERTAIN	PROTEASE/CONFLEX (SEKINE)		PLANT PROTEIN TWO	HOMOLOGOUS HEVEIN-LIKE	CITCAD DAMPATTER	JECTEN INDING PROJEIN UDA;	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA:	LECTIN, HEVEIN DOMAIN, UDA.	SUPERANTIGEN, SACCHARIDE	BINDING	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING	SIGNALI ING BLOTTEN BRIDGE	PROTEIN CYTOKINE SIGNALLING	PROTEIN	BLOOD COAGULATION INHIBITION
Coumpound		N1G9 (IGG1=LAMBDA=); CHAIN: L. H:	MONIOCI ONIAI ANIMIDONIA	F11.2.32; CHAIN: L, H, M, N;	HIV-1 PROTEASE PEPTIDE;	(Y) (Z)			BLOOD COAGULATION	FACTOR VIIA: CHAIN: 1. H.	SOLUBLE TISSUE FACTOR:	CHAIN: T. U. D.PHE.PHE.ARG.	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	AGGLUTININ ISOLECTIN VI;	CHAIN: A	AGGLUTININ ISOT ECTIN	VI/AGGLITTININ ISOI ECTIN V.	CHAIN: A;	AGGLUTININ ISOLECTIN	I/AGGLUTININ ISOLECTIN V/	CHAIN: A;		TUMOR NECROSIS FACTOR	KECEPIOK; CHAIN: A, B;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;		FLAVORIDIN; 1FVL 4 CHAIN:
SEQFOL D score									50.68										,				60.34	02.34					
PMF score		00.1	1 00	2											0.01		-0.12			0.00						0.36			0.04
Verify		0.35	0.30												0.40		90.0	-		-0.20			1			-0.34			-0.37
Psi Blast		1.6e-93	3.2e-93						6e-10					1	1.1e-07		3e-08			60-99			36-12	71-22		3e-12			1.26-12
END		249	251						195					0	××		88			88			192			203		101	5
STAR T AA		21	22						64					2	7		12			12			37			57		3.1	1
CHAI N ID		H	H						7						<		¥			⋖			A			٧			
PDB ID		Ingp	2hrp	•	_				ldan		-	-		Palot	ם ו		leis		十	Ten2			lext			lext ,	_	14/1	
SEQ ID NO:		1759	1759						1762				-	1767	70/1		1762		1370	1/07			1762	_		1762		1762	1

												_																		_		•
PDB annotation		GP IIB/IIIA ANTAGONIST 1FVL 9	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I	RECEPTOR, STINFRI; INCF 8 BINDING PROTEIN, CYTOKINE	INCF 19	SIGNALLING PROTEIN TYPE I	RECEPTOR, STNFR1; INCF 8 RINDING PROTEIN CYTOKINE	INCF 19	COMPLEX (BLOOD	COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INFIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL	
Coumpound		NULL IFVL 5	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A, B: INCF 5	£, 117.51	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A,	B; INCF 3	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;	•					!	ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;	
SEQFOL	D score			66.44				55.28			57.36														65.03							
PMF	score		-0.12		0.23														0.15												0.12	
Verify	score		0.17		-0.24													•	0.05												-0.14	
Psi Blast			4.5e-19	1.3e-20	7.5e-09			7.5e-11			3e-14								3e-17						1.5e-18						3e-18	
END	AA		184	203	140			189	}		176					_			121						161						161	
STAR	TAA		15	48	17			55	3		41	-				_			19	<b>`</b>					57	; 					28	
CHAI	NID				A			A			1																					
PDB	B		1klo	Iklo	1ncf			1ncf			1 pfx	 [							1sk7	73851					Iskz	!	,				1skz	
SEO	ΒŞ	5	1762	1762	1762			1762			1762	}							1767	20					1762	1					1762	

<u> </u>				<del>,</del>						~~~~
PDB annotation		STRUCTURE, FACTOR XA INHIBITOR, 2 SIRINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SIRINE PROTEASE INHIBITOR, THIROMBOSIS		TREFOIL FAMII.Y OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL			SIGNAL TRANSDUCTION PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGNIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGAIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
Coumpound			ANTISTASIN; CHAIN: NULL;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BETA-SPECTRIN; IBTN 4 CHAIN: NULL: 1BTN 5	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;
SEQFOL	D score				61.72		97.20			
PMF	score		-0.08	-0.15		0.13		0.70	0.24	0.01
Verify	score		0.13	0.36		0.12		-0.02	0.52	0.04
Psi Blast			4.5e-17	9e-33	0.0014	1.5e-18	6e-29	0.003	0.0043	1.2e-11
END			204	190	191	133	191	234	347	349
STAR	TAA		86	35	06	13	32	200	245	245
CHAI	N ID			Ą	Ą	Ą	٧		٧	¥
PDB	9		1skz	Ivmo	2psp	9wga	9wga	1btn	1byn	Ibyn
SEQ	a ö		1762	1762	1762	1762	1762	1768	1768	1768

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN NF1-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NF1, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGININE FINGER	SIGNALING PROTEIN NF1-333; NEUROFIBROMIN, TYPE I NEUROFIBROMATOSIS, NF1, RAS, GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION, GTP 3 HYDROLYSIS, PATIENT MUTATION, ARGININE FINGER	
	ENDOC	ENDOCY SANDWI DOMAIN	SIGNAI BAM32 PHOSPI TETRAI TRANSI	SIGNAI BAM32 PHOSPI TETRAI TRANSI ADAPT	SIGNAI NEURO GAP, 2 CANCE GTP 3 E	SIGNAI NEURO GAP, 2: CANCE GTP 3 E	
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	NEUROFIBROMIN; CHAIN: A;	NEUROFIBROMIN; CHAIN: A;	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL
SEQFOL D score					108.36		
PMF score		0.54	0.36	0.70		0.99	0.37
Verify score		0.47	0.07	-0.29		0.21	0.33
Psi Blast		4.5e-05	6e-05	96-06	7.5e-68	7.5e-68	4.5e-05
END AA		362	235	239	687	682	239
STAR T AA		247	173	173	400	416	173
CHAI N ID		Ą	⋖	₹	∢	⋖	
PDB ID		1dqv	l fao	1fb8	Infl	Infl	1pls
SEQ ID NO:		1768	1768	1768	1768	1768	1768

								•	
PDH annotation		SIGNAL TRANSDUCTION SON OF SEVENLESS, PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDITCTION	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGITIL ATION CANCER	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGITATION RNP DOMAIN RNA
Coumpound	WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	SOS 1; CHAIN: NÜLL;	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CAIR) 1857 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	P120GAP; CHAIN: NULL;	P120GAP; CHAIN: NULL;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*
SEQFOL D score								183.05	
PMF score		0.39	0.16	0.22	0.05	0.49	1.00		-0.19
Verify score		-0.48	0.17	0.22	-0.14	0.13	0.62		0.05
Psi Blast		0.00015	3e-05	6e-06	0.0043	1.5e-09	1.5e-91	1.5e-91	3.2e-14
END		235	245	349	347	349	712	718	205
STAR T AA		162	184	247	245	246	397	397	126
CHAI N ID			₹						∢
PDB 1D		1pms	Iqqg	lriw	lrsy	lrsy	lwer	lwer	1b7f
SEQ ID NO:		1768	1768	1768	1768	1768	1768	1768	1770

PDBCHAISTARENDPsi BlastVerifyPMFIDN IDT AAAAScorescore	STAR END Psi Blast Verify T AA AA score	END Psi Blast Verify AA score	Psi Blast Verify score	Verify	ļ	PMF score		SEQFOL D score	Coumpound	PDB annotation
									UP*UP*UP*UP*U)- CHAIN: P, Q;	COMPLEX
1b7f A 132 314 1.6e-37 0.24 -0.02	132 314 1.6e-37 0.24	314 1.6e-37 0.24	1.6e-37 0.24	0.24		-0.02			SXL-LETHAL PROTEIN; CHAIN: A. B. RNA (5'-	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA: SPLICING
									R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*U}- CHAIN: P, Q;	REGULATION, RNP DOMAIN, RNA COMPLEX
1b7f A 236 425 4.8e-34 0.63 1.00	236 425 4.8e-34 0.63	425 4.8e-34 0.63	4.8e-34 0.63	0.63		1.00	-		SXL-LETHAL PROTEIN; CHAIN:	RNA-BINDING PROTEIN/RNA TRA
									A, B, RNA (5'-	PRE-MRNA; SPLICING
									R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	KEGULA IION, KNP DOMAIN, KNA COMPLEX
1b7f A 348 431 4.8e-14 0.63 0.51	348 431 4.8e-14 0.63	431 4.8e-14 0.63	4.8e-14 0.63	0.63		0.51	<u> </u>		SXL-LETHAL PROTEIN; CHAIN:	RNA-BINDING PROTEIN/RNA TRA
									A, B; RNA (5'-	PRE-MRNA; SPLICING
								-	R(P*GP*UP*UP*UP*UP* Im*Im*Im*Im*In CIA'NI. D O.	REGULATION, RNP DOMAIN, RNA
751	200 00 7 1	1 7 20 0 000	1 7 20		1	100	_		OF OF OF OF OF OF PRINTE	CENT BECTT ATTONIBNA BOT V(A)
1cvj A 136 320 1.0e-39 0.09 -0.01	136 320 1.56-39 0.09	320 1.0e-39 0.09	1.6e-39 0.09	6.09		10.01			FOLTDENTLATE BINDING	DENE KEGOLATION/KINA FOLI(A)
									FROIDIN I, CHAIN: A, B, C, D, E B B B G H: RNA (S)	PROTEIN-RNA COMPLEX GENE
									R(*AP*AP*AP*AP*AP*	REGULATION/RNA
									AP*AP*AP*A)-3'); CHAIN: M, N,	
							_		O, P, Q, R, S, T;	
lcvj A 238 431 6.4e-34 0.40 0.86	238 431 6.4e-34 0.40	431 6.4e-34 0.40	6.4e-34 0.40	0.40		98.0			POLYDENYLATE BINDING PROTEIN 1: CHAIN: A. B. C. D.	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,
									E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
									R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
									AP*AP*AP*A)-3'); CHAIN: M, N,	
1cvi B 136 300 1.6e-32 0.07 -0.11	136 300 1.6e-32 0.07	300 1.6e-32 0.07	1.6e-32 0.07	0.07		-0.11	-		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
									PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
									E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
									R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
						,	_		AP*AP*AP*A)-3'); CHAIN: M, N,	
									O, P, Q, R, S, T;	
1cvj B 238 409 6.4e-28 0.45 0.89	238 409 6.4e-28 0.45	409 6.4e-28 0.45	6.4e-28 0.45	0.45		68'0			POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
									FROIEIN I; CHAIN: A, B, C, D, F F G H: RNA (5'-	BINDING FROIEIN I, PABE I; KRM, PROTEIN RNA COMPLEX GENE
							4		- 2) 13 177 (17 (2 ( 1 ( 1 ( 1 ( 1 ( 1 ( 1 ( 1 ( 1 ( 1	

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PDI3 annotation	REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROYEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA. BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA-
Coumpound	R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O. P. O. R. S. T.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;
SEQFOL D score									
PMF score		0.76	0.65	0.25	0.68	0.19	0.27	-0.19	-0.03
Verify score		0.33	0.17	0.03	0.78	0.04	0.52	0.03	0.48
Psi Blast		1.6e-12	6.4e-21	1.6e-21	1.6e-12	3.2e-21	4.8e-13	8e-14	3.2e-18
END		435	402	405	435	322	431	218	319
STAR T AA		352	238	238	352	233	346	136	237
CHAI N ID		Ф	[Li	н	Ξ	V	A	۷	A
PDB ID		lcvj	lcvj	lcvj	levj	Z8p1	Z8p1	1492	1d9a
SEQ ID NO:		1770	1770	1770	1770	1770	1770	07.71	1770

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PDB annotation	BINDING DOMAIN	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN
Coumpound		UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HNRNP AI; CHAIN: NULL;	HNRNP A1; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;
SEQFOL D score									
PMF score		0.12	0.07	-0.09	0.95	0.94	-0.19	0.16	0.68
Verify score		0.57	0.30	0.17	0.21	0.83	0.03	0.78	0.91
Psi Blast		1.6e-11	3.2e-12	4.8e-45	1.6e-40	1.3e-16	6,4e-20	4.8e-22	9.6e-15
END		315	313	314	425	431	213	314	425
STAR T AA		230	222	129	231	350	136	237	351
CHAI N ID			4			,	۲	∢	A
PDB ID		1fht	1fjc	lhal	lhal	lhal	1hd1	1hd1	1hd1
SEQ D		1770	1770	1770	1770		1770	1770	1770

PDF annotation	RIBONUCLEOFROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING,
Coumpound	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 15XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL 5	MUSASHI1; CHAIN: A;	MUSASHII; CHAIN: A;	MUSASHI1; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD
SEQFOL D score						<u>.</u>			
PMF score	0.15	-0.15	0.13	-0.18	0.17	0.99	0.25	0.70	0.88
Verify score	0.06	0.21	0.51	0.11	0.74	0.91	0.36	0.42	0.75
Psi Blast	4.8e-19	1.6e-18	3.2e-13	1.3e-14	6.4e-19	4.8e-14	1.1e-19	4.8e-14	6.4e-18
END	427	319	429	213	314	425	322	431	314
STAR T AA	238	223	341	136	237	351	236	348	236
CHAI	∢	1		А	Ą	∢			4
PDB ID	lqm9	1sxl	1sxl	2mss	2mss	2mss	2sxI	2sxl	2u2f
SEQ NO.	1770	1770	1770	1770	1770	1770	0//1	1770	1770

SEQ ID	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
					-				SUBUNIT; CHAIN: A;	U2 SNRNP, RBD, RNA-BINDING PROTEIN
1770	2up1	4	128	319	4.8e-47	0.00	0.09		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2
1770	2up1	4	231	433	1.6e-43	09.0	0.52		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP AI, UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN AI
1770	3sxl	∢	133	307	3.2e-36	0.22	-0.02		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1770	3sxl	4	236	425	1.46-32	0.32	0.96		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1772	lalh	∢	363	445	3.2e-31			74.27	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1772	Imey	O	138	219	9.6e-44	-0.22	0.04		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ ID	PDB	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTI:IN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	Imey	O	166	247	4.8e-46	0.35	0.96		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	Imey	U	194	275	4.8e-47	0.14	1.00	,	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZING FINGER/DNA) ZINC FINGER, PROTI:IN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	Imey	O	222	303	1.3e-47	0.54	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTIEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRIJCTURE, COMPLEX (ZINC FINGER/DNA)
1772	lmey	ပ	250	331	3.2e-48	0.24	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTIZIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	lmey	U	278	359	1.1e-49	0.71	1.00		DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1772	Imey	υ	306	387	3.2e-50	0.74	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)			~	~		
Coumpound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN; C. F. G:
SEQFOL D score						102.60	
PMF score	1.00	1.00	1.00	1.00	1.00		1.00
Verify	0.69	-0.02	0.37	0.52	0.31		60.0
Psi Blast	1.6e-51	4.8e-51	9.6e-51	1.6e-50	1.6e-50	1.6e-50	6.4e-34
END	415	443	471	499	527	528	531
STAR T AA	334	362	390	418	446	446	474
CHAI N ID	U	U	U	U	ပ	ပ	၁
PDB ID	lmey	Imey	lmey	lme <u>y</u>	lmey	Imey	lmey
SEQ ID NO:	1772	1772	1772	1772	1772	1772	1772

PDB annotation	(ZINC FINGER/ONA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTIJIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTIM-DNA	CBYSTAL STRICTIBE COMPLEY	(ZINC FINGER/ONA)	COMPLEX (TRANSCRIPTION PEGIT ATTOMANA) COMPLEY	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		TFIIIA; CHAIN: A, D; 5S PIBOSOMAI PNA GENE:	CHAIN D E E				TEITIA: CHAIN: A D: 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;
SEQFOL D score																										100.49	
PMF score		0.05		•	0.29				0.54					0.06	2					0.99							
Verify score		0.55			-0.73				0.24					0.28	27.0					0.07							
Psi Blast		9.6e-11			1.6e-09				1.3e-35					4 86-37	(C-20:+		•			3.2e-38						3.2e-38	
END		161			7.1				312					368	2					452						497	
STAR T AA		164		•	44				167					223	777					307			-			334	
CHAI N ID		G			O				4	_				۵						A			_			V	
PDB ID		1mey			Imey				1tf6					1166	2					1tf6						1tf6	
SEQ ID NO:		1772			1772		_		1772					1777	7///					1772	`					1772	

PDB annotation	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF score		0.95	0.94	0.11	0.72
Verify		-0.06	0.01	0.07	-0.21
Psi Blast		1.6e-37	1.4e-36	4.8e-32	1.5e-23
END		509	529	247	275
STAR T AA		363	391	143	169
CHAI N ID		<b>∀</b>	∢	U	၁
PDB ID		1tf6	11f6	1ubd	lubd
SEQ ID NO:		1772	1772	1772	1772

ıtion		IPTION ING-YANG 1; IATION,	, YY1, ZINC 2 A-PROTEIN IPLEX	IPTION ING-YANG 1;	1ATION, YY1, ZINC 2	A-PROIEIN PLEX		IPTION ING-YANG 1:	IATION,	YYI, ZINC2	PLEX		PTION	ING-YANG 1;	VVI ZPIC 2	A-PROTEIN	PLEX		
PDB annotation	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTISIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTILIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TD ANSON INTERNAL	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGIII.ATION/DNA) YING-VANG 1:	TRANSCRIPTION INITIATION	INITIATOR ELIMENT, YYI, ZINC 2 FINGER PROTEIN DNA PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGILLATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	IKANSCKIPIION INIIIATION,	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	
Coumpound		C; ADENO- O VIRUS P5 LEMENT DNA;	CHAIN: A, B;		INITIATOR ELEMENT DNA; CHAIN: A, B;			YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	LEMENT DNA;	CHAIN: A, B;			_		CHAIN A R.				
SEQFOL D score																			
PMF		1.00		1.00				1.00		,			1.00			_			
Verify score		0.13		0.02			•	0.21					0.36						
Psi Blast		4.5e-43		1.6e-32				1.5e-46					4.8e-34						•
END		303		303	.,,,,,,	-		359				—	359	<del></del>					
STAR T AA		661		202				223					258	,					
CHAI N ID		၁		၁				ပ ပ					C						
PDB ID		lubd		lubd				lubd					pqn1						
SEQ ID NO:		1772		1772				1772					1772						

PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
SEQFOL D score					82.44
PMF score		1.00	0.90	1.00	
Verify score		0.06	10.0-	0.01	
Psi Blast		6e-52	98-51	36-50	9e-51
END		472	90 90	527	528
STAR T AA		360	မာ ဗာ ဗာ	416	420
CHAI N ID		ပ	O	၁	C
PDB ID		lubd	lubd	lubd	lubd
SEQ NO.		1772	1772	1772	1772

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PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTISIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEINGMA)	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; BLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZING PROTEIN/DNA- BILL, COMPLEX (DNA- BILL) CHOREN COMPLEX (DNA-	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI:
Coumpound	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		ADKI; CHAIN: NULL;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score									
PMF		1.00	9	-0.18	0.13	0.95	1.00	0.99	86.0
Verify		0.11	,	0.11	-0.10	0.26	0.51	0.21	0.31
Psi Blast		8e-3 <i>5</i>	00 11	96-14	3.2e-29	3e-58	9e-64	1.5e-63	1.5e-67
END AA		527	100	3.5	246	389	417	445	501
STAR T AA		426	130	661	102	197	278	306	362
CHAI N ID		O			4	∢	∢	<b>V</b>	4
PDB ID		pqnl	2adr	T C C C C C C C C C C C C C C C C C C C	11 <b>8</b> 7	2gli	2gli	2gli	2gli
SEQ ID NO:		1772	1777	7//1	7//7	1772	1772	1772	1772

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ç	A	OIN	TAA	AA		score	score	D score		
										GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1772	2gli	A	362	501	1.5e-67			88.77	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1772	2gli	<b>∀</b>	390	524	1.5e-49	-0.07	0.84		ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1772	2gli	A	398	529	1.6e-34	0.24	1.00	,	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
F. C.	Ö 23		C)	Sh Vh	4.55.55 50.55 50.55	(5)	3.37		TRANGORIPTION PACTOR PML; CHAIN: NULL;	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1774	1chc		=	59	1.3e-11	-0.50	0.52		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1774	Ichc		15	63	3.2e-06	-0.28	0.39		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1774	1fbv	4	41	69	1.2e-12	0.41	0.41		SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,
1774	1fbv	A	15	59	3.2e-06	-0.34	0.21		SIGNAL TRANSDUCTION	LIGASE CBL, UBCH7, ZAP-70, E2,

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PDB annotation	UBIQUITIN, E3, PHOSPHORYI.ATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C34C4)	CONTRACTILE PROTEIN TRIPLE- HELIX COILEI) COIL.	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS.
Coumpound	PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	NUCLEAR FACTOR XNF7; CHAIN: NULL;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RAGI; CHAIN: NULL;	RAG1; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				54.69	·		
PMF score		0.36	0.74		0.84	0.01	0.19
Verify score		-0.23	0.21		SO : 0	-0.19	-0.07
Psi Blast		1.5e-13	4.5e-14	3e-06	수 당 다 다	6.4e-14	4.5e-07
END AA		128	70	304	00	109	414
STAR T AA		93	11	63	erd p.d	0	248
CHAI N ID		1	Ą	A		=	A
PDB ID		lfre	1g25	Iquu	Jume	Irmd	1cun
SEQ ID NO:		1774	1774	1774	V. L. L.	1774	1775

PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE		TRANSCRIPTION HELIX-BUNDLE	TRANSCRIPTION TRANSCRIPTION, RNA POL YMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, EXTREMOPHILE		
Coumpound		ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	RNA POLYMERASE II; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII
SEQFOL D score								
PMF score		-0.13	-0.12	0.18	0.52	0.51	1.00	0.75
Verify		0.34	0.10	0.21	-0.14	-0.51	0.16	-0.07
Psi Blast		9e-10	4.5e-09	9000.0	4.5e-06	0.00045	1.6e-10	4.5e-11
END		93	124	553	 78	343	345	343
STAR T AA			6	516	-	291	286	287
CHAI N ID		A	A		∀.			
PDB		- 1cun	lez3	1chc	1eo0	19ур	100	1tfi
SEQ ID		1776	1776	1777	1780	1780	1780	1780

		r-,		1															
PDB annotation		SIGNAL TRANSDUCTION SRC HOMOLOGY DOMAIN: SIGNAT	TRANSDUCTION, SH3 DOMAIN, EPS8, PROLINE RICH PEPTIDE	TRANSFERASE IL-2-INDUCIBLE T. CELL KINASE; TRANSFERASE,	COMPLEX, KINASE	KINASE KINASE, SH3 DOMAIN,	PHOSPHOTRANSFERASE, 2 PROTO- ONCOGENE AND TIPLE DOMAIN	LEUKEMIA	COMPLEX (TRANSFERASE/PEPTIDE)	COMPLEX	(TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN	TRANSFERASI: TYROSINE-PROTEIN	TRANSDUCTION, 2 SH3	SIGNALING PROTEIN/TRANSFERASE NAK:	COMPLEX, SIGNAL	TRANSDUCTION,	DOMAIN (PTB), ASYMMETRIC CELL	DIVISION	COMPLEX (SH3 DOMAIN/TRAL FNHANCER) SPC-HOMOLOGY 3
Coumpound	(TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	EPS8; CHAIN: A, B;		ITK; CHAIN: NULL;		ABL TYROSINE KINASE;	67770		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41;	CHAIN: B, D, F, H;		HEMOPOIETIC CELL KINASE;	C. E. C. D. E. I.	NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE;	CHAIN: B;				FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF
SEQFOL D score								i				•							
PMF score		0.01		0.82		0.92			0.84			1.00		0.63	, ,				1.00
Verify		-0.85		0:30		-0.29			-0.27			-0.27		-0.04					-0.15
Psi Blast		1.5e-14		3e-14		1.2e-11			le-11			4,5e-12		0.003					6e-11
END		510		507		208			208			805	,	148				١	207
STAR T AA		458		436		459			459	-		459		δ Σ					459
CHAI N ID		V				_			∢			∢		∢					₩
PDB ID		laoj		lawj		Iawo			zggī		;	- I no I		T dam				3.1	II I
SEQ ID NO:		1781	,	18/.1		18/1			1/81			1/81	1701	1/01				1701	1/01

PDB annotation	DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN		COMPLEX (KINASE/PEPTIDE)
Coumpound	PROTEIN; CHAIN: B, D;	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	GRB2; CHAIN: A; SOS-1; CHAIN: B;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA;
SEQFOL D score					
PMF		1.00	0.84	0.74	0.01
Verify		0.07	-0.33	-0.35	-0.41
Psi Blast		16-11	1.4e-12	3e-13	4.8e-19
END	<b>5</b>	208	508	510	581
STAR	84	457	454	446	456
CHAI		∢	A	⋖	A
PDB	3	Ifyn	1gbq	1gbr	11ck
SEQ	Ö	1781	1781	1781	1781

r Dis annotation			(TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX	JEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) UTANT PWT; KTH FTON	PEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) UTANT PWT; UTANT SH3 KELETON SE TYROSINE OR COMPLEX, TED KINASE, 2	PEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) (UTANT PWT; (UTANT, SH3 KELETON SE TYROSINE OR COMPLEX, TED KINASE, 2 ATION LOOP CYTOSKELETON, CYTOSKELETON,	PEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) UTANT PWT; UTANT, SH3 KELETON SE TYROSINE OR COMPLEX, TED KINASE, 2 THON LOOP CYTOSKELETON, I DOMAIN EIN KINASE SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE, SINE KINASE,	PEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) UTANT PWT; UTANT PWT; UTANT, SH3 KELETON SE TYROSINE DR COMPLEX, ED KINASE, 2 CYTOSKELETON, DOMAIN EIN KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B DR KINASE, B	PEPTIDE) SRC, SH3 DS, NON-PEPTIDE MPLEX PEPTIDE) UTANT PWT; 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FDIS and		COMPLEX	(I KANSTEKASETET IIDE) SKC, SH. DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TP ANSER A SERVED TO SERVED TO SERVED A SERVED TO SERVED A SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVED TO SERVE	CIRCULAR PERMUTANT; SHA	CIRCULAR PERMUTANT PRY ELEMENTS, 2 COMPLEX (TRANSFERASEPEPTIDE) CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2				
-	VIN: B; 1LCK 15	C-SRC; CHAIN: C; NL1 (MN7- MN2-MN1-PLPPLP); CHAIN: N; (C	Ш		ii ii	N: \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	IN; CHAIN: FIC CELL CHAIN: A; FRIN; CHAIN: A; TEIN KINASE	IN; CHAIN:  TIC CELL CHAIN: A;  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE  TEIN KINASE	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
1LCK 14 CHAIN: B; 1LCK 15		C-SRC; CHAIN:		ALPHA SPECTRIN; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN NULL; HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	ALPHA SPECTR NULL; HAEMATOPOET KINASE (HCK); ALPHA II SPECT	ALPHA SPECTR NULL; HAEMATOPOET KINASE (HCK); ALPHA II SPECT TYROSINE-PRO BTK; CHAIN: A;	ALPHA SPECTRIN; CF NULL; HAEMATOPOETIC CE KINASE (HCK); CHAIN TYROSINE-PROTEIN ; BTK; CHAIN: A; BTK; CHAIN: A; RHOSPHOTRANSFERA PROTO-ONCOGENE T KINASE (E.C.2.7.1.112) (SH3 DOMAIN) 1SHF 4	ALPHA SPECTRIN; CHAIN: NULL; HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A; ALPHA II SPECTRIN; CHAIN TYROSINE-PROTEIN KINAS BTK; CHAIN: A; PHOSPHOTRANSFERASE FY PROTO-ONCOGENE TYROSI KINASE (E.C.2.7.1.112) 1SHF (SH3 DOMAIN) 1SHF 4 NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: A;
_									
		1.00	1 00	7.0	0.15	0.15	0.15	0.15	0.15 0.15 0.81 0.81
		0.18	0.21		-0.31	-0.31	-0.31 0.20 -0.05	-0.31	-0.31 -0.20 -0.05 -0.64
		3e-11	3e-10		3.2e-18	3.2e-18 1.5e-10	3.2e-18 1.5e-10 3e-12	3.2e-18 1.5e-10 3e-12 7.5e-11	3.2e-18 1.5e-10 3e-12 7.5e-11
		507	208		581	581	581	508 508 508	581 508 508 153
		459	457		456	456	456 457 455	456 457 455 459 ·	456 457 459 · .
		O .			A	<b>4 4</b>	<b>4 4 </b> ∢	<b>₹ ₹ ₹</b>	<b>₹ ₹ ₹ ₹</b>
!		Inlo	1pwt		1qcf	1qcf 1qkw	Iqcf Iqkw Iqiy	1qef 1qkw 1q!y 1shf	Iqef Iqkw Iqly Ishf
Αö		1781	1781		1781	1781	1781 1781 1781	1781 1781 1781 1781	1781 1781 1781 1781

PDB annotation	TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE		ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
Coumpound	KINASE; CHAIN: NULL;	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	APOLIPOPROTEIN E; CHAIN: A;	ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;
SEQFOL D score								
PMF score		0.04	0.04	-0.06	0.30	0.28	0.00	0.18
Verify		0.07	0.20	0.04	-0.22	0.11	-0.41	-0.04
Psi Blast		1.1e-07	1.6e-05	3e-13	7.5e-19	4.5e-07	1.5e-08	1e-09
END AA		198	126	259	298	260	298	394
STAR T AA		36	6	24	78	118	138	246
CHAI N ID		4	A	A	æ	A	<b>∀</b>	∢
PDB		lbgl	1624	Icun	1dn1	lez3	lez3	1ez3
SEQ ID		1782	1782	1782	1782	1782	1782	1782

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PDB annotation		MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX		DNA-BINDING HMGA DNA- BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-BOX 1AAB	SIGNALING PROTEIN GUANINE	NUCLEOTIDE BINDING PROTEIN 1;	GBP, GTP HYDROLYSIS, GDP, GMP,	INTERFERON INDOCED, DYNAMIN 2 RFI ATED I ARGE GTDASE	FAMILY, SIGNALING PROTEIN	SIGNALING PROTEIN GBP, GTP	HYDROLYSIS, GDP, GMP,	INTERFERON INDUCED, DYNAMIN	Z KELATED, LARGE GIPASE	FAMILY. GMPPNP, GPPNHP.	SERINE/THREONINE PROTEIN	KINASE TRANSFERASE,	SERINE/THREONINE-PROTEIN	KINASE, 2 PROTO-ONCOGENE,	ZINC, ATP-BINDING, PHORBOL-	ESTER BINDING						SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI: INCF 8
Coumpound		SSO1 PROTEIN; CHAIN: A;	SSOI PROTEIN; CHAIN: A;		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	INTERFERON-INDUCED	GUANYLATE-BINDING	PROTEIN I; CHAIN: A;			INTERFERON-INDUCED	GUANYLATE-BINDING	PROTEIN 1; CHAIN: A;			RAF-1; CHAIN: NULL;					DNA BRIDING LIGH	MODIT TEV CROIM PROTERY	MODILII I GROOF PROTEIN FRAGMENT R (HMGR) (DNA	BINDING 1HMF 3 HMG.BOX	DOMAIN B OF RAT HMGD	(NMR, 1 STRUCTURE) 1HME 4	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,
SEQFOL	2026				,				-																		
PMF		0.04	0.03		0.03	0.19					0.04				5	0.03					000	3					0.12
Verify		-0.09	-0.28		-0.24	0.02					0.02				0.40	-0.40					-0.29	ì					0.02
Psi Blast	1	7.5e-07	le-11		0.00012	4.5e-05	-				0.00015				200	0.003					0.0045						0.006
END	107	485	280		763	2333					2333				0	66					753	)					141
STAR		283	29		716	2237					2237				0,7	מא					716	)					17
CHAI		∢	∢			⋖					⊲;																V V
PDB	i i	01110	1ff0		laab	1dg3					ItSn				1 620	- hart					1hme						Incf
SEQ ID	NO:	1/82	1782		1783	1783					5871				1793	1/02					1783						1783

PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	PHOSPHOTRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
Coumpound	B; INCF 5 BI	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL; PI	PROTEIN KINASE C, GAMMA C, TYPE; CHAIN: NULL; PI PI TYPE	LYMPHOID ENHANCER-GBINDING FACTOR; CHAIN: A; HUDNA (5'-CHAIN: B; DNA (5'-TICHAIN: C; B)	PROTEIN KINASE C, GAMMA C. TYPE; CHAIN: NULL; P. P. T. TYPE	QGSR ZINC FINGER PEPTIDE; C CHAIN: A; DUPLEX CLIGONUCLEOTIDE BINDING Z SITE; CHAIN: B, C; P!	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO
SEQFOL D score								
PMF score		0.23	0.31	0.41	0.31	0.01	0.45	-0.13
Verify score		0.02	-0.09	-0.35	-0.13	-0.65	-0.30	0.07
Psi Blast		0.003	0.00075	0.006	7.5e-05	60000	3.2e-26	3.2e-12
END		50	50	66	763	137	130	232
STAR T AA		21	21	69	716	100	62	178
CHAI N ID					A		Ą	
PDB ID		lptq	Itbn	1tbn	2lef	Itbn	1a1h	1bbo
SEQ ID		1783	1783	1783	1783	1784	1785	1785

PDB annotation	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NICLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	TUMOR SUPPRESSOR, 3 MTS1.	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE	6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN:	́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́́					CYCLIN-DEPENDENT KINASE	6; Chain: A; Figinr4D; Chain:   B:	î			CYCLIN-DEPENDENT KINASE 6: CHAIN: A: P19INK4D: CHAIN:	B;			CYCLIN-DEPENDENT KINASE
SEQFOL D score																						
PMF score		0.29			0.19	0.04							0.00					0.37				0.15
Verify score		-0.09			-0.01	0.14							-0.17					0.01				-0.12
Psi Blast		4.8e-29			8e-27	6.4e-17							6.4e-26					1.3e-23				6.4e-25
END		125		<del></del>	160	560							160					183				130
STAR T AA		3			21	443							21					20				1
CHAI N ID		В				В							В		_			В				A
PDB ID		lawc			1bd8	1bi7							1blx					1blx				1bu9
SEQ ID		1788			1788	1788					1		1788					1788				1788

	T	7	<del></del>				T	<del></del>	<del></del>
PDis annotation	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEJENDENT KINASE,	SIGNALING PROTEIN HELIX-TURN-	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REP!AT, 2 CDK 4/6	INHIBITOR ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	SIGNALING PROTEIN RUBI, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING	PROTEIN DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITIN, DE NOVO PROTEIN,	UBIQUITIN SIGNALING PROTEIN NEDD8; NEDD8, NEDD-8, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2	PROTEIN
Coumpound	6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIRITOR B. CHAIN: A.	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	UBIQUITIN-LIKE PROTEIN 7, RUB1; CHAIN: A;	ID8 UBIQUITIN; CHAIN: A;	UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	UBIQUITIN TETRAUBIQUITIN 1TBE 3
SEQFOL D score									
PMF score		90.0	0.10	0.37	0.01	0.92	0.76	0.75	0.94
Verify score		0.14	-0.12	0.01	0.14	0.17	0.02	0.22	0.48
Psi Blast		1.6e-17	1.3e-25	3.2e-24	1.6e-20	1.4e-20	1.6e-27	6.4e-20	3.2e-27 (
END AA		292	161	129	127	194	196	195	193
STAR T AA		443	18	-	61	124	124	124	124
CHAI N ID		A	¥	∢		A	A	A	В
PDB ID		1d9s	lihb	1ihb	Imyo	1bt0	1c3t	Indd	1tbe
SEQ NO:		1788	1788	1788	1788	1791	1791	1791	1791

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PDB annotation		UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION		MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION		ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT		ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT		MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC- DOMAIN, RESIDUES 1 - 75; CERIUM-
Coumpound	CHROMOSOMAL PROTEIN UBIQUITIN 1UBI 3	UBIQUITIN CORE MUTANT ID7; CHAIN: A;	ELONGIN B; CHAIN; A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;		M-PMV MATRIX PROTEIN; CHAIN: NULL;	M-PMV MATRIX PROTEIN; CHAIN: NULL;		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN IA; CHAIN: B;		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;		TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CALMODULIN; CHAIN: NULL;
SEQFOL D score						69.49						57.92		
PMF score	99:0	0.55	0.15		0.64			0.00		0.00			0.25	-0.01
Verify score	0.19	0.39	-0.54		-0.22			-0.04		-0.04			0.30	0.12
Psi Blast	4.8e-29	3.2e-28	6.4e-05		3.2e-36	3.2e-36		0.0075		0.0075		6.4e-36	6.4e-36	4.8e-16
END AA	196	196	181		92	35		227		235		382	379	309
STAR T AA	124	124	124		1	1		157		165		225	241	241
CHAI N ID		A	<b>∀</b>					В		В				
PDB ID	1ubi	1nd7	1vcb		1bax	1bax		1dn1		ldn1		1aj4	1aj4	1ak8
SEQ No:	1791	1791	1791		1792	1792		1794		1795		1799	1799	1799

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PDB annotation	LOADED, CALCIUM-BINDING PROTEIN	CALCIUM-BINING CNTNC; CALCIUM-BINING, REGULATION, TROPONIC, CARDIAC MUSCLE 2	HYDROLASE, PHOSPHATASE,	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, MAMINOSI IPPRESESTON	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, BENDROMAL SPECIFIC GUANYLATE	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE	CALCIUM-BINDING CALCIUM. BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE			
Coumpound		CARDIAC N-TROPONIN C; CHAIN: NULL;	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B:	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	NEUROCALCIN DEL TA; CHAIN: A, B;	NEUROCALCIN DEL TA; CHAIN: A, B;	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT	CALCIUM-BINDING PROTEIN CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CT 1	CALCIUM-BINDING PROTEIN
SEQFOL D score			69.73				59.92			59.19
PMF score		-0.01		99.0	0.19	0.83		0.18	0.21	
Verify score		0.50		0.46	-0.02	0.64		0.25	0.05	
Psi Blast		1.4e-12	4.8e-42	4.8e-42	3.2e-11	6.4e-36	6.4e-36	3.2e-42	3.2e-47 (	3.2e-47
END		314	391	378	345	385	390	378	378	380
STAR T AA		241	233	240	202	224	224	241	241	241
CHAI N ID			В	В	∢	A	Ą	∢		
PDB ID		1ap4	laui	laui	1bjf			1cdm	lcll	IcII
SEQ ID NO:		1799	1799	1799	1799	1799	1799	1799		1799

PDB annotation		CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	BLOOD CLOTTING HELICAL, EF. HAND, BLOOD CLOTTING	STRUCTURAL PROTEIN HELIX- TURN-HELIX	STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM	LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN,
Coumpound	CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; 1CMF 7	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	APO CIB; CHAIN: A	CARDIAC TROPONIN C; CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: A;	TROPONIN C; CHAIN: A;	CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	GUANYLATE CYCLASE ACTIVATING PROTEIN 2;
SEQFOL D score													
PMF score		0.13	-0.06	09:0	0.07	69.0	0.12	0.60	0.16	0.21	0.18	0.03	0.99
Verify score		0.73	0.43	10.0	90.0	0.16	0.13	0.40	0.44	0.25	0.10	0.18	0.46
Psi Blast		4.8e-11	1.6e-25	3.2e-20	1.4e-12	8e-36	1.3e-44	8e-11	3.2e-24	9.6e-10	1.3e-19	3.2e-15	1.6e-29
END		309	378	388	306	379	378	309	378	306	379	341	392
STAR T AA		242	310	241	183	241	241	247	316	238	313	221	241
CHAI N ID				<b>⋖</b>	⋖	¥	¥	A	A	A	A	A	A
PDB ID		1cmf	lcmf	1dgv	1dtl	1dt]	lexr	1771	1771	1fi5	1fi5	1fpw	1jba
SEQ NO:		1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799

		_			_																		_							
PDE annotation	GUANYLYL CYCLASE 2	CALCIUM-REGULATED MISCIE	CONTRACTION MUSCLE	CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	CONTRACTION	CALCIUM-REGULATED MISCI F	CONTRACTION MUSCLE	CONTRACTION, CALCIUM-	BINDING, TROFONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	REGULATED 3 MUSCLE	CONTRACTION	CALCIUM-BINDING PROTEIN EF-	HAND ITNX 14	CALCIUM-BINDING PROTEIN EF. HAND 17NX 14											
Coumpound	CHAIN: A;	TROPONIN C; CHAIN: NULL;				-			TROPONIN C; CHAIN: NULL;								IROPONIN C; ITNX 4 CHAIN:	Thomas in a series	INOPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CONTRACTILE SYSTEM	PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM	PROTEIN TROPONIN C 1TOP 3	CALCIUM BINDING PROTEIN	CALMODULIN (/TR=2=C\$	FRAGMENT COMPRISING	RESIDUES 78 - 148 1TRC 3 OF	THE INTACT MOLECULE) ITRC	4	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$
SEQFOL D score									63.35							80.5	61.09			64.51								··		
PMF		0.48																50.0	50.0		1	0.41	,	-0.05				-	800	60.0-
Verify score		0.10											. ,					-0.72	77:0		000	0.02		0.28					Ì	0.03
Psi Blast		3.2e-37							3.2e-37				•			4 80.26	00.50	4 Re-36	25.20	3.2e-38	135.70	3.25-38	7 11	0.46-11					$\dagger$	1.16-24
END		378						3	3/9							378	2	378	2	382	370	0/0	306	9		-			270	0/5
STAR T AA		232							733							233	}	236		/77	73.6	2	242	747					314	
CHAI N ID																							4	<del></del>					A	
PDB ID		1tcf						3.71	511							Ithx		1tnx		don	iton		Ĭ.						1trc	$\dashv$
SEQ ID NO:		1799						1200	1/22							1799		1799	1200	1133	1799	`	1799	``					1799	

PDB annotation	3 OF ) ITRC	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	IN: A, MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN		TL; CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN	TDE; COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), DING ZINC FINGER, DNA-BINDING PROTEIN	-
Coumpound	FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN; NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;
SEQFOL D score			56.76	·					
PMF score		0.07		0.33	0.04	0.13	0.12	0.35	86.0
Verify score		-0.21		0.12	0.23	0.36	0.19	0.03	0.03
Psi Blast		1.6e-14	3.2e-46	3.2e-46	1.4e-20	9.6e-10	1.3e-19	1.6e-12	4.8e-19
END		309	381	378	382	306	379	210	238
STAR T AA		180	239	241	241	238	313	120	158
CHAI N ID		<b>V</b>	A	<b>V</b>	U			4	4
PDB ID		lvrk	lvrk	lvrk	1 wdc	3ctn	3cm	lalh	lalh
SEQ ID NO:		1799	1799	1799	1799	1799	1799	1801	1801

Supple   Cital   Star   Ext)   Fei Blast   Vertry   PME   SRQFOL   Coumpound   PDB santodifican		<del></del>	<del></del>						1	
Pub   CHAI   STAR   END   Fsi Blast   Verify   PMF   SEQFOL	PDB annotation	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, INA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, UNA-BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA)
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score   Score	Coumpound	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING STTE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: R. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
PDB   CHAI   STAR   END   Fsi Blast   Verify   Score	SEQFOL D score	84.50								
PDB   CHAI   STAR   END   Fsi Blast   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Far   Fa	PMF score		1.00	0.41	0.57	0.66	0.78	0.15	1.00	1.00
PDB   CHAI   STAR   END   FSi Blast	Verify score		0.23	-0.16	0.22	0.11	0.07	0.17	0.45	0.54
PDB   CHAI   STAR	Psi Blast	4.5e-37	1.1e-29	9.6e-22	1.6e-19	3e-19	3e-21	3.2e-26	8e-30	
PDB CHAI	END AA	296	377	377	404	454	481	481	509	510
PDB	STAR T AA	214	270	270	298	298	353	382	429	429
PDB	CHAI	A	Ą	A	∢	Ą	∢	∢	∢	A
SEQ 1D 1801 1801 1801 1801 1801 1801	208 CC	lalh	ialh	lalh	lalh	lalh				
	S E S	1801	1801	1801	1801	1801	1801	1801	1801	1801

PDB annotation		ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTORE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, FROIEIN-DNA INTERACTION. PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX
Coumpound		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	
SEQFOL	D score																														
PMF	score		1.00			1.00			0.36		-			1.00					1.00					1.00					1.00		
Verify	Score		-0.09			0.28			0.10					0.42					0.55					0.35					0.56		
Psi Blast			1.1e-30			7.5e-34			8e-30					1.4e-37					3.2e-47					3.2c-48					4.8e-49		
END	¥¥		537			565			210					238					266					294					322		
STAR	I AA		457			485			119					157					185	}				213					241		
CHAI	<u>2</u>		A			A			U					S	_				ن	)				C	)				U		
PDB	3		1a1h		-	lalh			lmev	`		-		lmey					1mev					Imev	}				Imey		
SEQ	ΑÖ		1801			1801			1801					1801					1801					1801	3				1801	·	

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PDB annotation	(ZINC FINGER/I)NA)	COMPLEX (ZINC FINGER/DNA) ZINC	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/I)NA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/LINA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/E)NA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DINA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC.FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC: FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2
Coumpound		DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSOS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	,		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;
SEQFOL D score		101.14																														
PMF score						0.51				-0.17					0.70					0.24				1	0.07					 0:1	•	
Verify					,,,,,	-0.00	•		,	0.01	-				0.42					0.41					0.26	_				0.51		
Psi Blast		4.8e-49			07.07	4.86-40				1.1e-20					1.3e-22				;	8e-41			***		3.2e-45					1.6e-49		
END AA		323			27.0	//ς			1	453				,	481				137	455		,			481					509		
STAR T AA		241			020	607			200	/67				0	353				257	32/				201	361					428	_	
CHAI N ID		ن ن			0	د				ر.					۔۔				1	 د					— ر				,	۔۔۔		
PDB ID		lmey			10001	ımey			1	ımey					Imey				1 20021	liney	-			+	ııııcy				+	Imey		1
SEQ NO:		1801			1001	1001			1851	1901				1001	1801				1801	1001				1001	1001				100	1001		

	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
	,							•	
									CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
ပ		456	537	1.6e-49	-0.03	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
								PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
ပ		484	565	1.6e-49	0.25	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								CONSENSOS ZINC FINGER PROTEIN; CHAIN; C, F, G;	FINGER, FROI EIN-DNA INTERACTION, PROTEIN DESIGN, 2
									CRYSTAL STRUCTURE, COMPLEX
		200	101	6 40 17	0.72	100		TB ANSCRIBTION BACTOR IIIA:	CONDI EV (TP ANISCPIPLIONI
<		795	401	0.46-17	57.0	10:0-		CHAIN: A; SS RNA GENE;	REGULATION/DNA) TFIIIA; 5S
								CHAIN: E, F;	GENE; NMR, TFIIIA, PROTEIN, DNA,
									TRANSCRIPTION FACTOR, 5S RNA 2
									GENE, DNA BINDING PROTEIN,
			_						ZINC FINGER, COMPLEX 3
									(IKANSCKIFIION REGIII.ATION/DNA)
⋖		112	247	1.4e-22	0.08	0.22		TFIIIA: CHAIN: A. D: 5S	COMPLEX (TRANSCRIPTION
:		:	:	\ !				RIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX
								CHAIN: B, C, E, F;	(TRANSCRIPTION
									REGULATION/DNA), RNA
							,	,	POLYMERASE III, 2 THE ANSCEIPTION PRITTY ATION TRIC
									FINGER PROTEIN
₹		157	325	3e-61			114.65	TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION
								KIBOSOMAL KNA GENE;	KEGULATION/DNA) COMPLEX
					-			C. C. C. C. C. 1.	REGULATION/DNA). RNA
									POLYMERASE III, 2
									TRANSCRIPTION INITIATION, ZINC
_									FINGER PROTEIN

PDB innotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE 111, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DINA) COMPLEX (TRANSCRIPTION REGULATION/DINA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC
Coumpound	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
SEQFOL D score					
PMF	0.99	1.00	0.24	0.28	66:0
Verify score	0.37	0.15	0.04	-0.15	0.23
Psi Blast	9.6e-31	1.4e-35	1.3e-25	1.3e-34	1.6e-35
END	303	324	495	547	565
STAR T AA	158	186	298	382	429
CHAI N ID	¥	∢	Ą	A	4
aga ID	1466	1176	11(6	1476	1466
SEQ ID NO:	1801	1801	1801	1801	1801

PDB annotation	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGIT ATTOM/DNA) VING-YANG 1:	TRANSCRIPTION INITIATION,	FINGER PROTEIN, DNA. PROTEIN	KECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I;	IRANSCRIPTION INITIATION, INITIATOR FLEMENT VY1 ZINC 2	FINITED DEOTEIN THAT DEOTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I;	TRANSCRIPTION INITIATION,	TRICER PROFESSION 111, CHACA	FINGER PROTEIN, DNA-PROTEIN	ATT ANSOR INTON	REGULATION/DNA)	COMPLEX (TRANSCRIPTION
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;		YYI; CHAIN: C; ADENO-	INITIATOR ELEMENT DNA;	Cimin. A, D,			YYJ; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INTITATION ELEMENT DINA;   CHAIN: A R:	CITAIN: A, B,				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, D;				YY1; CHAIN: C; ADENO-
SEQFOL D score					92.90																			
PMF score		1.00								1.00							1.00							1.00
Verify score		0.25								0.35							0.15	y.						0.17
Psi Blast		6e-43 _.			7.5e-48					7.5e-48							7.5e-51							1.6e-32
END		266			267					294							322							322
STAR		157			159					186							217				<del></del>			221
CHAI N ID		ပ			ပ					U							၁							ပ
PDB ID		lubd			1ubd					Iubd							1ubd							lubd
SEQ DD NO:		1801			1801					1801							1801			_				1801

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PDB annotation	REGULATIONINA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIL ATIONINA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION, 3	COMPLEX (TRANSCRPTION REGULATIONDNA) YING-YANG 1; TRANSCRPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	CEGULATION/DINA) COMPLEX (TRANSCRIPTION REGULATION/DINA) YING-YANG 1; TRANSCRIPTION INITIATION
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:
SEQFOL D score					
PMF score	·	0.99	-0.02	0.64	0.36
Verify score		-0.16	0.04	0.23	0.26
Psi Blast		3.2e-26	1.66-24	1.5e-30	6.4e-29
END		377	453	509	481
STAR T AA		249	305	351	360
CHAI N ID		υ	υ	O	ນ
PDB ID				. Inpq	lubd
SEQ ID NO:		1801	1801	1801	1801

PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	
Coumpound	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3
SEQFOL D score					
PMF score		0.65	1.00	0.98	0.10
Verify score		0.07	0.30	-0.10	0.53
Psi Blast		3.2e-31	4.5e-40	8e-34	36-18
END		509	565		377
STAR T AA		387	454	464	294
CHAI N ID		O	U	U	<b>∀</b>
PDB 1D		lubd	lubd	lubd	2drp
SEQ S		1801	1801	1801	1801

				•						
PDJ8 annotation		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZING FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, SINC FINGER, COMPLEX (DNA-	COMPLEX (DNA-BINDING  COMPLEX (DNA-BINDING  PROTEIN/DNA) FIVE-FINGER GLI;  GLI, SINC FINGER, COMPLEX (DNA-	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; GLI, SINC FINGER, COMPLEX (DNA-BINDING)	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; GLI, SINC FINGER, COMPLEX (DNA-BINDING) PROTEIN/DNA)	COMPLEX (DNA-BIDDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BIDDING)	COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING)	COMPLEX (DNA-BINDING
Coumpound	DNA 2DRP 4	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII;
SEQFOL D score		100.58								
PMF score			1.00	0.90	0.81	0.49	-0.02	0.87	0.75	0.69
Verify score			0.25	0.15	0.01	0.11	0.15	0.40	0.25	0.39
Psi Blast		1.1e-58	3e-57	1.1e-58	3.2e-23	1.1e-37	8c-30	6.4e-32	1.5e-48	1.6e-33
END		296	296	322	404	511	508	536	565	564
STAR	,	157	157	185	249	297	360	424	428	436
CHAI N ID		∢	¥	¥	A	Ą	A	∢	A	A
PDB ID	:	. 2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli
SEQ ID NO:		1801	1801	1801	1801	1801	1801	1801	1801	1801

PDBCHAISTARENDPsi BlastVerlfyPIDN IDT AAAAScorest	STAR END Psi Blast Verlfy TAA AA score	END Psi Blast Verify AA score	verify score		PI S	PMF score	SEQFOL D score	Coumpound	PDB annotation
						1		CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
						Ì			
lafb 1 89 252 1.5e-21	252		1.5e-21			•	59.81	MANNOSE-BINDING PROTEIN- A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1b08 A 118 249 3e-31 0.35 0.83	249 3e-31 0.35	3e-31 0.35	0.35		0.83			LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COLLED- 2 COIL, LUNG SURFACTANT, SUGAR BINDING PROTEIN
1b6e 123 253 4,5e-29	253	<u> </u>	4.5e-29			}	74.73	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD
1b6e 126 251 4.5e-29 0.57 0.98	251 4.5e-29 0.57	4.5e-29 0.57	0.57		0.98	j		CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD
1bj3 A 125 250 8e-25	250		8e-25			ł	67.59	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER,
•	•	•	•					BINDING PROTEIN B; CHAIN: B;	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1du8 A 103 249 1.2e-27 0.06 0.18	249 1.2e-27 0.06	1.2e-27 0.06	0.06		0.18			SURFACTANT PROTEIN A; CHAIN: A;	MEMBRANE PROTEIN SP-A; SP-A:PHOSPHOLIPID MOLOLAYER COMPLEX
1dv8 A 126 250 1.5e-28 0.47 1.00	250 1.5e-28 0.47	1.5e-28 0.47	0.47		1.00	Į.		ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1dv8 A 126 252 1.6e-28 0.35 0.48	252 1.6e-28 0.35	1.6e-28 0.35	0.35	-	0.48	)		ASIALOGL YCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD
le87 A 125 250 1.5e-27 0.79 0.65	250 1.5e-27 0.79	1.5e-27 0.79	0.79		0.65	}		EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL

PDB annotation	RECEPTOR, LIJUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR	C-TYPE LECTIN ALPHA-HELICAL	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-1 YPE CRD MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,	LECTIN	METAL BINDING PROTEIN	PANCREATIC STONE PROTEIN, PSP;	PANCREATIC STONE INHIBITOR,	LITHOSTATHINE	METAL BINDING PROTEIN	PANCREATIC STONE PROTEIN, PSP;	PANCREATIC STONE INHIBITOR,	LITHOSTATHINE	COMPLEX (NK RECEPTOR/MHC	CLASS I) H-2 CLASS I	HISTOCOMPATIBILITY ANTIGEN,	B2M; NK-CELL SURFACE	GLYCOPROTEIN YEI/48, NK CELL,	INHIBITORY RECEPTOR, MHC-I, C-	TYPE LECTIN-LIKE, 2	HISTOCOMPATIBILITY, B2M, LY49,
Coumpound		MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN: NULL: 1HUP 5	COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;		COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:	NOLL		LITHOSTATHINE; CHAIN: A;				LITHOSTATHINE; CHAIN: A;				MHC CLASS I H-2DD HEAVY	CHAIN; CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	HIV ENVELOPE	GLYCOPROTEIN 120 PEPTIDE;	CHAIN: P; LY49A; CHAIN: C, D;		
SEQFOL D score		63.07	65.37				61.47					66.78						21.12	/4.13											
PMF score														, ,	0.80							,	0.60			-				
Verify score														1	0.75							3	09'0		_					
Psi Blast		3e-27	1e-24				6e-25					36-23		1	3e-28			30.70	07-20			†	1.5e-30					_		
END		249	250				252				250	707		250	767			250	707			250	723							
STAR T AA		86	125				125				701	071		11.4	+11			114	<u>.</u>			122	173						_	
CHAI N ID			Ą				<b>T</b>								τ			4					 ر							
PDB ID		Ihup	lixx				X				Ě			†	noh i	~ ~~		lodd			-	+	cohi							
SEQ ID NO:		1802	1802				7081				1800	7001		1800	1902		_	1802				1800	1002							

PDB annotation	COMPLEX (NK RECEPTORMHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-1, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49	LECTIN SUB-MBP-C; IRDL 9 C-1 YFE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20		ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN		LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR
Coumpound	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	MANNOSE-BINDING PROTEIN- C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;
SEQFOL D score		61.44	63.45		61.86	60.17	
PMF score	0.43			0.41			0.83
Verify	0.81			0.52			0.35
Psi Blast	1.3e-27	1.2e-26	4.5e-23	1.3e-29	1.3e-25	1.5e-21	3e-31
END	253	251	252	250	251	291	288
STAR T AA	130	136	68	123	136	127	157
CHAI N ID	Ω		-	ď	A		<
PDB ID	1903	Irdi	1rtm	2afp	2msb	lafb	1508
SEQ ID	1802	1802	1802	1802	1802	1803	1803

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PDB annotation	BINDING PROTEIN	NY CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN-	LIKE, NKU NK CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN.	LIKE, NKD COLLAGEN BINDING PROTEIN IX	BP; IX-BP; COAGULATION FACTOR	IX-BINDING, HETERODIMER, VENOM HABIT 2 SNAVE C TYPE	LECTIN SUPERFAMILY, COLLAGEN	COLI A CENT BY THE COLI	BP; IX-BP; COAGULATION FACTOR	IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE	LECTIN SUPERFAMILY, COLLAGEN BINDING PROPERI	MEMBRANE PROTEIN C. TYPE	LECTIN-LIKE DOMAINS		MEMBRANE PROTEIN SP-A; SP-	A:PHOSPHOLIFID MOLOLAYER	SIGNALING PROTEIN HEPATIC	LECTIN HI; C-1 YPE LECTIN CRD	SIGNALING PROTEIN HEPATIC	LECTIN HI; C-1 YPE LECTIN CRD	HEMATOPOIETIC CELL RECEPTOR	ACTIVATION INDUCER MOLECULE	(AIM), EA 1, HEMATOPOIETIC CELL	RECEPTOR, LEUCOCYTE, C.TYPE
Coumpound		CD94; CHAIN: NULL;	CD94; CHAIN: NULL;	COAGULATION FACTOR IX-	BINDING PROTEIN A; CHAIN:	A; COAGULATION FACTOR IX- BINDING PROTEIN B: CHAIN:	B;	COAGIII ATTON FACTOR IV	BINDING PROTEIN A; CHAIN:	A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN:	ģ	FLAVOCETIN-A: ALPHA	SUBUNIT; CHAIN: A; FI AVOCETEN A: BETA	SUBUNIT; CHAIN: B	SURFACTANT PROTEIN A;	CHAIN: A;	ASIALOGLYCOPROTEIN	RECEPTOR 1; CHAIN: A;	ASIALOGLYCOPROTEIN	KECEPIOR I; CHAIN: A;	EARLY ACTIVATION ANTIGEN	CD69; CHAIN: A;		
SEQFOL D score		73.97		68.01																-			_	<del>, , , , , , , , , , , , , , , , , , , </del>	
PMF score			96.0					0.48					-0.06			0.18		0.46		00.1	970	6.6			
Verify			0.57					0.16					0.38			90.0		0.13	1,7	74.0	07.0			-	
Psi Blast		4.5e-29	4.5e-29	1e-24				1e-24	-				4.5e-24			1.2e-27		4.8e-25 (	$\dagger$	07-50.1	1 50-27			_	
END		292	290	289				288			•••		290			288		288	280	607	2%0				-
STAR T AA		162	165	164				591					165		1	142		165	165		164		-	_	
CHAI N ID				Ą				A					Δ,			<		₹	\ \ \	:	A		-		
PDB ID		1b6e	1b6e	1bj3				1bj3				$\dashv$	1038		+	onpi	+	, avai	1dv8		1e87				
SEQ ID NO:	2001	1803	1803	1803				1803					1803		1900	1903	000.	5081	1803		1803				

PDB annotation	6 333	LECTIN-LIKE, 2 NKD, KLR	SUGAR BINDING FROIEIN C-1 1FE LECTIN, MANNOSE RECEPTOR	C-TYPE LECTIN ALPHA-HELICAL	COILED-COIL 1HUP 12	C-TYPE LECTIN ALPHA-HELICAL	CONCETT ATTON FACTOR BINDING	IXX-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-1 YPE CKU MOTIF 1 OOP EXCHANGED DIMER	COAGIL ATION FACTOR BINDING	TX/X-RP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IXXX-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	DXX-BP COAGULATION FACTOR	BINDING, C. I'YPE LECTIN, GLA-	DOMAIN 2 BINDING, C-1 YFE CKU	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,	LECTIN	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN	
Coumpound	-		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	MANNOSE-BINDING PROTEIN;	1HUP 4 CHAIN: NULL; 1HUP 5	MANNOSE-BINDING PROTEIN;	IHOF 4 CHAIN: NOLL, INO. 3	COAGULATION FACTORS IX/X-BINDING PROTEIN:	CHAIN: A, B, C, D, E, F;		COACITI ATTION EACTORS	TAY BUILDING DECTEIN:	CHAIN: A B. C. D. E. F.			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:	NULL		LITHOSTATHINE; CHAIN:	NULL	LITHOSTATHINE; CHAIN: A;	
SEQFOL	D score			63.43			, ,	65.74								61.53							-						67.30			
PMF	score		0.95			0.40					9	0.48									0.48	•				68.0					0.86	
Verify	score		0.62			0.33						0.32									0.38					0.77					0.75	1
Psi Blast			1.5e-25	30-27	1	3e-27		1e-24				le-24				50-05	77.00				6e-25					30-25	}		3e-25		30-28	24-20
END	AA		288	288	907	289		289				788				201	167				290	}				201	<u> </u>		291	} 	201	177
STAR	TAA		165	150	200	164		164				165				151	104				165	}				165	}		165	}	153	177
CHAI	A IS		V					W W				Ą				6	η				ď	<b>1</b>									<	4
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SEQ	ВŞ	į	1803	1000	5081	1803		1803				1803					1803				1803	7607				10/13	2001		1803	6	1003	1803

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PD:B annotation	PANCREATIC STONE PROTEIN, PSP. PANCREATIC STONE INHIBITOR, LITHOSTATHINF	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP, PANCREATIC STONE INHIBITOR, THE COST.	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,	B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-1, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M. LY49	LY-49	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN	B2M; NK-CELL SURFACE	INHIBITORY RICEPTOR, MHC-1, C-TYPE LECTIN-1, IKE, 2	HISTOCOMPATIBILITY, B2M, LY49, LY-49	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING	LECTIN SUB-M3P-C; IRDL 9 C-TYPE	LECTIN, CALCIUM-BINDING PROTEIN IRDI. 20		
Coumpound		LITHOSTATHINE; CHAIN: A;	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B;	HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2. MICROGLOBULN; CHAIN: B;	HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE:	CHAIN: P; LY49A; CHAIN: C, D;		MANNOSE-BINDING PROTEIN- C; IRDL 6 CHAIN: 1, 2; IRDL 7	MANNOSE-BINDING PROTEIN-	C; IKUL 6 CHAIN: 1, 2; IRDL 7	LECTIN MANNOSE-BINDING	PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM
SEQFOL D score		73.96							,	61.70			64.49	
PMF score			09.0		0, 0	0.43					0.70			
Verify score			0.60			0.81		<del></del>			0.41			
Psi Blast		3e-28	1.5e-30		135.02	1.36-27				1.2e-26	1.2e-26		4.5e-23	
END		291	292		202	767				780	289		291	
STAR T AA		153	162		160	6			ļ	5/1	176		127	
CHAI N ID		∢	ပ	-	c	1					1		7	
PDB ID		1qdd	1403		1003	3			F	Irai	Irdi		E E	
SEQ ID NO:		1803	. 1803		1803				1803	1003	1803	2001	1802	

PDB annotation	TOUR OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERS	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C. 2 TYPE LECTIN, ANTIFREEZE PROTEIN			HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION			CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
Coumpound	3 IRTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALMODULIN; CHAIN: A;
SEQFOL D score		-	61.86						
PMF score		0.41		0.54	0.87	0.36	0.49	09.0	0.93
Verify score		0.52		0.57	0.10	-0.07	-0.04	0.23	0.11
Psi Blast		1.3e-29	1.3e-25	1.3e-25	4.8e-24	1.6e-29	8e-36	8e-32	9.6e-34
END		289	290	288	08	18	81	81	81
STAR T AA		162	175	176		-	-	<u>∞</u>	-
CHAI N ID		A	A	A	В	⋖			4
PDB ID		2afp	2msb	2msb	laui	1cdm	1cll	1cmf	lexr
SEQ ID	ÿ.	1803	1803	1803	1804	1804	1804	1804	1804

PDI3 annotation	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE	CONTRACTION		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING	PROTEIN/PEPTIDE)	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,	SNRNP, RIBONUCLEOPROTEIN CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Coumpound	CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: NULL;	CONTRACTILE SYSTEM	PRUTEIN TROPONIN C 1TOP 3 CALCIUM BINDING PROTEIN CALMODULIN (TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	4 CALMODULIN; CHAIN: A; RS20; CHAIN: B;		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;
SEQFOL D score									
PMF score	0.89	1.00	0.95	0.98	0.98		1.00	0.99	0.98
Verify score	0.39	0.23	0.25	0.52	0.30		0.60	0.58	0.57
Psi Blast	8e-30	1.6e-24	1.6e-24	1.4e-30	3.2e-35		8e-24	8e-24	6.4e-34
END	81	81.	81	81	82	3	067	250	227
STAR T AA	14	-	-	12	1		+ 11	114	4
CHAI N ID	A			∢	A		c	Ö	A
PDB ID	1771	Itef	1 top	1trc	lvrk	1001		1a9n (	1 d0b1
SEQ ID NO:	1804	1804	1804	1804	1804	1806		1806	1806

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PDB annotation	ADHESION CELL ADHESION I FITCINE RICH	REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSIAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT		CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	CYLINDER, DYNEIN, 2 CHI AMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BEIA-BEIA-ALPHA	CHLAMYDOMONAS, FLAGELLA		COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE, NUCLEOTIDE EXCHANGE 2
Coumpound	n reconstant prin. Citatal. A.	INTEKNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A.C. RAB	GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFE RASE BETA SUBUMIT: CHAIN:	B. D.	OUTER ARM DYNEIN; CHAIN: A:		OUTER ARM DYNEIN; CHAIN:	<b>A</b> ;	OUTER ARM DYNEIN; CHAIN:	A;			NUCLEOTIDE EXCHANGE FACTOR GRPE; CHAIN: A, B; MOLECULAR CHAPERONE
SEQFOL D score																	
PMF score		1.00	0.99		0.88				0.78		0.46		0.01			-	0.11
Verify score		0.39	0.51		0.45				-0.40		-0.60		-0.30				-0.10
Psi Blast		1.3e-32	3.2c-25		3.2e-17				3e-14		1.6e-28		3.2e-13				0.0015
END		235	249		207		· · · · · · ·		191		251		179				398
STAR T AA		25	132		84				1111		125		E				250
CHAI N ID		A	A		A	•			A		4		4	<u>.</u>			∢
PDB ID		140b	Idce		1dce				1ds9		1ds9		1469	<u>}</u>			1dkg
SEQ	ÖN	1806	1806		1806				1806		1806		1808	2001			1809

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PDB annotation	FACTOR, COIL ED-COIL, COMPLEX (HSP24/HSP20)	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COLLED COLL, CONTRACTILE PROTEIN				HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPIATASE,	HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE,	HYDROLASE HYDROLASE UTEROFERRIN, TRAP, PAP, TARTRATI: RESISTANT ACID PURPLE ACID PHOSPHATASE.	TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOENZYME, ITTEROFFREN HYDDOL A SE	HYDROLASE (PHOSPHORIC MONOESTER) PURPLE ACID PHOSPHATASE, HYDROLASE (PHOSPHORIC MONOESTER)
Coumpound	DNAK; CHAIN: D;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;		LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4		PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;	II PURPLE ACID PHOSPHATASE; CHAIN: A;		PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;
SEQFOL D score							61.74		63.06		
PMF score		-0.07	0.07		0.28			0.34		<u> </u>	0.52
Verify score		90.0	-0.12		0.21			-0.19			0.01
Psi Blast		3e-08	7.5e-13	7	1.6e-05		4.5e-10	4.5e-10	0.00014		1.5e-12
END AA		367	374		528		310	239	320		247
STAR T AA		143	102		439		32	39	28		10
CHAI N ID		В	ď		∢		∢	∢	A		4
PDB ID		1dn1	Iquu	1	Ises	+	Iqhw	lqhw l	lute		4kbp /
SEQ ID NO:		1809	1809	0,0	1812		81	1814	1814		1814

PDB annotation	PATA PRIDENCE DE CHEIN/RNA TRA	RNA-BINDING ENGLEMENT PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	METAL TRANSPORT MAYS, STOOTS, CALGRANULIN A CALCIUM- BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR_RELATED PROTEIN 8, S100 PROTEIN		NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN OF SNRNY A PROTEIN; RNA BINDING DOMAIN; NUCLEAR PROTEIN	RNA BINDING DOMAIN KNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME
Coumpound	IN TAXABLE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE TO SERVICE	SXL-LETHAL PROTEIN; CHAIN; A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*) I IP*( IP*( IP*UP*UP*U IP*)	NUCLEOLIN RBD2; CHAIN: A;	MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score								
PMF score		0.46	0.12	0.21	0.13	0.55	0.31	0.18
Verify score		-0.30	-0.15	0.07	-0.32	0.29	0.31	-0.10
Psi Blast		3.2e-05	9.6e-09	0.0045	3.2e-05	0.003	0.0093	6.4e-05
END		272	250	149	272	267	256	257
STAR T AA		195	180	101	195	188	195	195
CHAI N ID		A	A	A				A
PDB U		1b7f	156	1mr8	1sx1	2u1a	2ula	3sxl
SEQ	NO:	1815	1815	1815	1815	1815	1815	1815

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PDB annotation	DOSAGE COMPENSATION	-	ļ · · · · ·	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD,	HYDROLASE HAD-FAMILY ALPHA/BETA CORE DOMAIN, MG(II) BINDING SITE, 5-2 HELIX	BUNDLE	DEHALOGENASE DEHALOGENASE, HYDROLASE		ELECTRON TRANSPORT ELECTRON	IKANSPORT, IRON-SULFUR	TRANSPORT INON-SILETTE	ELECTRON TRANSFER (IRON-	ELECTRON TRANSPORT TWO 4FE-	HYDROGENASE HYDROGENASE	CYTOCHROME CS53, ELECTRON	TRANSFER COMPLEX		HYDROGENASI: HYDROGENASE,	CYTOCHROME C553, ELECTRON TRANSFER COMPLEX		
Coumpound			EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	PHOSPHONOACETALDEHYDE HYDROLASE; CHAIN: A, B, C, D;	1 2 1141 6 4 615	DETALOGENASE; CHAIN: NULL:		7-FE FERREDOXIN; CHAIN:	7-FF FFRREDOYIN: CHAM.	NULL;	FERREDOXIN; ICLF 5 CHAIN:	2[4FE-4S] FERREDOXIN; CHAIN: A	FEI-HYDROGENASE (LARGE	SUBUNIT); CHAIN: A; [FE]-	SUBUNIT): CHAIN: D:	CYTOCHROME C553; CHAIN: E	[FE]-HYDROGENASE (LARGE	HYDROGENASE (SMALL	SUBUNIT); CHAIN: D;	CYTOCHROME C553; CHAIN: E
SEQFOL D score			,													<del>-</del>					
PMF score			-0.14	0.05	0.64	010			-0.19	-0.17		-0.17	-0.12	1.00				1.00			
Verify score			-0.00	-0.84	0.20	0.12	3		0.05	0.17		0.43	0.53	0.37				0.23			
Psi Blast			3.2e-09	0.006	96-06	3e-10			8e-14	1.1e-10		1.1e-10	1.6e-11	6.4e-68				36-92			-
END		200	305	69	143	316			219	254		661	200	519				504	····		
STAR T AA		30.	7/3	39	38	28			137	176	100	137	137	136			Ē	1/3			
CHAI N ID			∢	В	₹								A	A		-		c			
PDB ID		101	ICKI	lek1	1 fez	1zm			1bc6	1bc6	31-1	ICIL	1dur	1e08			9001				
SEQ ID NO:		1810	6101	1819	1819	1819			1820	1820	020	1820	1820	1820			1820	7070			

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PDB annotation	OXIDOREDUCTASE OXIDOREDUCTASE	OXIDOREDUCTASE OXIDOREDUCTASE	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM	HYDROGENASE FE-ONL Y HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN 1WO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIFLE
Coumpound	PERIPLASMIC HYDROGENASE	PERIPLASMIC HYDROGENASE 1: CHAIN: A:	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L,	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M:	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M;		ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE
SEQFOL D score	232.77		223.69						52.84	
PMF		1.00		1.00	1.00		0.01	0.36		0.43
Verify		0.33		0.40	0.61		-0.18	-0.09		-0.34
Psi Blast	1.4e-85	1.4e-85	4.5e-92	3.2e-68	4.5e-92		6e-09	1.5e-07	9e-12	9e-12
END	574	572	524	519	504		344	207	302	340
STAR T AA		69	117	122	173		104	51	54	56
CHAI N ID	4	4	H	J	,-1		4	. ⋖	A	A
PDB	1feh	ifeh	lhfe	lhfe	lhfe		1cun	lcun	1quu	lquu
SEQ	NO:	1820	1820	1820	1820		1821	1821	1821	1821

PDB annotation	HELIX COILEI) COIL, CONTRACTILE PROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	ANTI-COAGULANT ANTI- COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	BLOOD COAGILATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COI:ACTOR/LIGAND)	APOPTOSIS TRAIL, DRS, COMPLEX	APOPTOSIS TRAIL, DRS, COMPLEX
Coumpound	ALPHA-ACTININ 2; CHAIN: A;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	HIRUSTASIN; CHAIN: NULL;	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U, D-PHE-PHE-ARG- CHLOROMETHYLKETONE CHEROMETHYLKETONE	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING I IGAND: CHAIN: D. E. I V. I.	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED
SEQFOL D score		51.57						
PMF score			-0.15	-0.03	-0.15	-0.19	-0.18	-0.12
Verify score			1.12	0.53	0.87	0.56	1.08	0.59
Psi Blast		9e-08	6e-11			7.5e-13	7.5e-11	4.5e-12
END		125	113	165	126	135	77	125
STAR T AA		29	45	36	4	7	2	31
CHAI N ID		L		<b>A</b>	V ,	۱ .	∢	Y
PDB ID		laut	16x7	1c2a	1c2a	Idan	1du3	1du3
SEQ ID NO:		1822	1822	1822	1822	1822	1822	1822

PDB annotation	VI THE CO. YOUR WAR	APOPTOSIS TRAIL, DR3, COMPLEA	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2	PLANT PROTEIN 1 WO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN 1 WO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,
		APOPTOS	SERINE P COAGUL, COAGUL, FETOMOI ANTIGEN PROTEIN ANTICOA	HOMOLOC DOMAINS	HOMOLOC DOMAINS	PLANT PRO HOMOLOC DOMAINS	SUGAR BINDINC LECTIN, HEVEIN SUPERANTIGEN	SUGAR BINDING LECTIN, HEVEIN SUPERANTIGEN	SUGAR BINDING LECTIN, HEVEIN SUPERANTIGEN	SUGAR I
Coumpound	APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN V; VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;
SEQFOL D score										
PMF score		-0.15	-0.14	-0.18	-0.12	0.16	0.17	-0.11	0.10	-0.17
Verify score		1.17	0.58	0.49	1:11	1.00	0.87	1.02	1.08	0.24
Psi Blast		6e-12	4.5e-11	1.4e-18	7.5e-19	1.4e-18	1.5e-19	1.2e-19	1.5e-19	7.5e-17
END		96	155		91	141	121	06	141	091
STAR T AA		6	47	12	4	52	19	4	52	75
CHAI N ID		A	I	A	<b>∀</b>	4	₹	. <b>A</b>	4	Ą
PDB ID		1du3	1dx5	1ehd	lehd	lehd	leis	leis	1eis	1eis
SEQ	Ö	1822	1822	1822	1822	1822	1822	1822	1822	1822

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PDB annotation	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE	SUGAR BINDING PROTEIN UDA:	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN I IDA:	LECTIN, HEVEIN DOMAIN, UDA,	SUPERANTIGEN, SACCHARIDE BINDING	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	HORMONE RECEPTOR HORMONE	RECEPTOR, INSULIN RECEPTOR	GI VCOPROTEIN GI VCOPPOTEIN	GI VCOPPOTERI CI VCOPPOTERI	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I	RECEPTOR, STAFRI; INCF 8
Coumpound	CHAIN: A;	AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN Y/ CHAIN: A;	AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN	I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN	MAGGLUTININ ISOLECTIN V/	CHAIN: A;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH	FACTOR RECEPTOR 1; CHAIN:	LAMININ: CHAIN: NI II I	LAMININ: CHAIN: NI II :	LAMININ; CHAIN; NULL;	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A,
SEQFOL D score									62.34										82.39	50.41	
PMF score		-0.13	-0.18	0.11		-0.14					-0.14		-0.14		-0.19		-0.15	-0.06			
Verify score		0.40	1.10	1.04		0.61					0.78		0.63		0.40		0.65	1.13			
Psi Blast		3e-18	6e-16	3e-21		6e-18			7.5e-20		7.5e-20		6e-13		1.5e-28		1.2e-19	7.5e-27	7.5e-27	1.5e-12	
END AA		121	06	141		160			177		175		128		178		178			171	1
STAR T AA		12		52		62	•		10		12		m		4		47	4	4	34	
CHAI N ID		<b>4</b>	<b>Y</b> .	A		<b>∀</b>			٧		∢		∢		∢	_				∢	
PDB ID		len2	len2	1en2		len2			lext		lext		lext		igi E		1klo	ıklo	1klo	Incf	1
SEQ ID NO:		1822	1822	1822		1822			1822		1822		1822		1822		1822	1822	1822	1822	

PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	EXTRACELLULAR MODULE OSTEONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	COMPLEX (BLOOD COAGULATIONINHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Coumpound	B; INCF 5	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score					55.26	
PMF score		-0.14	-0.19	-0.20		-0.20
Verify		0.68	0.10	0.14		0.44
Psi Blast		1.5e-12	6e-26	3e-23	3e-23	9e-14
END		155	171	179	178	123
STAR T AA		35	23	61	36	3
CHAI		A	∢	J	٦	L)
PDB ID		lncf	Inub	1pfx	Ipfx	1pfx
SEQ	NO:	1822	1822	1822	1822	1822

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PD/8 annotation	INHIBITOR, HIMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTIASE, CALCTUM- BINDING, HYDROLASE, 3	SERINE PROTITASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	SERINE PROTE ASE INHIBITOR SERINE PROTE ASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA NHIRITOR 2 SEPINE DE OCTOR SE
Coumpound		ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;
SEQFOL D score					63.90	
PMF score		0.54	-0.06	0.11		-0.12
Verify score		0.63	0.57	0.03		0.61
Psi Blast		1.2e-18	7.5e-21	7.5e-25	7.5e-25	1.5e-18 (
END		134	147	. 921	180	117
STAR T AA		55	43	71	71	∞
CHAI N ID						
PDB ID		1skz	1skz	1skz	I skz	1skz
SEQ ID NO:		822	1822	1822	1822	1822

PDB annotation	INHIBITOR, THROMBOSIS			ANTH COACIT ANT ANTI-	AN II-COAGOLANT PEPTIDIC COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR	APOPTOSIS TRAIL, DR5, COMPLEX					BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
Coumpound	1	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	+	HIRUSTASIN; CHAIN: NOLL;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND: CHAIN: D, E, F, J, K, L;	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NIMR\$) 1MHUA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MHUA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MRTA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MRTA 2	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score		107.39						65.07		63.47	
PMF score			0.03		0.07	-0.12	1.00		1.00		0.10
Verify			0.57		0.23	0.07	0.40		0.49		0.34
Psi Blast		6e-30	3e-26		4.5e-20	3e-08	9c-16	9e-16	9e-16	9e-16	7.5e-06
END		158	160		107	107	108	108	108	108	106
STAR T AA		2	2		50	49	78	78	78	78	54
CHAI N ID		A	<			<b>⋖</b>					L
PDB		9wga	9wga		1bx7	1du3	1mhu	1mhu	lmrt	1mrt	1xka
SEQ ID	NO:	1822	1822		1824	1824	1824	1824	1824	1824	1824

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PI)B annotation			CALCIUM-BINDING PROTEIN CALB; CALCIUM++/I)*HOSPHOLIPID BINDING PROTEIN 3 CALCIUM	BINDING PROTEIN, CALCIOM- BINDING PROTEIN CALCIUM-BINDING PROTEIN CALB; CALCIUM+FHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM4	BINDING PROTEIN TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES, PODIS: 1 EUPERAL	TRANSCRIPTION REGULATION ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS.	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS,	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-RIMMG	HYDROLASE HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING
Coumpound	METALLOTHIONEIN METALLOTHIONEIN ISOFORM IT AACTO 3	II #M123 METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT23	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;
SEQFOL D score		127.57							
PMF score	0.15		1.00	0.90	0.13	1.00	0.98	0.01	0.28
Verify score	-0.09		0.47	0.27	0.33	0.68	0.70	0.17	0.37
Psi Blast	1.3e-14	1.3e-14	4.8e-42	3.2e-37	0.00075	3.2e-46	1.46-27	1.1e-12	1.2e-15 (
END	108	108	491	646	109	484	639	480	639
STAR T AA	48	48	355	528	09	355	510	366	526
CHAI N ID			A.	A		A	A	4	V V
PDB ID	4mt2	4mt2	1a25	1a25	1bor	1byn ,	Ibyn /	lcjy /	1cjy A
SEQ ID NO:	1824	1824	1825	1825	1825	1825	1825	1825	1825

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PDB annotation		HYDROLASE	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER, CAI CHIM-RINDING.	PHOSPHOLPASE C, 3 PHOSPHOINGSITIDE-SPECIFIC	TIPID DEGRADATION PLC-D1:	PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID DEGRADATION 2 TRANSDICER.	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA	SANDWICH, CALCIUM ION, C2	ENDOCYTOSIS/EXOCYTOSIS BETA	SANDWICH, CALCIUM ION, C2	DOMAIN	TRANSFERASE CALCIUM++, PHOSPHOT IPIN BINDING PROTEIN	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	KINASE C	TRANSFERASE CALCIUM++,
Coumpound			PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B.			PATOSBIJORIOSITIDE SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	B;				PHOSPHOINOSITIDE-SPECIFIC	B.	î			SYNAPTOTAGMIN III: CHAIN:	A;	SYNAPTOTAGMIN III: CHAIN:	A:		PROTEIN KINASE C, ALPHA	IYPE; CHAIN: A;			PROTEIN KINASE C, ALPHA
SEOFOL	D score																\ \-									
PMR	score		0.62			ļ	0.12		·- <u></u>			0.58					-	0.1	27.0	0.40		96.0				0.31
Varify	score		0.19				-0.07					0.16					į	0.47		0.24		0.33				0.38
Dei Rlact	TOWN TO THE T		4.5e-15				6e-13					4.5e-15					000	3.26-88	3	4.8e-33		1.3e-45				6.4e-40
END	AA AA		467				620					467						649	į	671		494				929
CTAD	TAA		370				526					370				,	-	357		512		354				510
1 1 1	NED		A				A					В						⋖		٧		A				A
200	20 E		1djx				1djx					1djx						1dqv		1dqv		Idsy				1dsy
	E SEC	Q	1825				1825					1825			_			1825		1825		1825				1825

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PDB annotation	PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN	METAL BINDING PROTEIN RING FINGER PROTI:IN MATI; RING	HYDROLASE ('ALB DOMAIN; HYDROLASE ('2 DOMAIN; HYDROLASE, ('2 DOMAIN, CALB	HYDROLASE CALB DOMAIN; HYDROLASE, (22 DOMAIN, CALB	DOMAIN DNA-BINDING PROTEIN V(D)J	RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J	RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINICLEAR CLISTER ZINC	FINGER, DNA-BINDING PROTEIN								TRANSPORT PROTEIN FYVE
Coumpound	TYPE; CHAIN: A;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI;	PHOSPHOLIPASE A2; CHAIN: NULL;	PHOSPHOLIPASE A2; CHAIN: NULL;	RAG1; CHAIN: NULL;				CALCIUM/PHOSPHOLIPID BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTFIN	SYNAPTOTAGMIN I (FIRST C2	DOMAIN (CALB) IRSY 3	CALCIONIPHOSPHOLIPID BINDING PROTEIN	SYNAPTOTAGMIN I (FIRST C2	PHOSPHATIDYLINOSTTOL-3- PHOSPHATE BINDING FYVE
SEQFOL D score								;	81.61				+	•		
PMF		0.10	0.41	0.23	0.03						1.00		90 0	?		0.16
Verify		0.10	-0.18	0.31	0.21						0.81		0.48	)		0.04
Psi Blast		0.00045	1.5e-16	7.5e-17	0.003			1 80.46	4.06-40		4.8e-46 (		1.6e-27			0.00075
END		601	480	631	109			483	Ç Ç		482		636		i	91
STAR T AA		8	373	528	40			347	}	2.20	ccc		510			09
CHAI N ID		∢				,										∢
PDB CI		1g25	lrľw	Irlw	Irmd			Irsv	 }				lrsy			lvfy
SEQ NO:		1825	1825	1825	1825			1825		1076	192		1825			1825

PDB annotation		MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2- DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	
Coumpound		CHAIN: A;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	
SEQFOL	D score			71.27			69.53	72.01	
PMF	score		69.0		1.00	0.58			
Verify	score		0.40		0.62	0.53			
Pei Blast			3e-22	3e-22	3.2e-29	1.4e-46	4.8e-53	1.1e-60	
END	AA		120	131	496	649	169	170	
CTAB	TAA		01	ω	357	512	29	26	
CUAI	NB		В	В	A	A		4	
guu	<b>a</b> a		1zbd	1zbd	3rpb	3rpb	1cll	lvrk	
09.5	36	ö	1825	1825	1825	1825	1828	1828	

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PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COAGULATIONINHIBITOR) COMPLEX (BLOOD COAGULATIONINHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COAGULATION/INHIBITOR) BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGILATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/CO?ACTOR/LIGAND)	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
Coumpound	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG. CHLOROMETHYLKETONE	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE	CHANNER WITH CHAIN; C; DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN; H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN; X, Y;
SEQFOL D score	58.73			60.57	
PMF score		-0.17	0.96		0.99
Verify score		0.14	0.10		0.26
Psi Blast	1.3e-20	1.3e-20	6.4e-16	1.5e-22	6.4e-16
END	145	202	231	193	231 (
STAR T AA	47	73	152	54	152
CHAI N ID	J.	J	ъ	1	J
PDB ED	laut	laut	ldan	Idan I	ldva I
SEQ ID NO:	1833	1833	1833		1833

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PDB annotation		MATRIX PROTEIN  EXTRACELLULAR MATRIX,  CALCIUM-BINDING,  GLYCOPROTEIN, 2 REPEAT,  SIGNAL, MULTIGENE FAMILY,  DISEASE MUTATION, 3 EGF-LIKE  DOMAIN, HUMAN FIBRILLIN-1  FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	COMPLEX(SERINE PROTEASE(COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE(COFACTOR/LIGAND), BLOOD CLOTTING GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Commonad		FIBRILLIN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I; LAMININ; CHAIN: NULL; LAMININ; CHAIN: NULL; LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I; FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
TOTOTO	SEQFOL D score	56.72	54.06	70.82	64.61
5	score			0.43	-0.12
	Verity score			0.32	0.10
	Psi Blast	1.36-15	9e-14	16-28 1.1e-20	6e-35 6e-35
}	END	226	173	205	218
	STAR T AA	149	10	95	22 22
	CHAI N ID		A	4	л н
	PDB ID	lemn	lext	11ak 11klo 11klo	1pfx 1pfx 1pfx
!	SEQ ID	1833	1833	1833 1833	1833

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PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTIZASE, CALCIUM- BINDING, HYTROLASE, 3	SERINE PROTISASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGIJLATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
Commpound		FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: 1;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA
SEQFOL D score					55.94	
PMF score		0.07	0.62	0.98		0.18
Verify score		-0.16	0.07	0.30		0.04
Psi Blast		66-29	1.5e-21	6.4e-15	7.5e-24	7.5e-24
END		226	226	231	561	207
STAR T AA		92	156	156	16	92
CHAI N ID		L)	ı	J	J	1
PDB ID		Ipfx	lqfk	lqfk	1qfk	1qfk
SEQ NO:		1833	1833	1833	1833	1833

PDB annotation			PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN		
Coumpound		(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PHOSPHOLIPASE A2; CHAIN: A, B;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
SEQFOL	D score							59.27		78.80	
PMF	score		0.63	0.19	0.16	-0.12	0.64		0.06		_
Verify	score		-0.02	0.27	0.23	0.03	0.18		0.32		
Psi Blast			1e-23	le-23	3e-21	4.5e-18	3e-18	1.1e-21	1.16-21	7.5e-25	
END	¥¥		226	125	196	130	226	208	207	207	
STAR	TAA		137	43	72	34	156	91	92	28	
CHAI	NID					A	Н	L	1	4	
aua	2 8		1tpg	1tpg	1tpg	lvap	1xka	1xka	Ixka	9wga	
Caro	Z a ;	 Oz	1833	1833	1833	1833	1833	1833	1833	1833	

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PDB annotation	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN,	VISUAL PIGMENT SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RISTINAL PROTEIN, VISUAL PIGMENT		RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SI'LICING REGULATION, RNP DOMAIN, RNA COMPI EV	TRANSFERASIS TYPE II DNA- (CYTOSINE N4) METHYLTRANSFERASE, AMINO 2 METHYLATION, SELENOMETHIONINE, MULTIWAVELENGTH ANOMALOUS	GENE REGULATION/RNA POLY(A) GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULA TIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/INA
Соитроипа	RHODOPSIN; CHAIN: A, B	RHODOPSIN; CHAIN: A, B		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5:- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*IP*IP*IP*IP*IP*IP*IP*IP*IP*IP*IP*IP*IP	N-4 CYTOSINE-SPECIFIC METHYLTRANSFERASE PVU II; CHAIN: A;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N,	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'. R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T;
SEQFOL D score							
PMF score	-0.07	0.10		0.36	0.27	0.24	-0.19
Verify	0.11	-0.14		-0.03	-0.57	-0.34	0.05
Psi Blast	3e-20	7.5e-18		1.6e-19	4.5e-05	6.4e-23	3.2e-26
END	320	299		144	480	150	237
STAR T AA	4	4			433	59	75
CHAI N ID	∢	В		∢	∢	4	В
PDB ID	8841	1 f88		1671	0	levj	lcvj
SEQ ID NO:	1834	1834		1835	1835	1835	1835

PDB annotation	TRANSFERASE METHYL TRANSFERASE	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER	RNA BINDING PROTEIN KNA- BINDING DOMAIN	TRANSFERASE RRNA METHYLTRANSFERASE ERMC, COFACTOR ANALOGS	TRANSFERASE RRNA METHYLTRANSFERASE ERMC', COFACTOR ANALOGS	TRANSFERASE (METHYL TRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION	METHYLTRANSFERASE GNMT, S- ADENOSYL-L-METHIONINE):
Coumpound	GLYCINE N- METHYLTRANSFERASE;	CHAIN: A, B, C, D; HU ANTIGEN C; CHAIN: A;	MJ0882; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A:	ERMC' METHYLTRANSFERASE; CHAIN: A;	ERMC' METHYLTRANSFERASE; CHAIN: A;	CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;	GLYCINE N- METHYLTRANSFERASE;
SEQFOL D score											
PMF	0.17	0.16	0.75	0.62	0.03	0.83	0.06	0.58	0.05	0.66	0.05
Verify	-0.57	-0.02	0.37	0.19	-0.51	0.20	0.27	-0.06	-0.12	0.23	-0.47
Psi Blast	1.2e-14	3.2e-17	9.6e-20	1.3e-13	3.2e-11	1.3e-13	3.2e-23	6e-21	6.4e-05	1.5e-15	1.5e-10
END	492	144	567	139	280	492	144	592	524	538	492
STAR	424	72	421	73	402	420	74	410	413	424	426
CHAI	A	A	A	₹.	1	_	<b>∀</b>	<	4		4
PDB	1d2h	1d9a	1dus	1fjc	1g6q	1g6q	1hd1	1qam	Iqam	1vid	1xva
SEQ	NO: 1835	1835	1835	1835	1835	1835	1835	1835	1835	1835	1835

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	DD 5 cm of of c
ΑÖ	9	N ID	TAA	AA		score	score	D score		TO SUBOLITION
									CHAIN: A B.	GI VORIE MERITRY OF ANTONIO
1835	2mss	А	74	144	4.8e-18	-0.04	0.00		MUSASHII; CHAIN: A;	RNA BINDING PROTEIN RNA-
1835	2sxl		73	152	8c-18	0.04	0.35		SEX-LETHAL PROTEIN; CHAIN: NULL;	
1835	3sxl	A	61	137	8e-18	0.10	-0.05		SEX-LETHAL; CHAIN: A, B, C;	SPLICING RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME
										DOSAGE COMPENSATION
1836	lbuo	∢	4	85	3.2e-16	0.37	-0.05		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGIRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC
1836	1gof		204	505	1.6e-06	-0.33	0.34		OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE	LEUNEMIA, GEINE REGULATION
1836	1gof		217	450	7.5e-13	-0.42	0.13		(E.C.I.I.S.9) (FH 4.2) IGOF 3 OXIDOREDUCTASE(OXYGEN(	
1836	1gof		246	372	1.5e-15	-0.23	0.07		(E.C.1.1.5.9) (PH 4.5) 1GOF 3 OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
200,			1							
1837	Idan	7	285	370	4.8e-10	-0.00	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L. H.	BLOOD COAGULATION, SERINE PROTEASE COMPLEX COLFACTOR
					!				(-) (-)	THE THE POWER THAT CONTRACTOR

PDB annotation		2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERNE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)			HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
Coumpound		SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;
SEQFOL	D score						
PMF	score		-0.20	-0.20	-0.20	-0.19	-0.20
Verify	score		0.04	0.21	0.09	0.10	0.27
Psi Blast			1.1e-12	3.2e-08	4.8e-10	1.1e-12	3.2e-08
END	AA		449	583	370	449	583
STAR	TAA		361	530	285	361	530
CHAI	N II		1	1	٦	н	i i
PDR	a		1dan	Idan	1dva	ldva	1dva
SEO	je;	Ö	1837	1837	1837	1837	1837

PD)3 annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMANN, HUMAN FIBRILLIN-1	MATRIX PROTEIN MATRIX PROTEIN MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE BOWANN, HUMAN FIBRILLIN-I	MATRIX PROTIEN MATRIX PROTIEN EXTRACELLULAR MATRIX, CALCIUM-BININIG, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMANN, HUMAN FIBRILLIN-I	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HEIX CAI CHIM BINDING	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HEI IX CAI CHIM BINDING	BLOOD COAGULATION 2 SERINE
Coumpound	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN; NULL;  FIBRILLIN; CHAIN; NULL;  FIBRILLIN; CHAIN; NULL;	LOW-DENSITY LIPOPROTEIN I RECEPTOR; CHAIN: A;	LOW-DENSITY LIPOPROTEIN I RECEPTOR; CHAIN: A;	BLOOD COAGULATION FACTOR VILA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;
SEQFOL D score						
PMF score	-0.19	-0.17	-0.20	-0.20	-0.20	-0.20
Verify score	0.19	0.07	0.03	0.03	0.13	0.22
Psi Blast	1.4e-10	3.2e-09	4.8e-09	1.6e-11	4.8e-09	3.2e-08
END	185	227	583	182	221	583
STAR T AA	107	149	530	102	143	530
CHAI N ID				A	¥	7
PDB ID	lemn	lemn	lem <b>n</b>		1f5y	1fak
SEQ ID NO:	1837	1837	1837	1837	1837	1837

PDB								
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation		PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA;
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF	Coumpound		SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: 1;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA
PDB   CHAI   STAR   END   Psi Blast   Verify   Score	SEQFOL	D score						
PDB   CHAI   STAR   END   Psi Blast	PMF	score		-0.13	-0.19	-0.15	-0.19	-0.20
PDB   CHAI   STAR   END	Verify	score		0.22	0.16	0.03	0.02	0.08
PDB   CHAI   STAR	Psi Blast			1.16-12	1.6e-11	4.8e-10	6.4e-12	3.2e-08
PDB CHAI  ID NID  Ipfx L  Iqfk L  Iqfk L	END	AA		409	449	243	449	583
PDB IDF IDF IDF IDF IDF IDF IDF IDF IDF IDF	STAR	TAA		328	361	152	365	530
PDB DD DD DD DD DD DD DD DD DD DD DD DD D	CHAI	N ID		H	<u></u>	1	L)	T
SEQ ID NO: 1837 1837 1837	PDB	A		1pfx	l .	1qfk	1qfk	1qfk
	SEO	A S		1837	1837	1837	1837	1837

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PDN annotation	BLOOD COAGULATION, SERINE PROTEASE		BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, HIDERMAL 2	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROAGULATION FACTOR, SERINE PROAGULATION FACTOR, SERINE PROAGULATION FACTOR, SERINE	GROWIN FACTOR LINE DOMAIN		HYDROLASE HYDROLASE, NAD	OXIDOREDUCTASE OXIDOREDUCTASE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
Coumpound	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C:	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	S-ADENOSYLHOMOCYSTEINE HYDROI A SE: CHAIN: A B:	TROPINONE REDUCTASE-1; CHAIN: A, B;
SEQFOL D score								
PMF score		-0.19	-0.20	-0.20	-0.14	-0.14	0.00	0.21
Verify score		0.19	0.22	0.04	0.21	0.01	-0.09	0.34
Psi Blast		3e-15	1.6e-08	4.8e-11	9.6e-16	4.8e-16	0.0032	0.00064
END	i	470	585	158	403	476	207	215
STAR T AA		303	530	73	250	275	163	173
CHAI N ID		Ą	ı	7	A	4	Y	4
PDB ID		lvmo	1xka	1xka		9wga	1a7a	lael
SEQ ID NO:		1837	1837	1837		1837	1838	1838

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PDB annotation	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE	OXIDOREDUCTASE NAD- DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2 OXIDOREDUCTASE	OXIDOREDUCIASE (CH-UH(D)- NAD(A)) OXIDOREDUCTASE ICDO 15	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1CDO 15	OXIDOREDUCTASE SHOKI-CHAIN DEHYDROGENASE, OXIDOREDUCTASE	OXIDOREDUCTASE KETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD	OXIDOREDUCTASE BETA1 ADH; IDEH 9 NAD+ DEPENDENT
Coumpound	TROPINONE REDUCTASE-1; CHAIN: A, B;	CIS-BIPHENYL-2,3- DIHYDRODIOL-2,3- DEHYDROGENASE; CHAIN: NULL;	L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B;	ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	HUMAN BETAI ALCOHOL DEHYDROGENASE; 1DEH 7
SEQFOL D score				56.21			64.19		
PMF score	0.05	0.25	0.89		1.00	0.03		1.00	1.00
Verify score	0.44	-0.07	0.67		0.64	0.19		0.81	0.63
Psi Blast	0.00064	4.8e-05	0.00013	1.3e-76	1.3e-76	3.2e-05	4.8e-75	4.8e-75	3.2e-81
END	215	222	221	367	366	261	367	366	366
STAR T AA	173	173	173		25	173	-	26	25
CHAI	В		A	A	4	4	4	A	A
PDB ID	lael	1bdb	1c1d	1cdo	1cdo	1cyd	IdIt	1d1t	1deh
SEQ	NO: 1838	1838	1838	1838	1838	1838	1838	1838	1838

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P))B annotation	ALCOHOL DISHYDROGENASE 1DEH	OXIDOREDUCTASE BETA1 ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DI!HYDROGENASE IDEH	ALCOHOL DEHYDROGENASE	ALCOHOL DEHYDROGENASE OXIDOREDUCTASE DEHYDROGENASE, ALCOHOL,	NICOTINAMIDE COENZYME,   STEROID 2 BINDING					OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP		OXIDOREDUCTASE	OXIDOREDUCTASE, ZINC, NADP	OXIDOREDUCTASE	OXIDOREDUCTASE					
Соитроинд	CHAIN: A, B; 1DEH 8	HUMAN BETAI ALCOHOL DEHYDROGENASE; IDEH 7 CHAIN: A, B; IDEH 8	ALCOHOL DEHYDROGENASE,	ALCOHOL DEHYDROGENASE; CHAIN: A, B;		OXIDOREDUCTASE 3-ALPHA,	DEHYDROGENASE	COMPLEXED WITH	CARBENOXOLONE 1HDC 4	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A,	В, С, Д;	NADP-DEPENDENT ALCOHOL DEHVDROGENASE: CHAPL	B, C, D;	FLAVOCYTOCHROME C3	FUMARATE REDUCTASE; CHAIN: A. D:	OXIDOREDUCTASE QUINONE	COMPLEXED WITH NAMPH	1QOR 3	OXIDOREDUCTASE QUINONE	COMPLEXED WITH NADPH
SEQFOL D score		74.95								53.09						116.09				
PMF			1.00	1.00		0.45					00.	00.1		0.47					1.00	
Verify score			0.77	0.73		-0.03					0.00	65.0		0.28					0.75	1
Psi Blast		3.2e-81	1.6e-69	4.8e-77	10 50	7.0e-0/			;	1.66-51	160.51			0.0032		8e-70	<u> </u>		8e-70	
END		367	366	366	707	<b>+97</b>			3,5	369	267	<u> </u>		207		370		,	795	
STAR T AA		m	26	25	173	5/1				<del>5</del> 7	50	3	,	891		37	•	,	28	
CHAI N ID		4	¥.	¥		ζ .			\ \	€	4	4		₹		∢			<	
PDB ID		ldeh	le3i	1ee2	140	2011			1/201	Ive	1kev		,	1908		Iqor		+		
SEQ ID NO:		1838	1838	1838	1838				1930	000	1838		000	8581		1838		1020		

PDB annotation	OVIDOREDITOTA SE GITITATHIONE.	DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+	DEPENDENT ALCOHOL DEHYDROGENASE 2	GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE	OXIDOREDUCTASE GLUTATHIONE- DEPENDENT FORMALDEHYDE DEHXDROGENASE NAD+	DEPENDENT ALCOHOL	DEH I DROGENASE Z GLUTATHIONE DEPENDENT	FORMALDEHYDE DEHYDROGENASE	TRANSFERASE (METHYLTRANSFERASE) COMT;	TRANSFERASE,	METHYLIKANSFERASE, NEUROTRANSMITTER	DEGRADATION	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE	OXIDOREDUCTASE	OXIDOREDUCTASE	OXIDOREDIICTASE	OXIDOREDUCTASE		KINASE KINASE, SIGNAL	
Coumpound	1QOR 3	HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, R.	ú		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A,				CATECHOL O- METHYLTRANSFERASE;	CHAIN: NULL;			TRIHYDROXYNAPHTHALENE REDITCTASE: CHAIN: A. B.	NADP-DEPENDENT ALCOHOL	DEHYDROGENASE; CHAIN: A,	B, C, D;	DEHYDROGENASE; CHAIN: A,	B, C, D;	CALCHIM/CALMODULIN-	DEPENDENT PROTEIN KINASE;
SEQFOL D score		72.11												52.30					89 65	20000
PMF score					1.00				0.47				0.49			,	9. 			
Verify					0.60				0.51				-0.20				0.56			
Psi Blast		1.66-86			1.6e-86				0.0000				9.6e-05	4.8e-54			4.8e-54		00 00	9.06-09
END		367			366				268	·n			280	370	)		367		9,0	349
STAR T AA					27				164				173	24	4		52			12
CHAI		A			A								4		ζ		٧			
PDB		Iteh			Iteh				1vid				lybv	1-1/2	7 / Y		1ykf			1a06
SEQ	ÖZ	1838			1838				1838				1838	1020	1939		1838			1839

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PDR annotation	CALCIUM/CAL,MODULIN	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12;	SERINE/THRECONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE), PECEPTOP 2 SEPRIF (TEMPENINE	KINASE	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THRECONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SURINE/THREONINE	KINASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK, PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR I; TIVANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFER ASE
Coumpound	CHAIN: NULL;	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;			FK 506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;				C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			FGF RECEPTOR I; CHAIN: A, B;						
SEQFOL D score		58.79												62.45						-						70.22				<u></u>		
PMF score							90.0										,	0.00				0.01										
Verify score							-0.17										300	-0.33				-0.39					-					
Psi Blast		1.1e-15					1.5e-13						300	3.2e-27				1.5e-13			2,00	3.26-27				1.1e-26						
END AA		350					199						22.5	33/				19/			,;;	334				339						
STAR T AA		20				-	2,2						3	ر2			70	•			-	<b>,</b>				40						
CHAI N ID		മ				6	EQ.							<			\ \	τ.				<				∢						
PDB ID		1b6c	•			,	1000		_	~			1141.0	9,01			11.11	1038			+	1038			†	II.gk						1
SEQ ID NO:		1839				000	1839					,	1020	1639			1020	1032			1020	1037			1020	102%					_	

PDB annotation		PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FOFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	TRANSFERASE PIOU, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP			(TRANSFERASE/SUBSTRATE)
Coumpound	•	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	HUMAN CYCLIN-DEPENDEN I KINASE 2; CHAIN: NULL;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN:
SEOFOL	D score	71.37				61.82	
PMR	score		0.41	0.10	0.33		0.16
Verify	score		0.11	-0.20	-0.13		0.10
Dei Blact	T SI DIGGS	3.2e-26	3.2e-26	1.6e-27	1.4e-22	3.2e-26	3.2e-26
GNE	AA A	338	335	332	321	350	332
C.L. I.D	TAA	63	87	84	97	8	87
17710	NB	m	B	⋖		4	A
444	708 E	1fgk	lfgk	1fpu	lhcl	lir3	1ir3
	OF A	1839	1839	1839	1839	1839	1839

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PD3 annotation	TYROSINE KINIASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SITRSTRATE)	TYROSINE KINIASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	TRANSFERASF KDR; TYROSINE KINASE		CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE	PROTEIN	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECHIAR TRANSFERASE	COMPLEX (TRANSDUCER/TRANSDUCTION)	GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-	GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION.	PHOSPHORYLATION, G PROTEINS,	COMPLEX	(TRANSDUCER/TRANSDUCTION)	COMPLEX (7IN) BINGER (DNA)	COMPLEX (ZINC FINGER/DNA),
Coumpound	Ď	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;		TROPOMYOSIN; CHAIN: A, B, C, D		METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;						OGSR ZINC FINGER PEPTIDE:	CHAIN: A; DUPLEX
SEQFOL D score											11-11				
PMF		0.29	0.03		-0.20		-0.13	-0.19						0.00	
Verify score		-0.26	-0.38		0.14		0.19	0.53						-0.46	
Psi Blast		1.1e-24	1.6e-20		8e-09		1.3e-08	4.5e-09		***				8e-23	
END		347	336	į	176		164	112						161	
STAR T AA		84	87	(	7_		5	9						117	
CHAI N ID		¥	A		∢		٧	Д						A	
PDB ID		Iqcf	lvr2		g 131		Ireq	2trc						lalh	
SEQ ID NO:		1839	1839	0,01	1840		1840	1840						1841	

PDB annotation	Order	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	FROIDIN					•			COMPLEX (ZINC FINGER/DINA) ZINC FINGER, PROTEIN-DINA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
Coumpound		OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUFLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	TRANSCRIPTION REGULATION	EAST INCHASE TION   EACTOR ADDITION	130) 1ARD 3 (AMING	TERMINAL ZINC FINGER	DOMAIN (NMR. 10	STRUCTÚRES) 1ARD 4 (ADR1B)	1ARD 5	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;
SEQFOL	D score		75.37																										
PMF	score					0.93			0.25	Ì			0.33				0.87				0.81							0.22	
Verify	score					-0.18			0.06	2			-0.34				-0.66	!			-0.12						_	-0.12	
Psi Blast			6.4e-30			6.4e-30			3000	3.20-20			6.46-24	! }			6.4e-30	) ) )			1.6e-06							1.6e-38	
END	AA		249			247			201	107			400	2			428	ì			376							191	
STAR	T AA		991			167	}		10.6	<u> </u>			325	5			348	}		_	348							109	···
CHAI	MID		A			V	:			∢			4	<b>ć</b>			<b>\</b>	ζ										ပ	
PDB	<b>e</b>		lalh			1ath	:		;	lain			1014	19111			101	14111			lard							1mey	
SEQ	e è	2	1841			1841	1101		1	1841			1071	1501			1041	1041			1841							1841	

PDIS annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRIJCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/I)NA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/I)NA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN 2
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA CUTABLA B B B	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		Paris Cristian	DNA; CHAIN: A, B, D, E;	PROTEIN: CHARL OF O	INCIELLY, CHALLA: C, F, G;		Part Orrigin a	DNA; CHAIN: A, B, D, E;	CONSENSOS ZINC FINGER	FROIEIN; CHAIN; C, F, G;		Dark, Circum. n. n. n.	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROIEIN; CHAIN: C, F, G.
SEQFOL D score									83.84								•												<del>.</del>		
PMF score		86.0			00 -	2							66.0	77.0				0.00	77.0				0.80	70.0				6	 0.70		
Verify score		-0.01			0 11								0.14	+		•		0,40	2				010	61.0-				:	0.13	-	
Psi Blast		1.6e-47			1.6e-48				1.6e-48				8P-45	2			-	1.16-41				•	1 60.45	Ct-20:1		_		27 27	71-21-1		
END AA		219			247	:	•		248				282	}				400	3				428	3		_		247			1
STAR T AA		138			166				166				194					324					347	:			-	220	27		-
CHAI N ID		ບ			C				ပ				၁					၁					S	,			-	6	)		
PDB ID		Imey			Imey	`			Imey				lmey	•				lmey					Imey			-		Imev			1
SEQ ID NO:	]	1841			1841				1841				1841					1841					1841			_		1841			

PDB annotation	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTORE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	ZINC FINGER TRANSCRIPTION TACTOR SP1: 21NC FINGER	TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S GENE: NMR. TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION REGIII.ATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	CONTRICT TO ANGODIDATION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION REGULATION/DNA), RNA
Coumpound			DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER			SPIF2; CHAIN: NULL;		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	Citain: L, 1,				TEIIIA-CHAIN: A. D: 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;
SEQFOL D score																		24.20	2							
PMF			0.95			0.48				0.03		-0.11	• 4.00												0.49	
Verify			-0.26			0.03				-0.21		0.03													-0.25	
Psi Blast			6.4e-13			1 6e-13				8e-09		1.1e-20						22-22	2.25-33						3.2e-33	
END	en l		372			428	2			376		267	i					040	8/7						284	
STAR	WW T		345			401	Ē			348		105	3						711						139	
CHAI	OI N		G			ď	<u> </u>						¢						∢						V.	
PDB	3		1mey				comit -			1sp2		£ <del>+</del> 1	CIII					,	ltt6						1tf6	
SEQ	NÖ E		1841			1041	1041			1841		10/11	1041						1841						1841	

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PDE annotation	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTFIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION	REGULATIONDINA), RNA POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/J)NA) COMPLEX	REGULATION/DNA), RNA	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION	REGULATION(I)NA) YING-YANG 1;	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION 3 COMPLEY	(TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN DNA PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	,		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, E,	Circliv. D, C, E, f,		YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA:	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CIMIN: A, B,			VVI. CHABI. C. Apparo	I II; CHAIN: C; ADENO-
SEQFOL D score													77.97							
PMF score		0.19			0.04			0.19							-				0.78	7.7
Verify score		-0.30			-0.37			-0.16											-033	7
Psi Blast		4.8e-31			6.4e-34			3.2e-30			-		3e-32			-		-	3e-32	
END		437			488			219					248						247	
STAR T AA		297			348			109					140						143	
CHAI N ID		<b>4</b>			∢			ပ					C						C	
PDB ID	2	91110		77.57	0111			1ubd					1ubd						1ubd	
SEQ ID NO:	,	1841		1041	1+01			1841					1841	_					1841	

PDB annotation		REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN; C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1;
SEQFOL	D score			·		76.50	
PMF	score		0.04	0.40	0.01		0.62
Verify	score		-0.25	-0.46	-0.52		-0.12
Psi Blast			3.26-32	6.4e-30	4.8e-06	1.6e-32	6e-29
END	AA		281	428	371	283	252
STAR	TAA	·	174	332	323	138	140
CHAL	N II		ပ	U	∢	A	A
PDB	a		lubd	lubd	2drp	2gli	2gli
SEO	ja ş		1841	1841	1841	1841	1841

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PD B annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA).	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN AT DIA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRIIGTI IR AL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	ENDOCYTORIS/BYOCKERS	NSECT: PROTEIN, PROTEIN	COMPLEX. MULTI-SUBLINIT	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUILDE	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;		ALPHA SPECTRIN; CHAIN: A, B, C;	•		ALPHA SPECTRIN; CHAIN: A,	B, C;			on the same and the same same same same same same same sam	SYNIAXIN BINDING PROTEIN	I; CHAIN: A; SYNTAXIN IA; CHAIN: B:	SYNTAXIN BINDING PROTEIN	1: CHAIN: A: SYNTAXIN 1A:	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;			SYNTAXIN-14. CHAIN: A B C.	() (d (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	
SEQFOL D score																		-							
PMF score		-0.05		-0.17			0.00				000	-0.20		-0.20			-0.17			-0.19			-0.19		
Verify score		60.0		1.09			0.39				170	0.41		0.57			0.43	-	000	0.78			0.83		
Psi Blast		1.6e-32		1.5e-09			7.5e-05				4 50.10	01-20-4		1.5e-17			1.5e-11			1e-09			3e-16		
END		283		648			798				613	3		642			769		765	0/5			109	<del></del> -	
STAR T AA		146		511			995				437			481			513		447	Ì			485		
CHAI N ID		<b>A</b>		∢			∢				E C	1		В			ri Ti		\ 	ς .			A		
PDB ID		2gli		lcnu			lcnn				1dn1			1dn1		•	Igni		1072	3			lez3		7
SEQ ID NO:		1841	2,00	1845			1845				1845	!		1845		1046	1040	-	1845	}			1845		

PDB annotation	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCY LOSIS/EXOCY LOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPPNP, GPPNHP.	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	TRANSCRIPTION REGULATION SIGMA70; RNA POL YMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION	COMPLEX
Coumpound	SYNTAXIN-1A; CHAIN: A, B, C; END SYN SYN KD/		δ, В, С;	INTERFERON-INDUCED SIG GUANYLATE-BINDING HYI PROTEIN 1; CHAIN: A; 2 RI FAN		HUMAN SKELETAL MUSCLE CO ALPHA-ACTININ 2; CHAIN: A; HEI CO		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL; SIG SIGMA FACTOR; CHAIN: NULL;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL; SIC SIC RE	TRANSDUCIN; CHAIN: B, G; CO
SEQFOL D score	SYNTAXIN	SYNTAXII	SYNTAXII	INTERFER GUANYLA PROTEIN	SSO1 PRO	HUMAN S ALPHA-A	METHYL) MUTASE;	RNA POL SIGMA F	RNA POL SIGMA FA	TRANSDI
PMF score	-0.20	-0.17	0.00	-0.19	-0.20	-0.19	-0.08	-0.15	-0.20	-0.20
Verify score	1:1	0.98	0.21	0.74	0.55	0.70	0.48	0.76	0.40	0.22
Psi Blast	1.5e-16	3e-16	4.5e-05	3e-08	9e-13	3e-24	4.5e-31	4.5e-18	6e-17	1.5e-17
END	630	658	861	626	642	959	746	643	677	621
STAR T AA	511	526	739	485	485	460	451	485	486	488
CHAI N ID	A	A	⋖	٧	⋖	A	Ā			Ь
PDB ID	lez3	lez3	lez3	If5n	1fio	1quu	1req	Isig	1sig	2trc
SEQ	NO:	1845	1845	1845	1845	1845	1845	1845	1845	1845

PD 8 annotation	(TRANSDUCER/TRANSDUCTION) GT BETA-GANMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX	(TRANSDUCEIVTRANSDUCTION) COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX	(TRANSDUCER/TRANSDUCTION) COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
Coumpound	PHOSDUCIN; CHAIN: P;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;
SEQFOL D score				
PMF score		-0.19	-0.20	0.59
Verify score		0.29	0.23	-0.68
Psi Blast		1.56-20	1.5e-13	1.16-07
END		647	746	55
STAR T AA		513	577	29
CHAI N ID		<u>a</u>	Q	
PDB ID		2trc	2trc	1bor
SEQ SO BO		1845	1845	1849

PDB annotation	ACTIN BINDING PROTEIN ABP-120;	STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120;	ACTIN BINDING PROTEIN, STRICTURE, IMMUNOGLOBULIN,	GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120;	STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ACTIN	BINDING PROTEIN 120; ACTIN	BINDING PROTEIN,	IMMUNOGLOBOLIN, GELATION	+		BINDING PROTEIN,	IMMUNOGLOBULIN, GELATION	+	BINDING PROTEIN ACTIN	BINDING PROTEIN,	IMMUNOGLOBULIN, GELATION	FACTOR, ABP- 2 120	<u> </u>	BINDING PROTEIN 120; ACTUA	MANTINOGE OBLIEFY, GELATION	FACTOR, ABP-2 120		TRANSFERASE	
Coumpound	GELATION FACTOR; CHAIN:	NOTE;	GELATION FACTOR; CHAIN:	NULL;		GELATION FACTOR; CHAIN:	NOLL;	GET A TION EACTOR CHAIN: A.	B:	`		CHY AMONITA OTOB. CHAIN! A	GELATION FACTOR; CHAIN. A,   B;				GELATION FACTOR; CHAIN: A,	ú			GELATION FACTOR; CHAIN: A,	B;				GI VOINE N.	
SEQFOL D score	64.85							70 67	07.00																		
PMF			66 0	}		1.00							0.95		-		96.0				0.99				1	0.21	77.7
Verify			0.47	÷		0.54							0.11				0.52				0.52					000	20.02
Psi Blast	4.5e-30		4 50 30	4:36-30		1.3e-19			6e-36				1.6e-13				1.3e-19				6e-36	· ·				20.00	/.2e-00
END	200		907	476		499			515				494				528				528				-		351
STAR	397		000	398		398			306				359				395	,	_		397	}			-	  :  -	175
CHAI									⋖				A				A				4	4					Ą
PDB	Isi		_    -	Iksr		1ksr			1qfh				1qfh				1qfh				10fh	## 				-	1d2h
SEQ	8 S E	<u> </u>		1849		1849			1849				1849				1849				1940	10+2					1850

METHYLTRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN,	METHANOCOCCUS JANNASCHII TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED	ALFHA-BEIA, HEXAMER, 2 DIMER	ANTI-ONCOGENE, REPEAT, ANK	KEPEAT								COMPLEY (TB ANSCBIRTION	REGULATION/JNA) GABPALPHA:	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/I)NA), DNA-BINDING,	ANK VP IN PEDEATS	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA; GABPRETA : COMPI EX
METHYLTRANSFERASE; CHAIN: A. B. C. D:	MJ0882; CHAIN: A;	HNRNP ARGININE N- METHYLTRANSFERASE; CHAN: 1, 2, 4, 4, 6, 6,	VIII 111 1, 2, 7, 4, 7, 0,	TUMOR SUPPRESSOR PIGINK4A; CHAIN: NULL;	TB 4 Merrin 4 on my converse	IKANSFEKASE(PHOSPHOTRA NSFERASE) \$C-/AMP\$- DEPENDENT PROTEIN IN IN SE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	(CATALYTIC SUBUNIT) ALPHA	SER 139 1APM 4 REPLACED BY	ALA (/S139A\$) COMPLEX WITH	THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE DETTERGENT MEGA 8 1 APM 6	GA BINDING PROTEIN AL PHA:	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B:
					08.00	00.66			•												
	0.01	0.04		0.95									1.00		_	-				1.00	
	0.24	0.11		0.39					•				0.33								
	6.4e-09	1.3e-14		4.5e-32	4.5e-30		•				<del></del>		1.5e-36						1		
	294	292		899	349								604							) 50	
	177	148		538	-								447						1		
	⋖	1			E					•			<u> </u>								
;	Idus	1g6q		la5e	lapın		·				_	$\dashv$				_			┿		
	1850	1850	,	1853	1853							-					·- ·		十		$\dashv$
	METHYLTRANSFERASE; CHAIN: A. B. C. D:	METHYLTRANSFERASE; CHAIN: A, B, C, D; MJ0882; CHAIN: A;	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE;           1g6q         1         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N-METHYLTRANSFERASE;           CHAIN: 1, 2, 3, 4, 5, 6.         CHAIN: 1, 2, 3, 4, 5, 6.	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE;           Ig6q         I         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N-METHYLTRANSFERASE;           CHAIN: 1, 2, 3, 4, 5, 6;	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE; CHAIN: A; B, C, D; CHAIN: A;           Ig6q         I         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N-METHYLTRANSFERASE; CHAIN: I, 2, 3, 4, 5, 6; CHAIN: I, 2, 3, 4, 5, 6; CHAIN: I, 2, 3, 4, 5, 6; CHAIN: NULL;	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE; CHAIN: A, B, C, D;           1g6q         1         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;           1a5e         538         668         4.5e-32         0.39         0.95         TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE; CHAIN: A;           Lg6q         1         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;           1a5e         538         668         4.5e-32         0.39         0.95         TUMOR SUPPRESSOR PIGINK4A; CHAIN: NULL;           1apin         E         1         349         4.5e-30         99.80         TRANSFERASE(PHOSPHOTRA DEPENDENT PROTEIN KINASE	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE; CHAIN: A, B, C, D; CHAIN: A, B, C, D;           Ig6q         1         148         292         1.3e-14         0.11         0.04         HNRNP ARGININE N-METHYLTRANSFERASE; CHAIN: A, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 3, 4, 3, 4, 4, 3, 4, 3, 4, 4, 3, 4, 3, 4, 4, 3, 4, 4, 3, 4, 4, 3, 4, 4, 3, 4, 4, 3, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4,	1dus   A   177   294   6.4e-09   0.24   0.01   METHYLTRANSFERASE; CHAIN: A, B, C, D; M10882; CHAIN: A, B, C, D; M10882; CHAIN: A, C, D; M2   CHAIN: A, C, D; M2   CHAIN: A, C, D; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 3, 4, 5, 6; CHAIN: 1, 2, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4, 3, 4,	Idus         A         177         294         6.4e-09         0.24         0.01         METHYLTRANSFERASE;           Lig6q         1         148         292         1.3e-14         0.11         0.04         HINRNP ARGININE IN-METHYLTRANSFERASE;           La5e         238         668         4.5e-32         0.39         0.95         TUMOR SUPPRESSOR           Lapin         E         1         349         4.5e-30         99.80         TRANSFERASE(PHOSPHOTRA INFAL)           Lapin         E         1         349         4.5e-30         99.80         TRANSFERASE(PHOSPHOTRA INFAL)           Lapin         E         1         349         4.5e-30         99.80         TRANSFERASE(PHOSPHOTRA INFAL)           CATALYTIC SUBURITY ALPHA ISOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT WITH SIGOENZYME MUTANT SIGOENZYME MUTANT WITH SIGOENZYME MUTANT SIGOENZYME MUTANT SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGOENZYME SIGO	1dus A   177   294   6.4e-09   0.24   0.01   MIORRY: CHAIN: A, B, C, D;     1g6q   1   148   292   1.3e-14   0.11   0.04   HINRINP ARGININE N-METHYLTRANSFERASE;     1a5e   538   668   4.5e-32   0.39   0.95   TUMOR SUPPRESSOR     1apim   E   1   349   4.5e-30   99.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   99.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   99.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   99.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   TRANSFERASE(PHOSPHOTRA     1spim   E   1   349   4.5e-30   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   89.80   8	1dus   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN: A, B, C, D;     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   292   1.3e-14   0.11   0.04   HNRNP ARGININE N-     Lig6q   1   148   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149   149	1dus A   177   294   6.4e-09   0.24   0.01   MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, D; MIORB2; CHAIN: A, B, C, MIORB2; CHAIN: MIOLL; MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN: MIORB2; CHAIN:	1dus   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN: A; B, C, D;	1dus   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B, C, C, C, C, C, C, C, C, C, C, C, C, C,	1dus   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; A; B, C, D; CHAIN; C, C, C, C, S, S, C, C, C, C, S, S, C, C, C, C, C, C, C, C, C, C, C, C, C,	1dus	14ms   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN: A, B, C, D; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, C, C, C, C, C, C, C, C, C, C, C, C,	1dus   A   177   294   6.4e-09   0.24   0.01   MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, D; MJ0882; CHAIN: A, B, C, C, C, MJ082; CHAIN: A, B, C, C, C, MJ082; CHAIN: A, B, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: A, C, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, C, MJ082; CHAIN: B, C, C, C, C, C, C, C, C, C, C, C, C, C,	14us   A   177   294   6.44-09   0.24   0.01   METHYLTRANSFERASE; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, B, C, D; MI0882; CHAIN: A, C, B, C, C, C, C, C, C, C, C, C, C, C, C, C,	1dus   A   177   294   6.4e-09   0.24   0.01   MGTHYLTRANSFERASE; CHAIN: A, B. C, D; MJ082; CHAIN: A, B. C, D; MJ082; CHAIN: A, B. C, D; MJ082; CHAIN: A, B. C, D; MGTHYLTRANSFERASE; CHAIN: B, C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B. C, B

PDB annotation		(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TO ANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	-	GABPBETA1; COMPLEX	(TRANSCRIPTION PEGI II ATTON/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	+-		GABPBETAI; COMPLEA	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REFEATS,	╁		GABPBETAI; COMPLEX	REGULATION/DNA), DNA-BINDING,
Coumpound		DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA;	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DINA; CHAIN: D, E,			CA PRINCIPO DE CARENI AI DELA:	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;
SEQFOL	D score		94.92																	
PMF	score					1.00					00 1	1.00	<u>-</u>					1.00		
Verify	score					0.72					02.0	0.0						0.60		
Psi Blast			1.2e-45		-	6.4e-35					9, 0	1.2e-45						1.5e-44		
END	AA		705			704						737						770		
STAR	TAA		551			556						584						617		
CHAI	NID		В			В					-	<b>a</b>						В		
PINB	e		1awc			lawc						1awc						lawc		
SEO	i i	ON	1853			1853						1853						1853		

				1				Т								
PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, AMKYRIN REIPEATS, TRANSCEIPTION 2 EACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION)	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REFEATS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	GABPBETAL; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA) GARPAI DUA.	GABPBETAI; COMPLEX	REGULATION/DNA), DNA-BINDING,	Z NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPIEATS,	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SEKINE/I HREUNINE-PROTEIN KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	KECEPIOK 2 SEKINE/IHREONINE KINASE
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D. E:			FK506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B STIPPPEAMITY PECEPTOD	TYPE I; CHAIN: B, D, F, H;		
SEQFOL D score																
PMF		1.00		1.00				1.00				1.00	· · · · ·			-
Verify score		0.63		0.34				0.74			*	0.37				•
Psi Blast		1.5e-42		1.6e-32				36-35				3e-49				
END		805		802				828	_			276				
STAR T AA		651	1	656			100	/89				26		_		
CHAI N ID		щ		n			,	q				В				
PDB ID		Iawc		Iawc				2 2 2				1b6c				
SEQ ID NO:		1853	1062	1833			1963	661				1853				
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PDB annotation	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
Coumpound	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score									
PIMF score	0.49	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Verify score	0.37	99.0	0.58	0.76	0.32	0.51	0.21	0.77	0.63
Psi Blast	4.8e-10	4.5e-35	1.4e-40	1.5e-44	6e-42	1.5e-40	1.1e-36	3e-43	1.5e-41
END	574	605	637	673	739	805	610	673	743
STAR T AA	445	458	486	518	585	652	447	521	587
CHAI N ID							В	В	В
PDB	1bd8	1bd8	1bd8	1bd8	1bd8	1bd8	1blx	1blx	1blx
SEQ ID	NO:	1853	1853	1853	1853	1853	1853	1853	1853

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РДВ аппотатіоп	ALPHA/BETA, COMPLEX	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	HORMONE/OR OWTH EACTOR B18	INK4C; CELL CYCLE INHIBITOR	P18INK4C, TUMOR, SUPPRESSOR.	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEFENDENT KINASE,	HORMONE/GROWTH FACTOR	TRANSFERASE, CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, IKANSFERASE									SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
Соитроинд		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	Ď;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			TEBLISH OF THE	C-1 EKMINAL SKC KINASE;	CHAIN: A;		PHOSPHOTR ANSFER A SE	CAMP-DEPENDENT PROTEIN	KINASE CATALYTIC SUBUNIT	1CMK 3 (E.C.2.7.1.37) 1CMK 4	TRANSFERASE(PHOSPHOTRA	NSFERASE) CAMP-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (CAPK) 1CTP 3	(CATALYTIC SUBUNIT) 1CTP 4	ASE	7	CYCLIN-DEPENDENT KINASE
SEQFOL D score												· · ·								96.05	_			92.53							
PMF score		1.00					0.87				5	3				0 08	?												S.	2	3
Verify		09.0					0.16				0,60	2				0.81												1		0.36	1
Psi Blast		4.5e-41					8e-09				4 50-33				-	1.4e-45	-			1.5e-30			000	1.56-30				10.35	-	1.56-33	1
END		808					226				612	!				276				349			240	745				610	2	637	
STAR T AA		651					444				486					24						-	-	-			_	478	 :	510	
CHAI N ID		g					∢				4					A				ш			н				•		!	A	
PDB ID		1blx					Long				1bu9					lbyg			-+	Cm X			letn					1d9s	_	1d9s /	
SEQ ID NO:		1853				200	1853				1853					1853			$\dashv$	1853			1853	-				1853	_	1853	
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PDB annotation	HELIX, ANK YRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC- BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFEKASE FGFKIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATPBINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
Coumpound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;
SEQFOL D score							114.87		112.87
PMF score		1.00	1.00	1.00	0.92	0.51		1.00	
Verify score		0.65	0.36	0.43	0.54	0.13		0.46	
Psi Blast		7.5e-38	9e-37	1.2e-34	3e-34	4.5e-32	1.5e-45	1.5e-45	7.5e-45
END		673	743	773	807	694	293	276	292
STAR T AA		545	809	645	229	513	18	26	1
CHAI N ID		4	V	∢	∢	Ą	<b>4</b>	₹	В
PDB		1d9s	1d9s	1d9s	1d9s	1dcq	lfgk	1fgk	1fgk
SEQ	SO:	1853	1853	1853	1853	1853	1853	1853	1853

PDB annotation	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR,	PHOSPHOTRANSFERASE C-SRC, PHOSPHOTRANSFERASE C-SRC, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO- ONCOGENE, PHOSPHOTRANSFERASE	TRANSFERASIS P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571 ACTIVATION I OCE	PROTEIN KINASE CDK2; TRANSFERASI; SERINE/THREONINE PROTEIN KINASE, ATP-I3INDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORY A TION	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
Coumpound	FGF RECEPTOR 1; CHAIN: A, B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL: CHAIN: A. B:	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-A! PHA: CHAIN: D:	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; 1-KAPPA-
SEQFOL D score				92.94			
PMF score	1.00	1.00	1.00		1.00	1.00	1.00
Verify score	0.50	0.79	0.51		0.36	0.41	0.41
Psi Blast	7.5e-45	1.2e-46	7.5e-45	9e-28	3e-34	4.5e-46	6e-53
END	276	276	276	326	809	647	089
STAR T AA	26	26	49	61	484	458	486
CHAI N ID	B		Ą		4	D	D
PDB ID	1fgk	1fmk	1fbu	lhcl	lihb	1ikn	lika
SEQ ID NO:	1853	1853	1853	1853	1853	1853	1853

PDB annotation			TRANSCRPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,
Coumpound		B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL
SEQFOL	D score					114.32			
PMF	score		1.00	1.00	1.00		1.00	0.93	1.00
Verify	score		0.21	0.26	0.15		0.65	0.46	0.46
Psi Blast			6e-58	4,5e-52	1.3e-54	1.5e-46	1.5e-46	8e-13	9e-23
END	¥		749	775	810	306	276	523	563
STAR	TAA		551	584	219	10	56	445	458
СНАІ	SI N		D	D	D	∢	⋖		
PDB	A		likn	likn	likn	lir3	lir3	1myo	lmyo
SEQ	A Ş		1853	1853	1853	1853	1853	1853	1853

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PDB annotation	ACETY! ATTOM NAME AND DEBT ! T	ANK-REPEAT MYOTROPHIN,	ACELITEATION, NMR, ANK-REPEAT ANK-REPEAT MYOTROPHIN.	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYI ATION NAW ANY BEDEAT	ANK-REPEAT MYOTROPHIN.	ACETYLATION, NMR. ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPIRAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT).	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPI:AT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION
Coumpound		MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	A SEE SOUTH OF THE SEE SEE SEE SEE SEE SEE SEE SEE SEE S	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MVOTDOPLIMI. CITABLESTIFF	MIOINOPHIN; CHAIN: NOLL	MYOTROPHIN; CHAIN: NULL		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	£.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ř.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	÷.		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ř.	ME IVADA D BY COLLEGE	INF-NAPPA-B POS; CHAIN: A, C.
SEQFOL D score																_											<del>-</del>				
PMF		0.46	1.00	9	9.1	0.99	0.57	}	1.00		00.1		_		2	9					3:-		,		1	 9:	_			5	20.1
Verify score		-0.06	0.55	0.44	<i>†</i>	0.34	-0.03		0.37		0.50		_		65.0	70.0				6.4	4c.0			_		0.20	•			950	1
Psi Blast		8e-16	4.5e-32	1 50-36	1:3630	1.5e-32	3e-33		1.5e-30	,	be-43				30-50		-		-	1 70 52		-			1	1.36-35				1.5e-53	1
END		589	635	699	200	735	768		800	25					677	_				740	È				770	0 .				815	
STAR T AA		461	521	554		179	654		684	177					484	-				540	}				185	190				616	
CHAI N ID										2	4				田田	1				T.	,				Į.			-		Ε	
PDB ID		1myo	1myo	lmyo	,	1myo	lmyo		okmi	Infi	-				Infi					Inf			_		Infi	_				1nfi	
SEQ ID NO:		1853	1853	1853		1853	1853	3	1823	1853					1853					1853					1853	2				1853	

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PDB annotation	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	TRANSFERASE ALPHA BETA FOLD	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound	NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	MAP KINASE P38; CHAIN: NULL;	ERK2; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	LCK KINASE; CHAIN: A;	REGULATORY PROTEIN SWI6; CHAIN: A, B;	REGULATORY PROTEIN SWI6; CHAIN: A, B;	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score		92.67	97.49						
PMF score				1.00	1.00	0.10	0.00	96:0	1.00
Verify score				0.66	0.71	-0.40	-0.17	0.27	0.31
Psi Blast		3e-27	6e-29	1.5e-49	7.5e-50	1.5e-17	1.5e-40	3.2e-12	6.4e-12
END		359	358	276	276	592	759	503	578
STAR T AA		4	15	26	26	466	512	452	458
CHAI N ID				A	A	A	V	В	В
PDB		1p38	1pme	1qcf	1apc	1sw6	1sw6	1ycs	lycs
SEQ ID	Ö	1853	1853	1853	1853	1853	1853	1853	1853

PDE annotation	P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENEANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR STPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENEANKYRIN REPEATS)	COMPLEX (AN'TI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound		P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score				
PMF score		0.99	66:0	0.30
Verify score		0.09	0.26	-0.13
Psi Blast		66-33	1.4c-38	7.5e-33
END		099	726	608
STAR T AA		488	554	654
CHAI N ID		В	М	В
PDB ID		1ycs	1ycs	1ycs
SEQ NO:		1853	1853	1853

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PDB annotation	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERNE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING
Coumpound	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B:	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	RAB6 GTPASE; CHAIN: A;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;
SEQFOL D score	107.86	85.26			77.02		
PMF score			1.00	1.00		1.00	0.59
Verify score			0.43	0.55		0.48	0.12
Psi Blast	9e-31	9.6e-68	9.6e-68	1.6e-68	1.6e-68	6.4e-56	3.2e-53
END	356	171	173	173	174	171	176
STAR T AA	5	_		1	1	3	-
CHAI N ID		4	Ą	Ą	Ą	Ą	¥.
PDB ID	3erk	loly	lcly	lctq	lctq	1d5c	1486
SEQ ID NO:	1853	1854	1854	1854	1854	1854	1854

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY		COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-
Coumpound	GTP-BINDING PROTEIN YPT51; CHAIN: A;	RAP2A; CHAIN: NULL;	RAP2A; CHAIN: NULL;	RACI; CHAIN: NULL;	RACI; CHAIN: NULL;	ONCOGENE PROTEIN C-H-RAS P21 PROTEIN MUTANT WITH GLY 12 REPLACED BY PRO 1PLJ 3 (G12P) COMPLEXED WITH P3-1-(2- NITROPHENYL.)ETHYL- 1PLJ 4 GUANOSINE-5'-(B,G-IMIDO)- TRIPHOSPHATE 1PLJ 5	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;
SEQFOL D score			95.27	52.65			50.36	60.15
PIMF score	1.00	1.00			0.94	1.00		
Verify score	0.31	0.49			0.28	0.37		
Psi Blast	6.4e-55	4.8e-64	4.8e-64	1.1e-53	1.1e-53	4.8e-52	4.8e-36	8e-59
END	174	121	174	174	921	171	186	179
STAR T AA	1	-	-	-	2		2	1
CHAI N ID	¥						C)	Ą
PDB ID	1 <b>ek</b> 0	Ikao	1kao	1mh1	1mh1	lplj	Ігтр	1zbd
SEQ ID NO:	1854	1854	1854	1854	1854	1854	1854	1854

PDB annotation	BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (SERINE PROTEASE/INHIBITOR) SKIN- DERIVED ANTILEUKOPROTEINASE (SKALP); HYDROLASE, SERINE PROTEASE, 3D-STRUCTURE, ZYMOGEN, PANCREAS, 2 SIGNAL, COMPLEX (SERINE PROTEASE/INHIBITOR)
Coumpound		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;	ELASTASE; CHAIN: E; ELAFIN; CHAIN: I;
SEQFOL D score			54.33	68.59		
PMF		96.0			0.99	0.48
Verify		0.43			0.27	-0.71
Psi Blast		8e-59	3.2e-50	1.16-59	1.1e-59	3.2e-16
END AA		176	193	174	174	72
STAR T AA		4	-	2	4	29
CHAI N ID		A	V	¥	A	
PDB ID		1zbd	2ngr	3rab	3rab	1fle
SEQ ID NO:		1854	1854	1854	1854	1856

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	PDE annotation	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R- ELAFIN, ELASTASE INHIBITOR		SIGNALING PROTEIN GTP-BINDING PROTEINS PROTEIN PROTEIN	COMPLEX, EFFECTORS		SIGNALING PROTEIN PROTEIN-	PROTEIN COMPLEX,	ENDOCYTOSIS/EXOCYTOSIS G	PROTEIN, GTPASE, RAB6.	VESICULAR TRAFFICKING	G PROTEIN G PROTEIN, RAS, ARF,	AKF6, MEMBRANE TRAFFIC	ENDOCYTOSIS/EXOCYTOSIS G	PROJEIN, VESICULAR TRAFFIC,	OIL HIDROLISIS, TPI/KAB 2	FRUIEIN, ENDIDEYTOSIS, HYDROLASE	SIGNALING PROTEIN ARF-LIKE	PROTEIN 3, ARL3; PROTEIN-GDP	COMPLEX WITHOUT MAGNESIUM,	ARF FAMILY, RAS 2 SUPERFAMILY,	G-DOMAIN	PROTEIN TRANSPORT GDP-	BINDING, MEMBRANE TRAFFICKIN,	NON-MYRISTO'YLATED 1HUR 16
	Countpound	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	R-ELAFIN; CHAIN: NULL;		RAS-RELATED PROTEIN RAP- 1A; CHAIN: A: PROTO-	ONKOGENE	SERINE/THREONINE PROTEIN KINASE CHAIN: B:	HIS-TAGGED TRANSFORMING	PROTEIN RHOA(0-181); CHAIN:	RAB6 GTPASE: CHAIN: A:			ADP-RIBOSYLATION FACTOR	o, Crally: A;	GIF-BINDING PROTEIN YPTSI;	CHAIN: A;			ADP-RIBOSYLATION FACTOR-	LIKE PROTEIN 3; CHAIN: A;				HUMAN ADP-RIBOSYLATION	FACTOR I; IHUR 5 CHAIN: A,	B; IHUK /
CEOEOI	D score				50.43																			83.99		
DMG	score	0.12	0.46					0.01		0.01			1.00	13	51.5				1.00		•					
Verify	score	-0.54	-0.02					-0.14		-0.22			0.11	70.0	90.0				0.50							
Psi Riaet		0.0011	1.6e-17		9.6e-25			1.6e-28		3.2e-30		1	4.8e-52	37078					1.1e-48				!	6.46-57		
END	AA.	80	72		177			185		183		į	161	183	3				190				†	787		
STAR	T AA	32	20		19			23		21		];	4	22	1				7					<u> </u>		1
CHAI	NID	Ą			<			<b>V</b>		A			∢	A	<u> </u>	· · · ·	-		~				\   	<		1
PDB	a	ligr	2rel	+	lcly			lcxz		1d5c		$\dagger$	Soal	1ek0				+	bzii				+	mir		<del> </del>
SEO	NO.	1856	1856		1857			1857		1857		1057	/601	1857					/581			_	1067			1

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PDB annotation	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Coumpound	FACTOR 1; 1HUR 5 CHAIN: A, B; 1HUR 7	RAP2A; CHAIN: NULL;	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	RAB3A; CHAIN: A;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING STE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score		50.54		·		58.29		·
PMF			-0.03	0.30	0.28		0.51	0.09
Verify score			0.22	-0.03	-0.07		0.40	-0.22
Psi Blast		1.6e-24	1.6e-27	3.2e-33	3.2e-30	3.2e-31	3.2e-31	3.2e-50
END		186	185	190	132	791	160	188
STAR T AA		19		22	52	76	08	107
CHAI N ID			Ф	A	4	¥	<b>⋖</b>	၁
PDB UD		1kao	11x4	3rab	lalh	lalh	1a1h	1mey
SEQ ID NO:		1857	1857	1857	1858	1858	1858	1858

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PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 CHANSCRIPTION	COMPLEX (TRANSCRIPTION COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; INITIATOR ELIMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GIT ZING EINGER GOMET EN COMP
Соитроинд	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score			62.32			
PMF score	0.17	0.98		0.24	0.39	0.10
Verify score	-0.18	0.17		0.14	-0.08	-0.10
Psi Blast	4.8e-50	1.4e-50	1.4e-50	3.2e-20	1.3e-34	3.2e-33
END	132	160	161	160	091	162
STAR T AA	51	79	62	08	56	
CHAI N ID	O	ပ	O	¥	v	A
PDB ID	1mey	lmey	Imey		Inpq	2gli /
SEQ NO:	1858	1858	1858	1858	1858	1858

PDB annotation	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZRIC FINGER DNA BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING	COMMITTED (PRICED (DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SILE; CHAIN: B, C;	QGSK ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score		58.21		60.10														
PMF			0.11			0.78			0.35		-0.13			0.10			1.00	
Verify			-0.37			-0.04			-0.23		0.07			-0.26			-0.03	
Psi Blast		4.8e-34	4.8e-34	6.4e-29		6.4e-29			4.8e-27		6.4e-15	} !		3.2e-25			1.6e-50	
END		188	188	198		197			237		273	) i		169	}		197	977 944
STAR T AA		51	59	115		117			145		212	1		%	<u> </u>		116	
CHAI N ID		¥	Ą	¥	- <u></u>	A			<b>∀</b>		4	<b>:</b>		4	<u>:</u>		O	
PDB ID		2gli	2gli	1a1h		lalh			lalh		1914			1a1h			1mev	<b>.</b>
SEQ ID		1858	1858	1859		1859			1859		1950			1859	}		1859	

116   198   1.6e-50   77   1.3e-46   -0.02   0.43   1.72   2.65   1.1e-33   -0.35   0.12   1.72   2.65   1.1e-41   -0.10   0.35   2.09   2.37   1.4e-11   -0.11   0.42   2.12   2.39   8e-06   -0.29   0.81   1.12   2.39   8e-06   -0.29   0.81   1.16   2.09   2.37   1.4e-11   -0.11   0.42   2.12   2.39   8e-06   -0.29   0.81   2.00   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.30   2.3	PDB ID	B CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PD.8 annotation
C 116 198 1.6e-50 70.79 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 144 237 1.3e-46 -0.02 0.43 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 172 2.65 1.1e-33 -0.35 0.12 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 185 1.1e-26 -0.22 0.00 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 209 237 1.4e-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 209 237 1.4e-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; C CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C C CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C C CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C C C C C C C C C C C C C C C C C C		+				21026	arone	D score		
C 144 237 1.3e-46 -0.02 0.43 DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN; C, F, G; C 172 265 1.1e-33 -0.35 0.12 DNA; CHAIN; C, F, G; C 172 265 1.1e-36 -0.22 0.00 DNA; CHAIN; C, F, G; C 185 141 1.4e-26 -0.22 0.00 DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN; C, F, G; C 18 169 1.1e-41 -0.10 0.35 DNA; CHAIN; A, B, D, E; C 19 237 1.4e-11 -0.11 0.42 DNA; CHAIN; A, B, D, E; C 19 237 1.4e-11 -0.11 0.42 DNA; CHAIN; A, B, D, E; C 19 212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION FACTOR ADRITOR ITO.	- 1 2	+		5						(ZINC FINGER/DNA)
C 172 265 1.1e-33 -0.35 0.12 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 172 265 1.1e-33 -0.35 0.12 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 85 141 1.4e-26 -0.22 0.00 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 88 169 1.1e-41 -0.10 0.35 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 209 237 1.4e-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION FACTOR ADRI (RESIDIEST ID)			116	198	1.6e-50			70.79	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
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C 85 141 1.4e-26 -0.22 0.00 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CNSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CNSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER PROTEIN; CANSENSUS ZINC FINGER									FROIEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
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C 88 169 1.10-41 -0.10 0.35 DNA; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC FINGER PROTEIN C, F, G; CONSENSUS ZINC	G .		ç	141		-0.22	0.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
C 88 169 1.1c-41 -0.10 0.35 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN FR J J O, Z D, Z D, Z D, Z D, Z D, Z D, Z D, Z									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
C 88 169 1.1c-41 -0.10 0.35 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; G 209 237 1.4c-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 312 239 8c-06 -0.29 0.81 TRANSCRIPTION REGULATION FACTOR ADRI (RESIDINES 130)									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
G 209 237 1.40-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; G 209 237 1.40-11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, C, C, C, C, C, C, C, C, C, C, C, C,		-+								CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
GONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;  G 209 237 1.40-11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, C, C, C, C, C, C, C, C, C, C, C, C,	~		 8	169		-0.10	0.35		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
G 209 237 1.40-11 0.42 DNA; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENS						-			CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
G 209 237 1.40-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 212 239 86-06 -0.29 0.81 TRANSCRIPTION REGULATION FACTOR ADRIC RESIDINES 130.									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
G 209 237 1.4e-11 -0.11 0.42 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FEATOR ADRIGMENTATION FACTOR ADRIGMENTATION FEATOR ADRIGMENTATION FEATOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR ADRIGMENTATION FACTOR FACTOR ADRIGMENTATION FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FACTOR FAC										CRYSTAL STRUCTURE, COMPLEX
212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FOLIATION FACTOR ADRI (RESID) is 5.30.	5		209	237		-0.11	0.42		DNA CHAIN A B D E.	CLINC FINGER DNA)
PROTEIN; CHAIN: C, F, G; 212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDURES 130)							!		CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER DPOTTINI DNA
212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESID) IES 130									PROTEIN; CHAIN: C, F, G;	INTERACTION PROTEIN DESIGN 2
212 239 8e-06 -0.29 0.81 TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDITES 130.										CRYSTAL STRUCTURE, COMPLEX
18.0 62.0-	1_		212	†	1	000	1.00			(ZINC FINGER/DNA)
FACTOR ADRI (RESIDITES 110.	,		1			67.0	0.81		TRANSCRIPTION REGULATION	
	- 1								FACTOR ADRI (RESIDITES 130	

PDB annotation		ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRUPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATIONA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION
Coumpound	159) IPAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOWAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) IPAA 6	SP1F2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;
SEQFOL D score				55.20	
PMF score		0.03	0.00		0.48
Verify score		-0.25	-0.52		-0.08
Psi Blast		3.2e-05	1.16-16	1.46-20	1.4e-20
END	-	239	169	201	198
STAR T AA		212	105	114	117
CHAI N ID			∢	<b>∀</b>	4
PDB ID		1sp2	11f3	1143	143
SEQ		1859	1859	1859	1859

	_	<del></del>																
PD/B annotation	REGIII ATTONIONANA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION  COMPLEX (TRANSCRIPTION  REGULATION/DNA) COMPLEX  (TRANSCRIPTION	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION ZINC	FINGER PROTITIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(1KANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2	I KANSCKIP I I ON I NI TIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGILL ATTOMANA) COMPLEY	(TRANSCRIPTION)	REGULATION/DNA), RNA	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTFIN
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F:		- TOTAL	RIBOSOMAL RNA GENE;	CIMIN: D, C, E, F;			IFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE:	CHAIN: B, C, E, F;			YY1: CHAIN: C: ADENO-	ASSOCIATED VIRUS P5	CHAIN: A B.	CILIM. C, D,
SEQFOL D score						2022	00.00	<u></u>	-									
PMF score		0.10		0.33							10.0				0.45			
Verify score		-0.24		-0.01					-	200	77.0	*****			-0.00			
Psi Blast		1.4e-28		1.1e-28		1 16-28				3 20 16					3e-22			
END		239		275		237				178	2				220			
STAR T AA	,	105		117		50	100			86	}	•			110			
CHAI N ID		∢		∢		A				4			······································		C			
PDB ID	1	9		1466		1tf6				1116					Iubd			
SEQ ID NO:	0.501	1839		1859		1859				1859					1859			

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADR1; CHAIN: NULL;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score			68.47			·
PMF score		0.07		0.98	0.37	0.33
Verify		-0.06		-0.27	-0.05	-0.22
Psi Blast		3.26-22	3.26-33	3.2e-33	3.2e-16	6.4e-33
END		265	198	197	171	199
STAR T AA		152	98	93	117	106
CHAI		ပ	O	O		∢
PDB		1ubd	Iubd	lubd	2adr	2gli
SEQ ID	NO:	1859	1859	1859	1859	1859

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PD)3 annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (DNA-BINDING BE COMPLEX (	BINDING FRO JEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)		COMPLEX (ZING FINGER/DNA) COMPLEX (ZING FINGER/DNA), ZING FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, I)NA-BINDING	PROTEIN	GENE REGULA TION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY	CRYSTALLOGRAPHY, 3 PROTEIN	STRUCTURE, PROMYELOCYTIC	GENE REGULATION POZ DOMAIN;	DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY
Coumpound	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SILE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;				PROMYELOCYTIC LEUKEMIA	CHAIN: A;	
SEQFOL D score	68.84				1	69.01							-	64.40		
PMF score		0.04		1.00			;	0.41		00:1						
Verify score		0.04		0.37			200	-0.35		0.40					·	
Psi Blast	6.4e-33	1.3e-31		4.8e-32	4 02 22	4.06-32	1	3.25-28	1	1.36-37				1.3e-37		
END	238	237		452	152	CC+	400	°	,01	971	************			126		
STAR T AA	83	96		3/1	277	7/6	300			+		•		<b>^</b>		
CHAI N ID	¥	4		∢	A	<del></del>	4	¢	\ \	¢					**	
PDB ID	2gli	2gli	15.11	1 a a a a a a a a a a a a a a a a a a a	1214		lalh		16110				+	ongr		
SEQ ID NO:	1859	1859	1050	0001	1860		1860		1860	}	_	-	_	1901		

PDB annotation	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSIAL SIRUCIURE, COMPLEA	CAIN THE CANCED ONLY ONLY	FINGER PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S KNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION	
Coumpound		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	TWO TELLY, CHAMES () 13 ()		DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		6	DNA; CHAIN: A, B, D, E;	PROTEIN CHAIN: C. F. G.	redient, circus, c, r, c,	,	TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;						TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: R, C, F, F.	CIEDIA: 2, 2, 2, 2,
SEQFOL D score									67.59																		
PMF score		60.0				1.00								0.71				0.23								0.11	
Verify		-0.44				0.14								-0.16				-0.48	:							-0.38	
Psi Blast		1.6e-47		•		1.3e-50			1.3e-50					3.2e-47				3.2e-19								1.66-31	
END		423				452			452	] !				488				488	<u>}</u>							490	
STAR T AA		336				370			370	·				398				300	<u>}</u>							371	
CHAI N ID		S	)			ပ			J	)				ပ				4	:							⋖	
PDB ID	<del> </del>	Imev				lmey			1mev	Camer				lmey				1	3							11.66	
SEQ D	Ö	1860	-			1860			1860	2001				1860				1040	2001		_					1860	

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PD:B annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTISIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELISMENT, YY1, ZINC 2 FINGER PROTISIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRAINSCRIPTION COMPLEX (TRAINSCRIPTION REGULATIONINA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION RECT ATOMANA	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA-	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI:
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score		·				
PMF score		0.92	0.89	0.10	-0.20	0.07
Verify score		-0.05	-0.03	-0.08	0.05	0.10
Psi Blast		1.16-32	6.4e-34	4.8e-24	1.6e-09	6.4e-34
END AA		448	488	493	313	452
STAR T AA		344	375	406	224	319
CHAI N ID		ပ	ပ	U	∢	∢
PDB ID		pqnl	lubd	p		2gli
SEQ D NO:		1860	1860			1860

PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	Lamber 1012	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	HYDROLASE UVRB, MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A, HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF44, HELICASE, DEAD-BOX PROTEIN	THE ASSESSMENT TO A COMPANY OF	IRANSPORT PROTEIN 1C4, OTFASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	TRANSPORT PROTEIN TC4; GIPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;		GTP-BINDING PROTEIN KAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;
SEQFOL D score								•					113.24
PMF score		0.11		0.18	0.46	0.39	0.24	0.55	-0.14	0.43		1.00	
Verify score		-0.09		0.13	0.05	-0.11	-0.27	0.23	0.09	0.06		0.35	
Psi Blast		1.6e-34		1.6e-13	1.6e-13	1.4e-07	6.4e-17	9.6e-39	4.8e-43	3.2e-91		7.5e-64	7.5e-64
END		490		630	630	662	859	029	321	029		211	217
STAR T AA		344		470	470	538	457	208	105	313		14	15
CHAI N ID		Ą		∢	A	A	Ą	¥	Ą	В		∢	∢
PDB		2gli		1c40	1d2m	1d2m	1d9x	1fuk	1fuu	1fuu		1byu	1byu
SEQ ID	Ö	1860		1861	1861	1861	1861	1861	1861	1861		1862	1862

1862   1619   A   17   181   86-65   0.44   1.00   GTP-BINDING PROTEIN RAN;   TRANSFORT PROTEIN TC4 CITPASE   1619   A   17   181   86-65   0.44   1.00   GTP-BINDING PROTEIN RAN;   TRANSFORT PROTEIN TC4 CITPASE   1619   A   17   181   86-65   0.45   1.00   GTP-BINDING PROTEIN RAN;   TRANSFORT PROTEIN TC4 CITPASE   1840   A   17   181   86-65   0.45   1.00   GTP-BINDING PROTEIN RAN;   TRANSFORT PROTEIN TC4 CITPASE   1840   A   17   181   86-65   0.45   1.00   GTP-BINDING PROTEIN RAN;   TRANSFORT PROTEIN TC4 CITPASE   1840   A   17   181   86-65   0.45   1.00   GTP-BINDING PROTEIN RAN;   1840   1840   A   17   182   6.46-64   0.65   1.00   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING PROTEIN RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GTP-BINDING RAN;   1840   GT			$\neg$			<del></del>	<del></del>			<del></del>
Q PDB         CHAI         STAR         END         Psi Blast         Verify         PMF         SEQFOL           1 byu         B         9         211         1.3e-65         0.44         1.00         109.68           2 lbyu         B         9         215         1.3e-65         0.51         1.00         109.68           2 lcly         A         16         181         8e-65         0.51         1.00         102.67           1 cly         A         17         181         8e-65         1.00         102.67           1 clq         A         17         182         6.4e-64         0.65         1.00         98.76           1 cdq         A         17         182         6.4e-64         0.65         1.00         95.76           1 cdq         A         17         182         3.2e-58         95.76         1.00         95.76           1 cdq         A         18         179         3.2e-60         0.68         1.00         95.76           1 cdq         A         18         179         9.6e-60         0.68         1.00         95.76	PDI! annotation	TRANSPORT PROTEIN TC4, GTPASE, NUCLEAR TRANSPORT,	TRANSPORT PROTEIN TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT,	SIGNALING PROTEIN SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING	PROTEIN SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX,	ANTIPARALLEI, COILED-COIL ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6,	VESICULAR TRAFFICKING ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS.
Q         PDB         CHAI         STAR         END         Fsi Blast         Verify         FMF           1         IDyu         B         9         211         1.3e-65         0.44         1.00           2         1byu         B         9         215         1.3e-65         0.51         1.00           2         1c1y         A         16         181         8e-65         0.51         1.00           1cq         A         17         181         8e-65         1.00           1cq         A         17         182         6.4e-64         0.65         1.00           1cq         A         17         182         6.4e-64         0.65         1.00           1cx         A         17         182         3.2e-58         9           1cx         A         18         179         3.2e-62         0.56         1.00           1ek0         A         18         179         9.6e-60         0.68         1.00	Coumpound	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINETHREONINE PROTEIN	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN:	A, FAN, CHAIN: B; RAB6 GTPASE; CHAIN: A;	GTP-BINDING PROTEIN YPT51; CHAIN: A;
Q         PDB         CHAI         STAR         END         Psi Blast         Verify score           1         IDyu         B         9         211         1.3e-65         0.44         1           1         Ibyu         B         9         215         1.3e-65         0.51         1           1         Icly         A         16         181         8e-65         0.51         1           1         Iciq         A         17         181         8e-65         0.51         1           1         Iciq         A         17         181         8e-65         0.51         1           1         Iciq         A         17         182         6.4e-64         0.65         1           1         Iciq         A         17         182         3.2e-58         1           1         A         17         182         3.2e-52         0.56         1           1         A         18         179         9.6e-60         0.68         1	SEQFOL D score		109.68		102.67		98.76			
Q         PDB         CHAI         STAR         END         Psi Blast           1         ID         N ID         T AA         AA         1.3e-65         C           1         Ibyu         B         9         215         1.3e-65         C           1         Iciy         A         16         181         8e-65         O           1         Iciy         A         17         181         8e-65         O           1         Iciy         A         17         182         6.4e-64         O           1ctq         A         17         182         6.4e-64         O           1cxz         A         19         182         3.2e-58         O           1d5c         A         18         179         9.6e-60         O           1ek0         A         18         179         9.6e-60         O	PMF score	1.00		1.00		1.00			1.00	1.00
Q         PDB         CHAI         STAR         END         Psi Blast           1         Ibyu         B         9         211         1.3e-65           1         Ibyu         B         9         215         1.3e-65           1         Ibyu         B         9         215         1.3e-65           1         Icly         A         16         181         8e-65           1         Ictq         A         17         181         8e-65           1         Ictq         A         17         182         6.4e-64           1cxz         A         17         182         6.4e-64           1cxz         A         17         182         3.2e-58           1d5c         A         18         179         3.2e-62           1ek0         A         18         179         9.6e-60	Verify score	0.44		0.51		0.65			.56	39.
Q         PDB         CHAI         STAR         END           1         Ibyu         B         9         211           1         Ibyu         B         9         215           1         Icly         A         16         181           1         Icly         A         17         182           1         Ictq         A         17         182           1cxz         A         17         182           1cxz         A         17         182           1d5c         A         19         182           1d5c         A         18         179           1ek0         A         18         179	Psi Blast	1.3e-65	1.3e-65	8e-65	8e-65		6.4e-64	3.2e-58		
2 1byu B CHAI   B   CHAI   B   CHAI   B   CHAI   B   CHAI   B   CHAI   B   CHAI   B   CHAI   B   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHAI   CHA	END	211	215	181	181	182	182	182	179	
2 1byu 2 1byu 2 1byu 2 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq / 1ctq /	STAR T AA	6	6	16	17	17	17	19	81	81
2 1byu 10 10 10 10 10 10 10 10 10 10 10 10 10 1	CHAI N ID	В	В	∢	¥	¥	A	<b>V</b>	A	4
	PDB ID	1byu	1byu	lcly	lcly	lctq	·			
	SEQ D NO:	1862	1862	1862	1862	1862	1862			

PDB annotation	HYDROLASE	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR	GTP-BINDING PROTEIN GTP. BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL	GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN)	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN),	SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)	GTPASE-ACTIVATING PROTEIN RHOGAP: COMPLEX (GTPASE	ACTIVATION/PROTO-ONCOGENE), GIPASE 2 TRANSITION STATE, GAP	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED	PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN,	EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN,
Coumpound		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	RAP2A; CHAIN: NULL;	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN	NUP358; CHAIN: B, D;		P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN	RHOA; CHAIN: B;		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;		·
SEQFOL D score		113.50		98.96	114.45					87.88			130.15		
PMF			1.00				1.00								
Verify score			0.80				0.45								
Psi Blast		3e-60	3e-60	9.6e-59	1.4e-60	-	1.4e-60			4.8e-55			4.8e-69	**************************************	
END		187	186	182	198		193			180			187		
STAR T AA		17	81	17	15		91			61			12		
CHAI		A	K		ပ		၁			В	=		4		
PDB		1ibr	1 ibr	lkao	1rrp		lmp			1tx4			1zbd		
SEQ ID		1862	1862	1862	1862		1862			1862	_,		1862		

	 _				_		_			_																							
PDB annotation	KAB3A, RABPHILIN	COMPLEX (G1P- BINDING/EFF!;CTOR) RAS-RELATED	PROTEIN RAB3A; COMPLEX (GTP.	BINDING/EFFI;CTOR), G PROTEIN,	EFFECTOR, RABCDR, 2 SYNAPTIC	EXOCYTOSIS, RAB PROTEIN,	MADSA, KABPITILIN	HYDROLASE G PROTEIN,	VESICULAR TRAFFICKING, GTP	HIDROLISIS, KAB Z PROTEIN,	NEUROTRANSMITTER RELEASE,	HYDROLASE	HYDROLASE G PROTEIN,	VESICULAR TIVAFFICKING, GTP	HYDROLYSIS, RAB 2 PROTEIN.	NEUROTRANSMITTER RELEASE.	HYDROLASE		COMPLEX (NUCLEAR	PROTEIN/RNA) COMPLEY	MICLEAR PROTEIN/RNA) DNA	SNRNP.RIBONI ICI. FOPROTEIN	RNA-BINDING PROTEINBNA TRA	PRE-MRNA SPITCING	REGILI ATTON DAM DOLLAND	COMPLEX	GENE REGIT A TION/PMA BOT WAY	BINDING PROTEIN 1 PART 1 PART	PROTEIN-RNA COMPLEX CENE	REGILI ATIONIONA	Christian		GENE REGULA TION/RNA POLY(A)
Coumpound	D 4 D 2 1 OTT 1 D 1	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;					RAB3A: CHAIN: A:	Manach, CHAIN: A;				DADA CHABIA	NABSA; CHAIN: A;						U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B":	CHAIN: B, D;		SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*IP*IP*IP*	UP*UP*UP*UP*U)- CHAIN: P. O:	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A. B. C. D.	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M. N.	O, P, Q, R, S, T;	POLYDENYLATE BINDING
SEQFOL D score										_		145.01	_			-								_		_				Н.			
PMF score	5	00:1					1.00						.,						0.52				0.43		_		0.57						0.43
Verify score	0.65	3	•				0.78											,	0.40				0.08				0.47					1	0.34
Psi Blast	4.8e-69		•		_		8e-70					8e-70	1				-	1	/0-20-7		-	1	3e-07				7.5e-07 (					1	1.36-07
END	185						182					182						202	707	-		200	_			$\dagger$	507					100	1
STAR T AA	14						13			-		13		_				135	3			120	001			130	000	•		_		136	000
CHAI N ID	A						∢					Ψ						В	}	_		4											
PDB ID	Izbd						3rab					3rab			_		-	la9n I	_			11,75				1cvi						Icvi F	1
SEQ ID NO:	1862					1,00	1802					1862						1864		_		1864				1864					_	1864	1
														_				_	_	_	_		_	-				_					J

PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	CITY CITY FEITH CONTRACTOR	RIBONOCLEOPROTEIN FTB. FTB. C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	NUCLEAR PROTEIN OF SNRAF A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN KNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	NUCLEOLIN RBD1; CHAIN: A;	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POL YP YRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score							
PMF score		0.21	0.99	0.15	0.43	0.95	0.48
Verify score		0.48	0.13	0.20	0.05	0.32	0.38
Psi Blast		6e-07	1c-08	6e-07	6e-07	7.5e-07	3e-07
END AA		196	195	961	195	196	207
STAR T AA		136	135	88	136	138	138
CHAI		¥	Д	4		<b>∀</b>	A
PDB		157	Inrc	Iqm9	2u1a	2up1	3sxl
SEQ ID	Ö	1864	1864	1864	1864	1864	1864

		_							
PDB annotation	SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION				COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-	EINDING PROTEIN COMPLEX (TRANSCRIPTION FACTORDNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-	BINDING PROTISIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH	3 REPEATS COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING 1 FITCHNE-BICH
Coumpound			LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.11.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-	t color at	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score									
PMF score			0.01		0.60	0.47		0.43	0.60
Verify score			-0.21		-0.88	-0.90		0.30	0.15
Psi Blast			3.2e-05		1.6e-21	1.2e-37		8e-08	1.4c-08
END			542		94	96		350	338
STAR T AA			439		-	-		183	209
CHAI N ID			∢		∢	¥		¥	¥
PDB ID			1ses		1xbr	1xbr		1a4y	la4y
SEQ NO: B			1865		1867	1867		1870	1870

PDB annotation	3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION,	EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	RNA BINDING PROTEIN TAP (NFXI); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	LIGASE CYCL, IN A/CDK2- ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE- RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F- BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE	TRANSCRIPTION RNA1P; RANGAP;
Coumpound		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	•	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	SKP2; CHAIN: Å, C; SKP1; CHAIN: B, D;	GTPASE-ACTIVATING
SEQFOL D score									:	
PMF score		0.25		0.12	0.25	0.03	0.00	0.51	0.72	0.27
Verify score		0.14		0.40	-0.10	0.03	-0.01	0.45	0.22	0.09
Psi Blast		3e-06		8e-07	0.00096	1.1e-06	1.1e-06	1.1e-46	4.8e-36	0.00064
END		373		333	354	306	306	349	349	347
STAR T AA		209		961	222	193	193	128	128	248
CHAI N ID		∢		4	4	A	В	∢	4	Ą
PDB ID		la4y		1d0b	1d0b	1601	1601	lfqv	162	1yrg
SEQ ID		1870		1870	1870	1870	1870	1870	1870	1870

			_								
PDB annotation	GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACJITYLATION, LEUCINE-RICH REPEATS		TRANSFERASE GRK-2, BETA- ADRENERGIC RECEPTOR KINASE I, BETA-ARK PLECKSTRIN	HOMOLOGY DOMAIN, PH DOMAIN, SIGNAL TRANSDUCTION, 2 G-BETA-GAMMA BINDING DOMAIN,	BETA-ADRENERGIC RECEPTOR 3 KINASE, BETA-ARK, G-PROTEIN COUPLED RECEPTOR KINASE (GRK-	SIGNAL TRANSDUCTION PROTEIN	CYTOSKELETON			MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN TAIL DOMAIN
Coumpound	PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;		G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;			BETA-SPECTRIN; 1BTN 4 CHAIN: NITT 1 BTN 5	BETA-SPECTRIN; IDRO 6 CHAIN: NIII.: IDRO 7	SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLOGY		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;
SEQFOL D score					· · · · · · · · · · · · · · · · · · ·					<b>†</b>	
PMF score		0.71		-0.03			96.0	0.21	0.11	0.53	500
Verify score	·	-0.03		0.08			0.19	0.22	0.13	0.05	3
Psi Blast		3.2e-09		4.8e-10			8e-12	1.5e-05	4.8e-10	1.6e-58	
END AA		338		291			271	264	271	464	
STAR T AA		209		168			172	182	186	149	
CEAI N ID									∢	A	
PDB ID		2bnh		1 bak			1btn		Idyn	1ef1	
SEQ NO:		1870		18/1			1871	1871	1871	1871	

PDB annotation	A A D I A R A R A R A R A R A R A R A R A R A	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN ARFI GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION		OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,
Coumpound		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	GRP1; CHAIN: A;	RADIXIN; CHAIN: A;	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT IPLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,
SEQFOL	D score				-		69.11	
PMF	score	0.80	69.0	0.65	0.01	0.09		0.54
Verify	score	0.31	0.14	0.49	-0.01	0.14		0.03
Psi Blast		3.2e-17	3.2e-17	4.8e-18	3.2e-58	1.4e-14	0	0
END	ΑA	269	269	272	464	285	390	387
STAR	T AA	170	170	172	134	169	S	∞
CHAI	9 2	<	4	Ą	¥		<b>4</b>	A
PDB	e e	Ifao	1fb8	1fgy	1gc7	Ipís	1a05	1a05
SEQ	ВŠ	1871	1871	1871	1871	1871	1872	1872

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DECARBOXYI ATING DEHYDROGENASE, LEUCINE 2	BIOSYNTHESIS OXIDOREDUCTASE OXALOSUCCINATE DECARBOXYLASE IDH-	OXIDOREDUCTASE (NAD(A)-CHOH(D)), NAJ)P, PHOSPHORYLATION, 2 GLYOXYI ATF RYPASS	OXIDOREDUCIASE OXALOSUCCINATE	DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(A)-	CHOH(D)), NAL)P, PHOSPHORYLATION, 2	GLYOXYLATE BYPASS	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,	DEHYDROGENASE, NAD-	BIOSYNTHETIC PATHWAY	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE	DEHYDROGENASE, NAD.	DEPENDANT ENZYME, 2 LEUCINE RIOSYNTHETIC PATEUMAY	OXIDOREDUCTASE IPMDH, IMDH;	OXIDOREDUCTASE,	BIOSYNTHETIC PATHWAY, 2 NAD.	DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE
В;	ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	,	ISOCITRATE DEHYDROGENASE; CHAIN:	NOLL,		3-ISOPROPYI MAI ATE	DEHYDROGENASE; CHAIN: A,	B;		3-1SUPKOPYLMALATE DEHYDROGENASE; CHAIN: A,	B;		3-ISOPROPYLMALATE	B: B;		10 Can Carre	DEHYDROGENASE; CHAIN: A,
			62.58			$\dagger$		•									7 1
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	1ai2	cia!	7						1cm7		<del></del>	_				-	1
	1872	1872				1872			1872			+				1872	
	B;	5 387 0 0.01 0.60 ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	lai2         5         387         0         0.01         0.60         ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	1ai2         5         387         0         0.01         0.60         ISOCITRATE DEHYDROGENASE; CHAIN: NULL;           1ai2         7         387         0         62.58         ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	1ai2         5         387         0         0.01         0.60         ISOCITRATE DEHYDROGENASE; CHAIN: NULL;           1ai2         7         387         0         62.58         ISOCITRATE DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; 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CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE;	1ai2   5   387   0   0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7   387   0   62.58   ISOCITRATE   DEHYDROGENASE; CHAIN: 1   1   1   1   1   1   1   1   1   1	1ai2         5         387         0         0.01         0.60         B;           1ai2         7         387         0         62.58         ISOCITRATE DEHYDROGENASE; CHAIN: NULL; NULL; NULL;           1cm7         A         1         382         0         62.58         ISOCITRATE DEHYDROGENASE; CHAIN: NULL; NULL; NULL; NULL; NULL;	1ai2   5 387   0 0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7 387   0   62.58   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1cm7   A   1 382   0   63.70   DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: DEHYDROGENASE; CHAIN: A   C   C   C   C   C   C   C   C   C	1ai2   5 387   0 0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7 387   0 62.58   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL; 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  NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;	1ai2   5 387   0 0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7 387   0 62.58   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   Cm7   A 1 382   0 63.70   3-ISOPROPYLMALATE   DEHYDROGENASE; CHAIN: A 1 389   0 0.004 0.01   0.01 0.01   0.01 0.01   0.01 0.01	1ai2   5   387   0   0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7   387   0   62.58   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1cm7   A   1   382   0   63.70   3-ISOPROPYLMALATE   B;   B;   B;   CHAIN: A, B;   Cm7   A   1   389   0   0.04   0.41   DEHYDROGENASE; CHAIN: A, B;   Cm7   A   1   389   0   0.04   0.41   DEHYDROGENASE; CHAIN: A, B;   Cm7   A   1   389   0   0.04   0.41   DEHYDROGENASE; CHAIN: A, B;   Cm7   A   1   389   0   0.04   0.41   DEHYDROGENASE; CHAIN: A, B;   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7   Cm7	1ai2   5 387   0 0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7 387   0   0.04   0.41   B;   Ca.58   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   DEHYDROGENASE; CHAIN: NULL;   DEHYDROGENASE; CHAIN: A   1 382   0   0.04   0.41   B;   DEHYDROGENASE; CHAIN: A   B;   B;   DEHYDROGENASE; CHAIN: A   B;   B;   DEHYDROGENASE; CHAIN: A   B;   B;   DEHYDROGENASE; CHAIN: A   B;   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   B;   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAIN: A   DEHYDROGENASE; CHAI	1ai2   5   387   0   0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;   NULL;	1ai2   5 387   0 0.01   0.60   ISOCITRATE   DEHYDROGENASE; CHAIN: NULL;   1ai2   7 387   0   0.04   0.41   DEHYDROGENASE; CHAIN: NULL;   1cm7   A   1 382   0   0.04   0.41   DEHYDROGENASE; CHAIN: A   B;   B;   CHAIN: A   B;   CHAIN: A   B;   CHAIN: A   B;   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAIN: A   CHAI	1ai2   5   387   0   0.01   0.60   Biscriftate	1ai2   5   387   0   0.01   0.60   B.S.	2 1ai2 5 387 0 0.01 0.60 BCHYDROGENASE; CHAIN: NULL; NULL; 1ai2 7 387 0 62.58 ISOCITRATE DEHYDROGENASE; CHAIN: NULL; 1cm7 A 1 382 0 0.004 0.41 DEHYDROGENASE; CHAIN: A B; 1cm7 A 1 382 0 6.042 3-ISOPROPYLMALATE B; 1cm7 A 1 382 0 6.042 3-ISOPROPYLMALATE B; 1cm7 A 1 382 0 6.042 3-ISOPROPYLMALATE B; 1cm7 A 1 382 0 6.042 3-ISOPROPYLMALATE B; 1cm7 A 1 382 0 6.042 3-ISOPROPYLMALATE B; 1cm7 A 1 382 0 6.004 0.41 DEHYDROGENASE; CHAIN: A, B; 1cm2 B; 1cm2 A 1 389 0 6.004 0.64 0.64 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.

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PDB annotation	DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH; 1IDM 7 CHIMERA 1IDM 20	OXIDOREDUCTASE IPMDH; 11DM 7 CHIMERA 11DM 20	OXIDOREDUCTASE IPMDH, IMDH; IXAC 10 OXIDOREDUCTASE, CHIMERA IXAC 21	OXIDOREDUCTASE IPMDH, IMDH; 1XAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION
Coumpound	В;	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	3-ISOPROPYLMALATE DEHYDROGENASE 2TZM6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE 2TZM6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA;
SEQFOL D score		54.18		50.68			68.62		
PMF score			0.42		0.46	0.57		0.51	0.22
Verify score			0.06		0.04	-0.03		0.44	0.11
Psi Blast		4.8e-95	4.8e-95	1.6e-96	1.6e-96	0	0	1.6e-23	4.8e-36
END		366	387	366	387	387	388	125	156
STAR T AA		42	6	45	6	9	9	10	10
CHAI N ID						4	<b>A</b>		В
PDB ID		lidm	lidm	lxac	lxac	Zayq	2ауд	1a5e	lawc
SEQ	Ö	1872	1872	1872	1872	1872	1872	1873	1873

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PD]3 annotation	REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING.	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABBBETA I. COMETER	(TRANSCRIPTION	REGULATION/ONA), DNA-BINDING,	ANKYRIN REPIEATS,	TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR, ANK YR IN MOTHE	TIMOR STIDDE ESCOP TIMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	COMPLEX (KINASE/ANTI-	ONCOGENE) CINK6; P16INK4A,	KINASE CYCI IN DEPENDENT	KINASE INHIBITORY 2 PROTEIN	CDK, INK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRISSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR PROTEIN/KINA (SP) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL.
Соитроинд	CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: R:	DNA; CHAIN: D, E;			Priority in Charles	FISHNK4D CDK4/6 INHIBITOR; CHAIN: NIII I.	CITATION IN OLE,	P19INK4D CDK4/6 INHIBITOR	CHAIN: NULL;		CYCLIN-DEPENDENT KINASE	O; CHAIN: A; MULTIPLE TUMOR STIPPRESSOR: CHAIN:	B;					ביי ביי שי שים ימתבת וא וסאס	6; CHAIN: A; P19INK4D; CHAIN:	B;	
SEQFOL D score	,																					_	
PMF score			1.00				0.11	1		96.0			0.62							0.15	}		1
Verify score			0.43				0.05	3		0.22	****	200	70.7							0.18			
Psi Blast			6.4e-33				3.2e-32			1.1e-23		70.00					-			8e-33			
END		ç	125				157			128	•	125	3							157	<del>70</del>		1
STAR T AA		c	7				13			m		10	2							13		-	
CHAI N ID		_	<b>-</b>									2	1		-					В			
PDB ID		Torrio	i awc				1bd8			1 pd8		1hi7	:							1blx	···		
SEQ ID NO:		1873					1873		0.00	18/3		1873								1873			

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PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT KINASE CELL CYCLE 2 CONTROL.	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	PISINK4C, I UMOK, SUFFKESSOK,	CICLIN-Z DEFENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/0	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	ANK-REPEAT MYOTROPHIN,	ACEI YLAIION, NMK, ANK-KEFEAI	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;	•		CYCLIN-DEPENDENT KINASE 6 INHIBITOR: CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				MYOTROPHIN; CHAIN: NULL		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score																										
PMF score		96.0				0.71			0.55			•	0.49	} ;	09.0			-	0.74	; ;				0.64		0.45
Verify score		0.42				0.16			0.15				0.05	3	0.23	<u> </u>			0.14	<u>-</u>				0.21		0.02
Psi Blast		1.6e-22				6.4e-34			4.8e-27				370-24	F4-74.0	6.4e-34	· •			1 60.26	1,00-20				1.3e-24		3.2e-40
END		128				153			130				121	101	153	3			120	172		-		127		212
STAR T AA		3				10			2	1			10	2	10	2			6	7				=		4
CHAI N ID		В				A			A	4		-	_	₹	4	<b>4</b>				∢						ជ
PDB ID		16lx				1bu9			15:10	3			1,20,	SKDT	11,44				1:1:	ouri				1myo		1nfi
SEQ ID	2	1873				1873			1873				1077	18/3	1973	701			1072	18/3				1873		1873

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PD)3 annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYP IN MOTTE	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTTE	COMPLEX (KINIASE/ANTI- ONCOGENE) CDK6, P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI- ONCOGENE) HEADER	COMPLEX (KINASE/ANTI- ONCOGENE) CIDKG, P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI- ONCOGENE) HIADER	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN CVC! IN DEPENDENT
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, F;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B:
SEQFOL D score		•					
PMF		0.81	0.31	0.01	0.68	0.00	0.31
Verify		0.03	0.03	-0.04	0.18	0.15	0.09
Psi Blast		3.2c-16	3.2e-27	1.4e-15	3.26-17	1.46-17	3.2e-25
END AA		120	153	120	120	153	153
STAR T AA		10	13	2		52	13
CHAI N ID					В	Ф	В
PDB ID		1a5e	1bd8	1bd8			1blx
SEQ ID NO:		1874	1874	1874	1874	1874	1874

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PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR F18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC- BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;
SEQFOL D score								
PMF score		-0.09	0.23	0.11	0.05	0.33	69.0	0.71
Verify score		0.08	-0,15	0.04	0.01	0.28	0.08	0.40
Psi Blast		1.6e-14	1.3e-29	1.3e-18	6.4e-28	1.6e-17	1.5e-12	4.8e-18
END		120	158	125	212	120	122	124
STAR T AA		2	13	2	54	10	13	2
CHAI N ID		В	A	4	4	4	A	Ą
PDB ID		1bkx	15u9	1bu9	1bu9	149s	1dcq	1ihb
SEQ	Ö	1874	1874	1874	1874	1874	1874	1874

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PDE annotation	INHIBITION	CELL CYCLE INHIBITOR P18-	INHIBITOR, PI8-INK4C(INK6), ANKYRN PEPIAT 2 CDV 4/6	INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACELYLATION, NMR, ANK-REPEAT COMPLEX (ANTI-	ONCOGENE/ANK YRIN REPEATS)	P33BP2; ANK YELN REPEATS, SH3, P53, TUMOR SUPPRESSOR.	MULTIGENE 2 FAMILY, NÚCLEAR	PROTEIN, PHOSPHORYLATION,	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)		COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, ENA-BINDING	COMPLEY /ZRESTED FRICER	COMPLETA (ZINC FINGER/DIA)	THE PRICED THE PROPERTY.	PROTEIN	COMPLEX (ZINC) FINGER/DNA)	COMPLEX (ZINC FINGER/DNA).	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR: CHAIN: A. B.	(r (r )		MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	P53; CHAIN: A; 53BP2; CHAIN:	B;							QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	OGSR ZINC FINGER PEPTIDE.	CHAIN: A: DI IPI EX	OI.IGONIICI FOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	_	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score											•											72.03				
PMF score		0.27			0.24	0.23	0.01								99.0			0.00								0.09
Verify score		-0.09		,	-0.17	0.30	-0.03			-		-			0.12			0.04							1	-0.14
Psi Blast		3.2e-27			1.1e-21	1.1e-21	4.8e-20			-				1	9.6e-26	<del></del>	·	7.5e-29				7.5e-29			1	1.36-39
END		211		120	138	159	193							22.0	333			336				365			503	202
STAR T AA		54			=	73	09							220	737			243				283			305	565
CHAI N ID		∢					В					-			<			A	-			∢			V	
908 E1		lihb		1 mrso	, myc	Imyo	lycs							1211		-		lalh			╅	lain			lath	$\neg$
SEQ NO.		1874		1874	107	18/4	1874							1877	/01			1877			100	1/01			1877	

PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGEK/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, FROIEIN-DINA	CBNCTAI CTRITCT DE COMPLEY	(7INC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTFIN-DNA	THISTORY TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE ST
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;		DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSOS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSTITUTE CHILD I HISTORY
SEQFOL D score																											98.05	
PMF score		90.0			000	3			0.37				0.07					0.95					1.00					
Verify score		-0.16			0.57				-0,46				-0.24	<u>;</u>				0.02					0.29			-		
Psi Blast		4.8e-42			10 11	1			3e-26	\ \ \ \			8e-40	?				1.3e-39					6.4e-50				8e-51	
END		263			207	200			335				307	3				335					363				364	
STAR T AA		191			771	201			190	<u>}</u>			217	<u>;</u>				266					282				282	
CHAI N ID		ပ			C	۔۔۔۔			ن	)		_	c	>				C					ပ				O	
PDB ID		1mey				ımey			lmev		,		1 Ven	- Comman				lmev					Imey				Imey	
SEQ ID		1877			1000	) o I			1877	,,,,,			1877	//01				1877					1877				1877	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ö	A	N ID	TAA	AA		score	score	D score		
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	U	310	391	8e-51	60.0	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTISIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	၁	338.	419	3.2e-51	0.43	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
. —						,			CONSENSOS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2
								J		CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	ပ	366	447	1.3e-50	0.28	00'1		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1877	Imev	J	394	473	4 80-47	0.20	1		DNA. CHARI. A B D E.	(ZINC FINGER/JINA)
		)	<u> </u>	?		2.0	9		CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
		_								CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/JONA)
1877	1mey	ပ	422	529	3e-40	-0.02	0.82		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
								=	PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1877	1mev	c	450	620	270.40	0.0	100			(ZINC FINGER/I)NA)
:	<u></u>	)	}	747		٥3	3.		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
					···				PROTEIN: CHAIN: C. F. G:	INTERACTION PROTEIN DESIGN 2
										CRYSTAL STRUCTURE, COMPLEX
1077	1	,	727			1			000	(ZINC FINGER/I)NA)
10/	ımey	اد	4/0	333	8e-34	0.46	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
	A	e N	TAA	¥		score	score	D score		
<u> </u>									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DINA)
	1mey	Ð	187	214	1.6e-11	-0.12	0.48		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
									PROTEIN: CHAIN: C. F. G:	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1	1mev	Ü	236	263	6.4e-12	-0.05	0.52		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
· 	}	)	1						CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRISIAL SIROCIONE, COMELEA (ZINC FINGER/DNA)
1	1en2		190	218	9.6e-07	0.02	0.09		SPIF2: CHAIN: NULL;	ZINC FINGER TRANSCRIPTION
	1		<u>}</u>	; ;						FACTOR SP1; ZINC FINGER,
										TRANSCRIPTION ACTIVATION, SP1
F	143	A	239	335	4.8e-17	0.27	0.07		TRANSCRIPTION FACTOR IIIA;	COMPLEX (TRANSCRIPTION
									CHAIN: A; 5S RNA GENE;	REGULATION/DNA) TFIIIA; 5S
									CHAIN: E, F;	GENE; NMR, TFIIIA, PROTEIN, DNA,
										TRANSCRIPTION FACTOR, 5S RNA 2
										GENE, DNA BINDING PROTEIN,
										ZINC FINGER, COMPLEX 3
			-							(TRANSCRIPTION
			:							REGULATION/DNA)
F	1tf6	A	162	316	8e-31	-0.24	0.11		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION
									RIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX
									CHAIN: B, C, E, F;	(TRANSCRIPTION
_										REGULATION/DNA), RNA
								_		POLYMERASE III, 2
	_									TRANSCRIPTION INITIATION, ZINC
+					,,,		2		THEIR A. CHAINE A D. CO.	COMPLEX (TP ANSCRIPTION
	1tf6	∢	239	400	9.6e-36	-0.06	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
$\mathbf{I}$										

									_													
PDE annotation	(TRANSCRIPTION REGULATION/JONA), RNA POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/J)NA) COMPLEX (TRANSCRIPTION	REGULATION(I), RNA POLYMERASE III, 2 IRANSCRIPTION INTIATION ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION PEGITI ATTOMINAL COLUMNIA)	(TRANSCRIPTION	REGULATION/INA), RNA	Th ANGCHITAGE III, 2	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGIL ATTONIONA) COMPLEY	(TRANSCRIPTION	REGULATION/DNA), RNA	TRANSCRIPTION INITIATION 2010	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	FOLYMERASE III, 2	FINGER PROTEIN	COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: B, C, E, F;		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F:			TFIIIA; CHAIN: A, D; 5S RIBOSOMAI, RNA GENF:	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE:	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S	KIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				YY1; CHAIN: C; ADENO-
SEQFOL D score			107.85	•			-	-														
PMF score					000	66.0					00.1		<del>-</del>			0.95						0.37
Verify score					50	70.0-					21.0				,	0.17		•				-0.39
Psi Blast			7.56-68		00 30	00-20				7	4.66-38				1	86-34						1.4e-26
END		į	4/1		151						110				53.1	100					33.5	252
STAR T AA			010		311	;				357	à				305						166	
CHAI N ID			€		<b>A</b>	<del></del> -					4		<del></del>		4						1	
PDB UD		1+66	9		11.66					1466					1+66						1hd	7
SEQ ID NO:		1877			1877					1877					1877				_		1877	1

PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN; C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
SEQFOL D score					
PMF score		86.0	0.86	1.00	0.95
Verify score		-0.00	-0.09	0.00	-0.13
Psi Blast		7.56-40	6.4c-33	3e-50	3.26-35
END		363	363	391	419
STAR T AA		243	246	287	318
CHAI N ID		O	O	ပ	O
PDB ID		1ubd	1ubd	lubd	1ubd
SEQ ID	Ö	1877	1877	1877	1877

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PDI annotation	INITIATOR ELIMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIL ATTOMANA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATION, INITIATION, INITIATION FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	KEGULATIONDNA) COMPLEX (TRÁNSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION(I)NA) COMPLEX (TRANSCRIPTION REGULATION(I)NA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATIONENA) COMPLEX (TRANSCRIPTION REGULATIONENA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATION, FINGER PROTEIN DNA-PROTEIN
Coumpound	CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY I; CHAIN: C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score		86.32			
PMF score			66.0	0.95	0.99
Verify score			0.26	0.03	0.10
Psi Blast		3e-48	1.16-47	4.8e-32	3e-48
END		448	474	473	501
STAR T AA		340	364	374	392
CHAI N ID		U	ပ	U	O
PDB ID		Iubd	lubd	1ubd	lubd
SEQ ID NO:		1877	1877	1877	1877

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TKANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INTITATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADRI, ZINC FINGER, NMR	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	COMPLEX (DNA-BINDING
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;   CHAIN: A, B;				ADRI; CHAIN: NULL;		ADRI; CHAIN: NULL;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GL11;	CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII;
SEQFOL D score																				93.76
PMF score		1.00		0.0					0.41	-, · · · -	0.63			0.80			0.41			
Verify score		0.12		-0.08					-0.48		-0.23			0.15			0.19			
Psi Blast		1.5e-48		8e-34					1.3e-14		1.6e-12			1.5e-46			3.2e-33			1.5e-66
END		530		529					216		309			365			390			421
STAR T AA		420		430					162		239			061			246			282
CHAI N ID		O		ပ										¥			A			⋖
PDB ID		Iubd		1ubd					2adr		2adr			2gli			2gli			2gli
SEQ ID NO:		1877		1877					1877		1877			1877			1877			1877

	L L	1	1.	Τ	Τ		T		Γ.		T		7		Т		Γ	
PDB annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING) COMPLEX (DNA-BINDING) PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)		HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN,	ATPASE, TRANSPORT	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN	ATPASE, TRANSPORT	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2	PROTEOLYSIS, PROTEASOME	CELL CYCLE CIXCOP; CDC6, CDC18, ORC1, AAA PROTEIN, DNA	REPLICATION INITATION 2 FACTOR, CELL CYCLE CONTROL	FACTOR	CHAPERONE AAA-ATPASE, CLPY,	CHAPERONE AAA-ATPASE, CLPY.	ATP-DEPENDENT PROTEOLYSIS	TRANSFERASE CK; NUCLEOTIDE	MONOPHOSPHATE KINASE,
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN;	CHAIN: A;	N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN;	CHAIN: A;	HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU;	CHAIN: E, F;	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HEAT SHOCK PROTEIN HSLU; CHAIN: A:	HEAT SHOCK PROTEIN HSLU;	CHAIN: A;	CYTIDINE MONOPHOSPHATE	KINASE; CHAIN: A;
SEQFOL D score					65.03													
PMF score		0.27	0.93				0.64		0.10		0.28	· ·	250	):.  -	0.23		0.15	
Verify score		-0.16	-0.16				0.35		-0.74		0.22		000	0.00	0.16		-0.51	
Psi Blast		1.5e-66	6e-53		3.2e-15		3.2e-15		3.2e-13		1.5e-15		Ť	07-20-1	4.5e-34	+	0.0045	
END		503	533		424		349		270		405		350	200	442		242	
STAR T AA		310	395		169		961		691		184		160	~~~	183		817	
CHAI N ID		Ą	Ą		∢		∢		щ		∢		4	¢	A		€	
PDB ID		2gli	2gli		1d2n	+	107n		le94	+			1041	1811	1g41	+	ZCIIIK	
SEQ ID NO:		1877	1877		1878	500	18/8		1878	1040	0/01		1878		1878	1070	0/01	

PDB annotation	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE			TRYPTOPHAN BIOSYNTHESIS TRYPTOPHAN INDOLE-LYASE; TRYPTOPHAN BIOSYNTHESIS, TRYPTOPHAN INDOLE-LYASE, PYRIDOXAL 2 5'-PHOSPHATE, MONOVALENT CATION BINDING SITE	LYASE ACC SYNTHASE, S- ADENOSYL-L-METHIONINE ETHYLENE BIOSYNTHESIS	RIFAMYCIN BIOSYNTHESIS (RIFD
Coumpound	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'- PHOSPHATE 1ARS 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'- PHOSPHATE 1ARS 4	TRYPTOPHANASE; CHAIN: A, B, C, D;	1-AMINOCYCLOPROPANE-1- CARBOXYLATE SYNTHASE; CHAIN: A, B;	3-AMINO-5-
SEQFOL D score	77.13			76.94	71.45		
PMF score		0.88	0.51			1.00	0.33
Verify score		0.08	-0.19			0.44	0.08
Psi Blast	1.6e-58	1.6e-58	1.6e-64	1.6e-64	4.8e-13	0	1.6e-10
END	499	517	457	208	523	515	304
STAR T AA	54	68	85	95	89	80	181
CHAI N ID	Ą	⋖			⋖	∢	A
PDB ID	lajs	lajs	lars	lars	1ax4	1b8g	1b9h
SEQ ID NO:	1882	1882	1882	1882	1882	1882	1882

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PDB annotation	;	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)	AMINOTRANSFERASE	AMINOTRANSFERASE, PYRIDOXAL FNZYME	AMINOTRANSFERASE	AMINOTRANSFERASE, PYRIDOXAL	ENZYME	TRANSFERASE TAT; TYROSINE	CATABOLISM, TRANSFERASE,	AMINOTRANSFERASE, 2	PYRIDOXAL-5'-PHOSPHATE, PLP	TRANSFERASE TAT; TYROSINE	CATABOLISM, TRANSFERASE,	AMINOTRANSFERASE, 2	PYRIDOXAL-5'-PHOSPHATE, PLP	TRANSFERASE TRANSFERASE,	AMINOTRANSFERASE, PYRIDOXAL	PHOSPHATE	LYASE CGS; LYASE, LLP-	DEPENDENT ENZYMES,	METHIONINE BIOSYNTHESIS	TRANSFERASE	AMINOTRANSFERASE FOLD,	LARGE PLP-BINDING DOMAIN,	SMALL C- 2 TERMINAL DOMAIN,	OPEN ALPHA-BETA STRUCTURE.	TRANSFERASE SHMT, SERINE	METHYLASE; ALPHA PLP	ASPARTATE, AMINO	TRANSFERASE, (AAT)-LIKE FOLD	LYASE FES CLUSTER	BIOSYNTHESIS, PYRIDOXAL 5'-
Coumpound		HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	ASPARTATE	A. B:	ASPARTATE	AMINOTRANSFERASE; CHAIN:	A, B;	TYROSINE	AMINOTRANSFERASE; CHAIN:	A, B;		TYROSINE	AMINOTRANSFERASE; CHAIN:	A, B;		CYSTALYSIN; CHAIN: A, B, C,	D, E, F, G, H;		CYSTATHIONINE GAMMA-	SYNTHASE; CHAIN: A, B, C, D;		MALY PROTEIN; CHAIN: A, B;					SERINE	HYDROXYMETHYLTRANSFER	ASE; CHAIN: A, B, C, D;		L-CYSTEINE/L-CYSTINE C-S	LYASE; CHAIN: A, B;
SEQFOL D score					134.98							158.29																				
PMF			1.00					1.00								1.00			0.13			1.00					1.00				0.87	
Verify score			0.52					0.24								0.34			-0.10			0.35					0.42				0.17	
Psi Blast			9.6e-84		9.6e-84			1.6e-67				1.6e-67				6e-52	ı		1.6e-08	•		4.5e-53					4.8e-07				9.6e-13	
END	_		515		514			220				220				514			302			514					415				514	
STAR T AA			102		83			99				35				125	-		144		,	128					182				123	
CHAI			∀		Ą			∢				∢				∀			∢			∢					₹		-		∢	
PDB U			1bjw		1bjw			15w0			,	Ibwo				lc/n		,	lcs1			1421					Idfo			1	Teln	
SEQ	NO:		1882		1882			1882			000.	1882				1882		-	1882		000.	7887					1882				1887	

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PDB annotation	PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME- PRODUCT COMPLEX	AMINOTRANSFERASE	TRANSFERASE, AMINOTRANSFERASE	AMINOTRANSFERASE	TRANSFERASE,	AMINOTRANSFERASE AROAT;	AMINOTRANSFERASE	AMINOTRANSFERASE AROAT;	AMINOTRANSFERASE																LYASE LYASE, PLP-DEPENDENT	ENZYME, PYRIDOXAL PHOSPHATE	AMINOTRANSFERASE PHEAT,	TYKAT, AROAT; AMINOTRANSFERASE, AROMATIC	
Coumpound		ASPARTATE	A. B. C. D:	ASPARTATE	AMINOTRANSFERASE; CHAIN:	AROMATIC AMINO ACID	AMINOTRANSFERASE; CHAIN:	AROMATIC AMINO ACID	AMINOTRANSFERASE; CHAIN:	A, B;	TRANSFERASE(AMINOTRANSF	ERASE) ASPARTATE	AMINOTRANSFERASE	(CASPAT) (E.C.2.6.1.1) 2CST 3	COMPLEXED WITH	PYRIDOXAL-5'-PHOSPHATE	AND MALEATE 2CST 4	TRANSFERASE(AMINOTRANSF	ERASE) ASPARTATE	AMINOTRANSFERASE	(CASPAT) (E.C.2.6.1.1) 2CST 3	COMPLEXED WITH	PYRIDOXAL-5'-PHOSPHATE	AND MALEATE 2CST 4	TYROSINE PHENOL-LYASE;	CHAIN: A, B;	TYROSINE	A.B. C. D. E. F:	
SEQFOL D score		79.51				74.67												75.00										·	
PMF score				1.00				0.88			0.95														0.34		0.95		
Verify score				90.0				-0.16			-0.13														0.01		-0.17		
Psi Blast		4.8e-52	-	4.8e-52		8e-53		8e-53			1.6e-58							1.6e-58							1.1e-48		9.6e-58		
END AA		516		452		488		457			517							499							208		457		
STAR T AA		76		68		79		85			81							88							110		08		
CHAI N ID		Ą		Ą		¥		A			A							Ą							¥		Ą		
PDB ID		1yaa		1yaa		2ayl		2ayi			2cst							2cst							2 <del>p</del> I		3tat		
SEQ ID NO:		1882		1882		1882		1882			1882							1882							1882		1882		

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SUBSTRATES, PLP ENZYME	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC STRETPATES IN PENITYSAE		•		HYDROLASE TYROSINE PHOSPHATEASE 1 AR PROTEIN	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROI ASE	HYDROLASE VIR; HYDROLASE, PROTEIN TASE	HYDROLASE VIR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE	TOTAL TOTAL	IMMUNOGLOBIJLIN
Parada de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de la casa de l	TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT DH 7.47AAT 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7, 47AAT 4		LAR; CHAIN: A, B;	PYSTI; CHAIN: NULL;	PYST1; CHAIN: NULL;	HUMAN VHI-RELATED DUAL- SPECIFICITY PHOSPHATASE CHAIN: A R.	HUMAN YII. RELATED DUAL- SPECIFICITY PHOSPHATASE CHAIN: A, B;		ANTIBODY CTM01; CHAIN: L,
	91.42		78.03			68.80		139.04			
		0.43			0.18		1.00		1.00		1.00
		-0.10			-0.13		0.57		0.74		0.30
	9.6e-58	6.4e-65	6.4e-65		1.1e-58	6.4e-24	6.4e-24	7.5e-31	7.5e-31		9.6e-82
	497	457	492		220	200	200	208	200		242
	95	73	88		3	52	55	37	50		20
	≺	∢	∢		В			∢	4		H
	3tat	7aat	7aat		llar	1mkp	Imkp	1vhr	lvhr		1ae6
	1882	1882	1882		1883	1883	1883	1883	1883		1884
		TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	3tat         A         95         497         9.6e-58         91.42         TYROSINE           AMINOTRANSFERASE; CHAIN:         A, B, C, D, E, F;         A, B, C, D, E, F;           7aat         A         73         457         6.4e-65         -0.10         0.43         TRANSFERASE(AMINOTRANSFERASE ERASE AMINOTRANSFERASE (B.C.2.61.1) COMPLEX WITH TATA TATA TATA TATA TATA TATA TATA T	3tat   A   95   497   9.6e-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; A, B, C, D, E, F; A   73   457   6.4e-65   -0.10   0.43   TRANSFERASE(AMINOTRANSFERASE (B.C.2.6.1.1) COMPLEX WITH TAAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   77aat   A   88   492   6.4e-65   78.03   TRANSFERASE (AMINOTRANSFERASE (AMINOTRANSFERASE (B.C.2.6.1.1) COMPLEX WITH TAAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4   7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT AT AT 4   PHOSPHATE AT PH 7.5 7AAT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT AT 4   PHOSPHATE AT 4   PHOSPHATE AT	3tat A   95   497   9.6e-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F, E, E, E, E, E, E, E, E, E, E, E, E, E,	31at A   95   497   9.66-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; A, B, B, B, B, B, B, B, B, B, B, B, B, B,	31at   A   95   497   9.6e-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; A, B, C, D, E, F; A, B, C, D, E, F; B, C, B, E, E, E, E, E, E, E, E, E, E, E, E, E,	31at	31at   A   95   497   9.6e-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; AMINOTRANSFERASE; CHAIN: Tast   A   88   492   6.4e-65   6.4e-65   78.03   TRANSFERASE(AMINOTRANSFERASE) ASPARTATE   AMINOTRANSFERASE AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRANSFERASE   AMINOTRA	Table   A   95   497   9.6e-58   91.42   TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F; AMINOTRANSFERASE; CHAIN: A   73   457   6.4e-65   -0.10   0.43   TRANSFERASE(AMINOTRANSFERASE)   TRANSFERASE(AMINOTRANSFERASE)   TRANSFERASE   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSFERASE (AMINOTRANSFERASE)   TRANSF	Jail   A   95   497   9.66-58   91.42   TYROSINE

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ВÖ	e e	N ID	TAA	AA		score	score	D score		
T			·						田	IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
1884	lafv	Н	20	244	8e-84	0.43	1.00		HUMAN IMMUNODEFICIENCY VIRUS TYPE I CAPSID CHAIN:	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1
									A, B; ANTIBODY FAB25.3	CA, HIV CA, HIV P24, P24; FAB, FAB
									FRAGMENT; CHAIN: H, K, L, M;	LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL
										CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1884	1bd2	E	21	261	1.2e-81			301.81	HLA-A 0201; CHAIN: A; BETA-2	COMPLEX (MHC/VIRAL
									MICROGLOBULIN; CHAIN: B;	PEPTIDE/RECEPTOR) HLA A2
									TAX PEPTIDE; CHAIN: C; T	HEAVY CHAIN; COMPLEX
									CELL RECEPTOR ALPHA;	(MHC/VIRAL PEPTIDE/RECEPTOR)
									CHAIN: D; T CELL RECEPTOR PETA: CHAIN: E:	
1884	1hd2	ţr.	22	196	1 2e-81	99.0	1.00		H.A-A 0201: CHAIN: A: BETA-2	COMPLEX (MHC/VIRAL
		)	}				1		MICROGLOBULIN; CHAIN: B;	PEPTIDE/RECEPTOR) HLA A2
									TAX PEPTIDE; CHAIN: C; T	HEAVY CHAIN; COMPLEX
									CELL RECEPTOR ALPHA;	(MHC/VIRAL PEPTIDE/RECEPTOR)
									CHAIN: D; T CELL RECEPTOR BETA: CHAIN: E:	
1884	1bec		21	261	1.5e-76			273.44	14.3.D T CELL ANTIGEN	RECEPTOR T CELL RECEPTOR 1BEC
									RECEPTOR; 1BEC 5 CHAIN:	14
1884	145;	H	20	244	1.3e-81	0.23	0.99		CHIMERIC GERMLINE	IMMUNE SYSTEM IMMUNE
									PRECURSOR OF OXY-COPE	SYSTEM
									CHAIN: L; CHIMERIC	
									GERMLINE PRECURSOR OF	
-	1,55	1	5	7,70	1 02 01	9	90		OXY-COPE CHAIN: H;	WANTEROCT OBJET IN EAD
1001	1600	<b>-</b>	07	#7	4.00-01	0.40	3.		CHAIN: CHAIN: 1:	ANTIBODY ANTIGEN HIV. 1 P24
									IMMUNOGLOBULIN HEAVY	CA
									CHAIN; CHAIN: H;	
1884	1fvd	В	20	247	1.1e-84	0.18	1.00		IMMUNOGLOBULIN FAB	

	T	<del></del>												_	
PDIs annotation				IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C	REGION, IMMUNOGLOBULIN	IMMUNOGLOBULIN, V REGION, C REGION HINGE REGION	IMMUNOCIONALIN	IMMUNOGLOBULIN VARIABLE	HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT,	MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMINOGI ORITIN	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN SIGNAI	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS		GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2
Coumpound	FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB	FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, ETEPET-COCCUIT IIGC 5.5	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IGGI INTACT ANTIBODY	MAB61.1.3; CHAIN: A, B, C, D	NIG9 (IGG1=LAMBDA=);	SINGLE-CHAIN ANTIBODY	FKAGMENI; CHAIN: A, C;		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;		HEAT SHOCK PROTEIN HSLU; CHAIN: A;		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score											277.99				
PMF score		1.00		0.98	0.82		1.00	1.00					0.04		1.00
Verify score		0.22		-0.00	0.07		0.21	0.22					-0.34		0.34
Psi Blast		1.6e-83		3.2e-90	3.2e-82		1.6e-83	9e-07			8e-71		0.0094		4.8e-24
END		247		282	282		244	130			262	$\dashv$	369		129
STAR		50		20	21		20	12			19		314		01
CHAI N ID		н		В	В		Н	٧	, , , , , , , , , , , , , , , , , , , ,		m P		∢	†	<
PDB ID		ligc		ligt	ligy		Ingp	lnqb			Itcr	+	1841	+	ongi
SEQ NO:		1884		1884	1884		1884	1884			1884		1885	1000	1080

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION				RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA		GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA
Coumpound		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*
SEQFOL D score		59.44								
PMF score			0.27	0.12		1.00	1.00		0.89	
Verify			0.31	0.36	ļ	0.53	0.41		0.41	
Psi Blast		4.8e-24	1.2e-32	6.4e-12		9e-05	3e-05		3e-05	
END		134	551	555		1410	1410	·	1410	
STAR T AA		6	291	301		1342	1342		1340	
CHAI		⋖				A	<b>V</b>		Ð	
PDB		1buo	1gof	1gof		1b7f	1cvj		lcvj	
SEQ ID	NO:	1886	1886	1886		1887	1887		1887	

		$\neg$		Τ	_																			
PDB annotation		RNA BINDING PROTEIN RNA-	BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING	DOMAIN, NUCLEOLUS	OUTER MEMBIVANE PROTEIN OSMOPORIN: OTITER MEMBRANE	PROTEIN, NON-SPECIFIC PORIN,	OSMOPORIN, 2 BETA-BARREL,	TO THOMPINE WITH		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE	PROTEASE			<u>.</u>				RNA-BINDING DOMAIN RNA. BINDING DOMAIN, ALTERNATIVE	SPLICING	RNA-BINDING PROTEIN SPLICING,	OZ SINKINF, KBD, KNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T; HU ANTIGEN C; CHAIN: A;		NUCLEOLIN RBD2; CHAIN: A;	OMBESE CHARL A P. C.	OMFA36; CHAIN: A, B, C;			OUTER MEMBRANE PROTEIN	PHOSPHOPORIN (PHOE) 1PHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;		RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C-	TERMINUS, OR SECOND RNA-	BINDING DOMAIN ISXL 3	PLUS N-TERMINAL MFT) 18X1	4 (NMR, 17 STRUCTURES) 1SXL	Chart Francis	SEA-LEIHAL PROTEIN; CHAIN: NULL;	TOWN TO THE PLANT THE	SPEICING FACTOR UZAF 65 KD	(v	SEX-LETHAL; CHAIN: A, B, C;	
SEQFOL D score																	7		<u>,                                    </u>		-		<u></u>	
PMF score		1.00	270	0.03	-0.20	2			-0.19	0,	61.0-	;	0.54					1 00	8	000	3		0.55	
Verify score		0.45	0.43	0.45	0.70	) ; ;			0.77	900	6.0	100	0.07					0.47	÷	0.44	•		0.01	
Psi Blast		4.5e-05	30-05	6	4.5e-09	}			7.5e-10	4 50.00		$\dagger$	51000.0					0.00015		1.36-05			6e-05	
END		1410	1417		207				218	700	t 024	13061	0651				-	1410		1410		925	1432	
STAR T AA		1342	1331		14				=	37	ì	1225	5251		-			1339		1342	•••	22.5	1339	
CHAI		Ą	<	!	Ą					4	:									A				
PDB ID		Id8z	1fjc	,	losm				1pho	1004		leyl					····	2sxl	-	2u2f		2cv1		
SEQ	Ö.	1887	1887		1887			100	188/	1887		1887						1887		1887	·	1887		

CEO	PDR	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e è	a	N IS	TAA	AA		score	score	D score		
2										SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1888	1b7f	A	1303	1371	9e-05	0.53	1.00		SXL-LETHAL PROTEIN; CHAIN:	RNA-BINDING PROTEIN/RNA TRA
									A, B; KNA (5'- R(P*GP*I JP*I JP*GP*UP*UP*	REGULATION, RNP DOMAIN, RNA
									UP*UP*UP*UP*U)- CHAIN: P, Q;	COMPLEX
1888		4	1303	1371	3e-05	0.41	1.00		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
3	?	!							PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; KKM,
									E, F, G, H; RNA (5'-	PROTEIN-KNA COMPLEA, GENE
									R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
									AP*AP*AP*A)-3'); CHAIN: M, N,	
									O, P, Q, R, S, T;	
1999	1,00,1	a	1301	1371	3e-05	0.41	0.89		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
1000	[	1	<u>.</u>	:		:			PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
									E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
									R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
			. 1,,,						AP*AP*AP*A)-3'); CHAIN: M, N,	
									O, P, Q, K, S, 1;	DNA BINING PROTEIN RNA.
1888	Id8z	⋖	1303	1371	4.5e-05	0.45	3 		HU ANTIGEN C; CHAIN: A;	BINDING DOMAIN
1888	1 610	A	1292	1378	3e-05	0.42	0.65		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN
	e e e e e e e e e e e e e e e e e e e	:	<u>!</u>		; 		•			C23; RNP, RBD, RRM, RNA BINDING
										DOMAIN, NUCLEOLUS
1888	losm	A	14	207	4.5e-09	0.70	-0.20		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMODORN: OFFER MEMBRANE
										PROTEIN NON-SPECIFIC PORIN,
										OSMOPORIN, 2 BETA-BARREL,
										TRANSMEMBRANE
1888	1pho		=	218	7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
1888	1004	4	37	204	4.5e-08	0.89	-0.19		ALPHA-LYTIC PROTEASE;	HYDROLASE DOUBLE BETA
200	77.		,							

PDE annotation	BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPI ICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPIJCING REGILATION, RNP DOMAIN, RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 15XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP* I IP*I IP*I IP*I IP*I I)- CHAIN: P. O.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (\$'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, Q, R, S, T;
SEQFOL D score							
PMF		0.54	1.00	0.99	0.55	00.1	1.00
Verify score		0.07	0.47	0.44	0.01	0.53	0.41
Psi Blast		0.00015	0.00015	1.3e-05	6e-0 <i>5</i>	9e-05	3e-05
END AA		1357	1371	1371	1393	1313	1313
STAR T AA		1286	1300	1303	1300	1245	1245
CHAI N ID				Ą	4	∀	¥.
PDB ID		Isxi	2sxi	2u2f	3sxI	1b7f	lcvj
SEQ ID NO:		1888	1888	1888	1888	6881	1889

PDB annotation	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING
Coumpound	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3); CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;
SEQFOL D score									
PMF score	0.89	1.00	0.65	-0.20	-0.19	-0.19	0.54	1.00	0.99
Verify score	0.41	0.45	0.42	0.70	0.77	0.89	0.07	0.47	0.44
Psi Blast	3e-05	4.5e-05	3e-05	4.5e-09	7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05
END	1313	1313	1320	207	218	204	1299	1313	1313
STAR T AA	1243	1245	1234	41	=	37	1228	1242	1245
CHAI N ID	В	A	Ą	4		A			Y
PDB ID	1cvj	1d8z	1fjc	losm	1pho	1qq4	1sxl	2sxl	2u2f
SEQ ID	1889	1889	1889	1889	1889	1889	1889	1889	1889

PDB annotation	PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPISNSATION	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER ()F IL-6 TYPE CYTOKINES, TFIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III		HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
Coumpound		SEX-LETHAL; CHAIN: A, B, C;	GP130; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES	FIBRONECTIN; CHAIN: A;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;
SEQFOL D score							57.74	
PMF score		0.55	0.23	0.70	0.94	-0.18		-0.06
Verify score		0.01	0.21	0.07	0.18	0.02		0.28
Psi Blast		66-05	1.6e-12	9.6e-11	1.2e-12	1.6e-16	6.4e-28	9.6e-17
END		1335	262	265	266	355	450	348
STAR T AA		1242	166	165	165	162	168	168
CHAI N ID		¥					A	₹ `
PDB ID		3sxl	15j8	1bpv	1bpv	1cfb	1fnh	1923
SEQ ID NO:		1889	1894	1894	1894	1894	1894	1894

		IN,	IN.	Ž Ž			<u>}</u>	ر د د	ď.		PE,	Æ		•		_
ıtion		STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRICTIDAL PROTEIN,	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRICTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRIICTIRAL PROTEIN			RNA BINDING PROTEIN/RNA XI RRPA: PROTEIN, RNA COMPTEY	NA,	PROTEIN-RNA 2 INTERACTIONS,	i, KINA 'A	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	CELL CYCLE/RNA DSRBDIII; NMR	J'RNA,	PROTEIN DSRBD, DROSOPHILA,		
PDB annotation		L PROTEIN TYPE-I	PROTEIN TYPE-II	PROTEI V TYPE-II JILAR 2 M USION PI			PROTEI	ANDED F	A 2 INTER	TEINKN	PE WWI	RNA DSE	PROTEIN	BD, DRO	z	
PI	PROTEIN	STRUCTURAL PROTEIN TENA FIBRONECTIN TYPE-III, HEPAI EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRICTIE AT BECTEN	STRUCTURAL PROTEIN TENA FIBRONECTIN TYPE-III, HEPA EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRICTI RAI PROTEIN	STRUCTURAL PROTEIN TENA FIBRONECTIN TYPE-III, HEPA EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN			RNA BINDING PROTEIN/RNA	DOUBLE STRANDED RNA	PROTEIN-RNA 2 INTERACTI	BINDING PROTEIN/RNA	SH3 PROTOTYPE PROTEIN DESIGN	CYCLE/	STRUCTURE, PROTEIN/RNA,	TEIN DSR	RNA 2 HAIRPIN	
	PRO	STR FIBR EXT ADH	STR FIBR EXT ADH	STRI FIBR EXTI ADH STRI	<del>  </del>		RNA XI R	Dog	PRO	BINE	SH3	CELI	STRI	PRO	RNA	
pun		: A, B;	: A, B;	: A, B;	GL YCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3		DOUBLE STRANDED RNA BINDING PROTEIN A: CHAIN:		R(*GP*GP*CP*GP*CP*GP*CP*G P*CP*C)_3'): CHAIN: C D E G:	יט ימ ימ יט י	HAIN: A;	MATERNAL EFFECT PROTEIN	l: A;	STAUFEN DOUBLE-STRANDED	(AIN;	
Coumpound		ç, CHAIN	4; CHAIN	4; CHAIN	OTEIN FOUR TO WARE III MESTRUCTO		STRANDE PROTEIN	(5'-	*CP*GP*	, CIIOII	OTYPE; C	L EFFEC	); CHAIN	DOUBLE	ING DON	
		TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	GL YCOPROTEIN FIBRONE (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 17		DOUBLE STRANDED RNA	A, B; RNA (5'-	R(*GP*GP P*CP*C)-3	- C- C)	WWPROTOTYPE; CHAIN: A;	MATERNA	(STAUFEN); CHAIN: A;	STAUFEN	KNA BINDING DOMAIN; CHAIN: B:	
SEQFOL D score								-							_	
PMF score		0.29	0.12	-0.20	0.49		0.42				0.41	0.70				
Verify score		-0.24	0.09	0.03	0.15		0.30	-,• -			-0.10	0.57				
Psi Blast		4.5e-13	9.6e-15	4.8e-15	3e-13		1.1e-07				0.0003	6e-12				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
END AA		261	349	450	265		293				49	293				ļ
STAR T AA		164	169	271	164		230				20	226				-
CHAI N ID		∢	Ą	A			≪				∀	₹				-
PDB ID	·	1914	1qr4	lqr4	1tt	7	1di2	<del></del> -		~+		lekz				
SEQ ID NO:		1894	1894	1894	1894		1895	•		1	1895	1895				

DOMAIN STAUFEN 1STU 13	STAUFEN; 1STU 4									
DOUBLE STRANDED RNA BINDING	MATERNAL EFFECT PROTEIN		0.25	0.18	3e-05	293	233		895   1stu	1895
BINDING	CHAIN: C;									
DOMAIN, PHOSPHOSERINE	Y(SEP)PT(SEP)S PEPTIDE;									
PROLINE ISOMERASE, WW	ISOMERASE NIMA- CHAIN: B;									
										SON.
		D score	score	score		AA		NID	6	A
PDE annotation	Coumpound	SEQFOL	PMF	Verify	Psi Blast	END	STAR	CHAI	PDB	SEO

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
770	26	0.949	0.664
71	23	0.996	0.936
72	28	0.929	0.700
73	26	0.976	0.875
74	17	0.919	0.828
775	28	0.976	0.653
76	30	0.996	0.894
777	17	0.953	0.784
778	22	0.982	0.872
79	19	0.890	0.552
80	18	0.984	0.958
81	19	0.981	0.916
82	19	0.995	0.971
83	21	0.980	0.904
84	21	0.980	0.904
185	16		
86	26	0.961	0.916
87	43		0.801
		0.992	0.943
88	41	0.937	0.604
89	43	0.994	0.659
90	29	0.986	0.848
91	37	0.984	0.878
92	19	0.942	0.693
93	22	0.982	0.872
95	19	0.993	0.931
96	22	0.992	0.807
97	28	0.990	0.919
98	23	0.896	0.747
99	23	0.985	0.951
000	21	0.989	0.925
001	11	0.900	0.758
002	18	0.933	0.634
004	16	0.881	0.607

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1005	18	0.964	0.812
1006	19	0.972	0.915
1007	24	0.997	0.929
1008	16	0.945	0.737
1009	31	0.957	0.775
1010	22	0.975	0.822
1011	28	0.946	0.799
1012	24	0.973	0.910
1013	29	0.968	0.769
1014	25	0.977	0.776
1015	41	0.986	0.847
1016	28	0.988	0.938
1017	23	0.976	0.897
1018	45	0.964	0.604
1019	28	0.948	0.776
1020	33	0.930	0.679
1021	18		0.594
1022	26	0.947	0.925
1023	41	0.942	0.703
1024	36	0.910	0.749
	24	0.988	0.919
1026	27	0.962	0.696
1027	23	0.965	0.693
1028	22	0.962	0.919
1030	24	0.943	0.832
1030	34	0.973	0.817
1032	22	0.947	0.677
1033	25	0.889	0.718
1034	27	0.962	0.856
1035	19	0.967	0.909
1036	39	0.986	0.922
1037	28	0.982	0.924
1038	44	0.974	0.662
1039	29	0.984	0.763
1040	22	0.974	0.796
1041	29	0.928	0.725
1051	23	0.966	0.812
1054	19	0.951	0.895
1055	16	0.927	0.827
1056	25	0.949	0.823
1058	28	0.980	0.848
1061	24	0.965	0.891
1062	25	0.946	0.860
1067	36	0.964	0.648
1074	32	0.941	0.669
1076	17	0.995	0.974
1083	18	0.968	0.799
1089	24	0.882	0.599
1091	38	0.991	0.904
1094	29	0.963	0.888
1096	19	0.892	0.715
1101	34	0.921	0.652
1102	20	0.951	0.839
1106	31	0.921	0.659
1110	36	0.992	0.917

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1174	18	0.975	0.958
1175	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197	15	0.977	0.966
1199	26	0.976	0.875
1200	28	0.973	0.822
1201	28	0.990	0.925
1205	22	0.982	0.933
1206	15	0.986	0.919
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226	20	0.987	0.916
1229	30	0.996	0.894
1230	41	0.983	0.791
1234	20	0.978	0.893
1239	17	0.953	0.784
1240	25	0.950	0.897
1241	20	0.974	0.912
1242	15	0.974	0.817
1247	35	0.973	0.795
1250	22	0.982	0.872
1251	18	0.983	0.927
1254	20	0.934	0.828
1255	16	0.952	0.807
1256	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	
1263	33	0.953	0.640
1264	24		0.707
1265	24	0.981 0.987	0.884
1266	21		0.914
1200		0.977	0.905

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283 1293	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1302	20 29	0.926	0.751
1310		0.981	0.937
1314	27	0.977	0.849
1314	24 23	0.977	0.845
1317		0.990	0.833
1317	25 16	0.971	0.894
1319	41	0.961	0.916
1328	17	0.980	0.681
1329	26	0.977	0.921
1331	25	0.993	0.894
1333	33	0.986	0.939
1340	43	0.992	0.811
1341	20	0.943	0.943 0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	0.848
1369	18	0.997	0.979
1373	16	0.979	0.964
1375	25	0.980	0.952
1376	37	0.989	0.822
1378	37	0.984	0.878
1379	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.649
1467	41	0.990	0.922
1468	20	0.991	0.954
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	<del>-   <u>5:</u>   11</del>	0.900	0.758
1493	18	0.933	0.634
1495	22	0.899	0.639
1496	40	0.953	0.668
1509	16	0.881	0.607
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	28	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	0.596
			0.769
1600	29	0.968	
1604	28	0.975	0.926
1613	25	0.977	0.847
1618	41		
1627	24	0.915	0.578
1630	24	0.950	0.737
1631	28	0.987	0.785
1632	19	0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556 0.679
1684 1687	18 25	0.930 0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760 1769	36	0.980	0.559 0.780
1771	10	0.880 0.922	0.678
1773	39	0.982	0.829
1778	34	0.982	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
1826	36	0.951	0.782
1832	19	0.983	0.888
1833	23	0.971	0.941
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.945	0.737

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	44	0.974	0.662
1850	26	0.974	0.730
1851	27	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

## TABLE 7

SEQ ID	Chromsomal location
1	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21	2
22	11
23	12g
27	22q11
28	6p
29	6p23
31	17g
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10q26.2-10q26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52	19cen-q13.2
53	3p26

SEQ ID	Chromsomal location
54	2p24.3
55	3p26
56	3p26
57	15
60	15
62	1p21.2-22.3
65	11q12-q13.1
66	xp11
67	20q11:21-q13.12
69	2
70	X
71	1
72	1q21.2-q21.3
73	17p11.2
74	X
75	19
76	9
80	19
83	6q16
85	15
86	12
87	17q22-q24
88	8q22-q23
90	15
91	14q32.3
94	14
95	7
96	10q26.1
97	9p21
98	16q24.3
99	5
101 102	15
103	19
104	6p21.3
105	11p15.3-p15.4 16
107	14q32.1-q32,2
111	
112	11q13   9
114	
115	2q35 22q13
116	16
117	16
118	16q24.3
120	19
122	i i
123	20
124	9
125	3
126	11
127	22q11.2
128	20q11.2-12
129	14
131	10q25.1
133	17p11.2
134	20
136	4p16.3
	·- ·

SEQ ID	Chromsomal location
137 SEQ 1D	12p13
138	19
139	1p34.1-p32
140	4 or 17
143	Xq13.1-13.3
144	3
145	3
146	5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167	6p21.3
168	16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	6p21.3
180	15q14
181	
183	5q 5
184	11
187	11
188	3p21.3
189	12p13-qter
190	12p13-qter
191	12p13-qter
192	12p13-qter
193	2934-935
194	2q34-q35
195	10
199	7q11-q22
200	7q22.1-7q31.33
201	3
202	19q13.4
203	3
205	Xq28
206	6
208	Xq26.2-27.2
209	4
210	4
211	1q31
212	19q12-19q13.1
213	6q23
····	

SEQ ID	Chromsomal location
214	10
215	1
216	1p32.2-34.2
217	8
218	11q13
219	1q21-q23
220	Xq28
221	16
222	17
223	1
224	19p13.3
225	19p11-q11
226	1
227	- li
228	- li
229	12
230	5
231	1p31
232	1p31 1p31.1-p22.3
233	22q11.23
234	22q12.1-q12.3
235	1
236	17
237	15
238	2p13
239	17
241	11p13
242	111
243	4q22-q24
244	12
245	19
246	5
247	14
248	16
249	14
250	4
251	19
252	9p22-p21_or_9p13
	11q
256 257	9q33-q34.1
258	12pter-p13.31
260	8
261	11q14
262	17
	17
263	
264	16q13-q21
265	16q13-q21
267	6q26-27
268	9q12-q21.2
269	9q12-q21.2
270	9q12-q21.2
271	19
272	1p34.1-35.3
273	11
274	11
275	X
277	2

SEQ ID	Chromsomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299	2p11
300	16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307	1p35-p34
308	9
309	16
310	21
311	12p13
312	1
313	
314	17
315	1q42-q43
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320	6p21.32-22.1
321	6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324	6p21.32-22.1
325	6p21.32-22.1
326	17
327	3
328	14
332	17
335	17
336	14q32
337	8q23
338	8q23
339	16q11.1-q11.2
340	8q22-q23
341	16p13.3
342	18
343	15
344	17
345	20q11.2-q13.1
346	20q11.2-q13.1
347	19q13.3
348	19

17q25.1   350   18   351   11   11   352   1   11   353   352   1   11   11   11   11   11   353   354   11q14   355   1q31   355   1q31   355   1q31   355   355   1q31   355   355   36   37   38   39   359   310   360   7q22   361   7q22   361   7q22   362   1q21.3   363   3   3   3   364   38q12   363   3   3   3   364   38q12   365   31p15   367   34   369   3p36   371   369   3p36   371   369   3p36   371   373   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3   3p3	SEQ ID	Chromsomal location
11   352	349	17q25.1
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\$25.1-31.1   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   114   115   115   114   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115   115		
11914   1355   1931   1931   1355   1931   1355   1931   1357   138   358   359   10   10   10   10   10   10   10   1		
1931   3356   31931   3357   18		
1q31   357   18   8   357   358   359   359   360   7q22   362   362   362   363   3   3   364   365   367   367   369   369   369   369   369   369   369   369   369   369   371   369   371   373   374   373   374   375   376   7q32-q34   377   7q32-q34   377   7q32-q34   377   378   320   338   361   369   369   369   369   369   369   369   371   373   374   375   374   375   376   376   377   378   378   378   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379   379		
18	355	lq31
358   3p   10   360   7q22   361   7q22   362   1q21.3   363   3   3   364   38q12   365   3   3   364   38q12   365   31p15   367   369   1p36.21   373   3   1q413.1-1q21.3   373   3   1q413.1-1q21.3   373   3   1q413.1-1q21.3   375   4   376   376   7q32-q34   377   7q32-q34   377   7q32-q34   378   20q13.1-q13.2   381   33   382   1q21.2-22   383   384   12   385   20q13.1   386   387   8q21.3-q22.1   388   31   388   31   398   315q22.1   399   391   391   391   391   394   3q23   395   315q24-q26   396   397   7q34-q36   399   2   2   400   6q21-22   401   6q21-22   402   404   404   11q13   405   17   408   409   10q23-q24   401   409   10q23-q24   401   409   10q23-q24   401   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   411   412   11p15   413   413   414   5p13-q26.1   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409   409	356	
10   360   7q22   361   7q22   362   1q21.3   363   3   3   364   18q12   365   11p15   367   369   1p36.21   371   6p12.3-21.1   373   14q13.1-14q21.3   374   15   375   4   376   377   7q32-q34   378   20q13.1-q13.2   381   13   382   1q21.2-22   383   16   387   388   11   388   31   386   387   388   31   388   31   388   31   388   31   388   31   388   31   388   31   386   387   388   399   395   399   399   399   399   399   399   399   399   399   399   399   399   399   390   390   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   399   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390   390		
360       7q22         361       7q22         362       1q21.3         363       3         364       18q12         365       11p15         367       14         369       1p36.21         371       6p12.3-21.1         373       14q13.1-14q21.3         374       15         375       4         376       7q32-q34         377       7q32-q34         378       20q13.1-q13.2         381       13         382       1q21.2-22         383       16         384       12         385       20q13.1         386       16         387       8g21.3-q22.1         388       11         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2		
361     7q22       362     1q21.3       363     3       364     18q12       365     11p15       367     14       369     1p36.21       371     6p12.3-21.1       373     14q13.1-14q21.3       374     15       375     4       376     7q32-q34       377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19 </td <td>359</td> <td>7-00</td>	359	7-00
362     1q21.3       363     3       364     18q12       365     11p15       367     14       369     1p36.21       371     6p12.3-21.1       373     14q13.1-14q21.3       374     15       375     4       376     7q32-q34       377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11 <td></td> <td>7,22</td>		7,22
363         3           364         18q12           365         11p15           367         14           369         1p36.21           371         6p12.3-21.1           373         14q13.1-14q21.3           374         15           375         4           376         7q32-q34           377         7q32-q34           378         20q13.1-q13.2           381         13           382         1q21.2-22           383         16           384         12           385         20q13.1           386         16           387         8q21.3-q22.1           388         11           389         15q22.1           390         17           391         17           394         8q23           395         15q24-q26           396         15q22           397         7q34-q36           399         2           400         6q21-22           401         6q21-22           402         14q24.3           403         2	362	1021 2
364         18q12           365         11p15           367         14           369         1p36.21           371         6p12.3-21.1           373         14q13.1-14q21.3           374         15           375         4           376         7q32-q34           377         7q32-q34           378         20q13.1-q13.2           381         13           382         1q21.2-22           383         16           384         12           385         20q13.1           386         16           387         8q21.3-q22.1           388         11           389         15q22.1           390         17           391         17           394         8q23           395         15q24-q26           396         15q22           397         7q34-q36           399         2           400         6q21-22           401         6q21-22           402         14q24.3           403         2           404         11q13		1421.5
365         11p15           367         14           369         1p36.21           371         6p12.3-21.1           373         14q13.1-14q21.3           374         15           375         4           376         7q32-q34           377         7q32-q34           378         20q13.1-q13.2           381         13           382         1q21.2-22           383         16           384         12           385         20q13.1           386         16           387         8q21.3-q22.1           388         11           389         15q22.1           390         17           391         17           394         8q23           395         15q24-q26           396         15q22           397         7q34-q36           399         2           400         6q21-22           401         6q21-22           402         14q24.3           403         2           404         11q13           405         17		
367       14         369       1p36.21         371       6p12.3-21.1         373       14q13.1-14q21.3         374       15         375       4         376       7q32-q34         377       7q32-q34         378       20q13.1-q13.2         381       13         382       1q21.2-22         383       16         384       12         385       20q13.1         386       16         387       8q21.3-q22.1         388       11         389       15q22.1         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24		
1p36.21   371   6p12.3-21.1   373   14q13.1-14q21.3   374   15   375   4   376   7q32-q34   377   7q32-q34   378   20q13.1-q13.2   381   13   382   1q21.2-22   383   16   384   12   385   20q13.1   386   16   387   8q21.3-q22.1   388   11   389   15q22.1   390   17   391   17   394   8q23   395   15q24-q26   396   315q22   397   7q34-q36   399   2   400   6q21-22   401   6q21-22   402   404   411   412   412   411   412   412   411   412   411   412   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   411   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412   412		
371       6p12.3-21.1         373       14q13.1-14q21.3         374       15         375       4         376       7q32-q34         377       7q32-q34         378       20q13.1-q13.2         381       13         382       1q21.2-22         383       16         384       12         385       20q13.1         386       16         387       8q21.3-q22.1         388       11         389       15q22.1         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24         410       19         411       11 <td< td=""><td></td><td></td></td<>		
373       14q13.1-14q21.3         374       15         375       4         376       7q32-q34         377       7q32-q34         378       20q13.1-q13.2         381       13         382       1q21.2-22         383       16         384       12         385       20q13.1         386       16         387       8q21.3-q22.1         388       11         389       15q22.1         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24         410       19         411       11         412       11p15         413 </td <td></td> <td></td>		
374     15       375     4       376     7q32-q34       377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
375     4       376     7q32-q34       377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
376     7q32-q34       377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
377     7q32-q34       378     20q13.1-q13.2       381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		7q32-q34
381     13       382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	377	7q32-q34
382     1q21.2-22       383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		20q13.1-q13.2
383     16       384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
384     12       385     20q13.1       386     16       387     8q21.3-q22.1       388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
385       20q13.1         386       16         387       8q21.3-q22.1         388       11         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24         410       19         411       11         412       11p15         413       12q13.2-q13.3         414       3p13-q26.1		
386       16         387       8q21.3-q22.1         388       11         389       15q22.1         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24         410       19         411       11         412       11p15         413       12q13.2-q13.3         414       3p13-q26.1		
387       8q21.3-q22.1         388       11         389       15q22.1         390       17         391       17         394       8q23         395       15q24-q26         396       15q22         397       7q34-q36         399       2         400       6q21-22         401       6q21-22         402       14q24.3         403       2         404       11q13         405       17         407       14         408       10         409       10q23-q24         410       19         411       11         412       11p15         413       12q13.2-q13.3         414       3p13-q26.1		20q13.1
388     11       389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
389     15q22.1       390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
390     17       391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	388	
391     17       394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
394     8q23       395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
395     15q24-q26       396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
396     15q22       397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
397     7q34-q36       399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
399     2       400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		7034-036
400     6q21-22       401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		2
401     6q21-22       402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
402     14q24.3       403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
403     2       404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
404     11q13       405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
405     17       407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	404	
407     14       408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	405	
408     10       409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	407	14
409     10q23-q24       410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1	408	10
410     19       411     11       412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		
412     11p15       413     12q13.2-q13.3       414     3p13-q26.1		19
413 12q13.2-q13.3 414 3p13-q26.1		
414 3p13-q26.1		11p15
		12q13.2-q13.3
416 17		
	416	17

Sq35   Sq35   Sq35   Sq35   Sq35   Sq24.3   12   Sq35   Sq24.3   12   Sq24.3   19   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3   Sq24.3	SEQ ID	Chromsomal location	
422     3       423     12       424     3p24.3       425     19       426     6p21.1-21.2       6     427       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       435     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p55.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     2q11.2       464     16       465     10       467     11q23       468     3       469     7q32			
12   12   12   13   12   142   142   15   15   15   15   15   15   15   1		2	
424     3p24.3       425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       430     2       432     14q31       433     17       434     22       435     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p55.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     10       457     p31.3-32.2       458     1       460     12       461     18p11.2       462     17       463     22q11.2       464     16       465     10       467     11q23       468     3       469     7q32       470     1       477     9p24.1-24.3       476     2       477     9p24.1-24.3       479     20 <td></td> <td colspan="2"></td>			
425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     22q11.2       464     16       467     11q23       468     3       469     7q32       470     1       471     19       473     19       473     19			
426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       435     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     10       457     p31.3-32.2       458     1       460     12       461     18p11.2       462     17       463     22q11.2       464     16       467     11q23       468     3       469     7q32       470     1       471     9p24.1-24.3       469     7q36       476     2       477     9p24.1-24.3       479     20       480     22q12.3			
427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       477     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p1.2       462     17       463     22q11.2       464     16       467     11q23       468     3       469     7q32       470     1       472     19       473     19       474     p3-3-34.3       475     7q36       476     2 <t< th=""><td></td><td></td></t<>			
428       22q13.2q13.31         429       11         430       2         432       14q31         433       17         434       22         436       7q35         440       8p11.2         441       11q12         443       5         5       444         41       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         41       11         455       17         456       10         457       p31.3-32.2         458       1         469       7p13-p11.2         460       12         461       18p11.2         463       22q11.2			
11			
430     2       432     14q31       433     17       434     22       435     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     22q11.2       464     16       467     11q23       468     3       469     7q32       470     1       472     19       473     19       473     19       473     19       473     19       474     p33-34.3       475     7q36       476     2			
432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     22q11.2       464     16       465     17       467     11q23       468     3       469     7q32       470     1       471     p33-34.3       475     7q36       476     2       477     pp24.1-24.3       479     20       480     22q12.3-13.1       481     16q22.1-q22.3       483	430		
433       17         434       22         436       7q35         440       8p11.2         441       11q12         443       5         444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         459       7p13-p11.2         460       12         461       18p11.2         462       17         463       22q11.2         464       16         465       17         467       11q23         468       3         469       7q32         470       1         472       19         473       19         474       p33-34.3         <			
434       22         436       7635         440       8p11.2         441       11q12         443       5         444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         459       7p13-p11.2         460       12         461       18p11.2         462       17         463       22q11.2         464       16         466       17         467       11q23         468       3         469       7q32         470       1         472       19         473       19         474       p33-34.3         475       7q36		12	
436       7q35         440       8p11.2         441       11q12         443       5         444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         459       7p13-p11.2         460       12         461       18p11.2         462       17         463       22q11.2         464       16         465       17         467       11q23         468       3         469       7q32         470       1         477       19         473       19         474       p33-34.3         475       7q36         476       2			
440       8p11.2         441       11q12         443       5         4444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         460       12         461       18p11.2         462       17         463       22q11.2         464       16         465       17         467       11q23         468       3         3       3         469       7q32         470       1         472       19         473       19         474       p33-34.3         475       7q36         476       2         477       9p24.1-24.3 <td< th=""><td></td><td></td></td<>			
441       11q12         443       5         444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         459       7p13-p11.2         460       12         461       18p11.2         462       17         463       22q11.2         464       16         465       17         467       11q23         468       3         469       7q32         470       1         472       19         473       19         474       p33-34.3         475       7q36         476       2         477       9p24.1-24.3         479       20			
4443       5         4444       1         445       13q13         446       17         447       17         448       1p35.2-36.13         449       6         450       15q24-q25         451       19         452       4         453       2         454       11         455       17         456       10         457       p31.3-32.2         458       1         459       7p13-p11.2         460       12         461       18p11.2         462       17         463       22q11.2         464       16         465       17         467       11q23         468       3         469       7q32         470       1         472       19         473       19         474       p33-34.3         475       7q36         476       2         477       9p24.1-24.3         479       20         480       22q12.3-13.1			
1		11412	
445     13q13       446     17       447     17       448     1p35,2-36,13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31,3-32,2       458     1       459     7p13-p11,2       460     12       461     18p11,2       462     17       463     22q11,2       464     16       465     11q23       467     11q23       468     3       469     7q32       470     1       472     19       473     19       474     p33-34,3       475     7q36       476     2       477     9p24,1-24,3       479     20       480     22q12,3-13,1       481     16q22,1-q22,3       483     19       484     19       489     6			
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447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4       453     2       454     11       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     22q1.2       464     16       465     17       467     11q23       468     3       469     7q32       470     1       472     19       473     19       474     p33-34.3       475     7q36       476     2       477     9p24.1-24.3       479     20       480     22q12.3-13.1       481     16q22.1-q22.3       483     19       484     19       489     6			
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454     I1       455     17       456     10       457     p31.3-32.2       458     1       459     7p13-p11.2       460     12       461     18p11.2       462     17       463     22q1.2       464     16       466     17       467     11q23       468     3       469     7q32       470     1       472     19       473     19       474     p33-34.3       475     7q36       476     2       477     9p24.1-24.3       479     20       480     22q12.3-13.1       481     16q22.1-q22.3       483     19       484     19       489     6			
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472     19       473     19       474     p33-34.3       475     7q36       476     2       477     9p24.1-24.3       478     6p22.1-22.3       479     20       480     22q12.3-13.1       481     16q22.1-q22.3       483     19       484     19       489     6			
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477     9p24.1-24.3       478     6p22.1-22.3       479     20       480     22q12.3-13.1       481     16q22.1-q22.3       483     19       484     19       489     6		/q50	
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928	2q21	
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936	7q35	
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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22	970	22
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30	978	30
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32	980	32
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37 38	985	37
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	988	40
41 42	989	41
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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176	1123	175
177	1124 1125	176
178	1126	177
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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921	1869	921
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923	1871	923
924	1872	924
925	1873	925
926	1874	926
927	1875	927
928	1876	928
929	1877	929
930	1878	930
931	1879	931
932	1880	932
933	1881	933
934	1882	934
935	1883	935
	1884	936
936		
937	1885	937
938	1886	938
939	1887	939
940	1888	940
941	1889	941
942	1890	942
943	1891	943
944	1892	944
945	1893	945
946	1894	946
947	1895	947
948	1896	948
<del></del>		<del></del>

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## **CLAIMS**

## WHAT IS CLAIMED IS:

- An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 948, a mature protein coding portion of SEQ ID NO: 1 948, an active domain coding protein of SEQ ID NO: 1 948, and complementary sequences thereof.
- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
  - 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

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- 4. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 5. A vector comprising the polynucleotide of claim 1.

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- 6. An expression vector comprising the polynucleotide of claim 1.
- 7. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 9. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949-1896).
  - 10. A composition comprising the polypeptide of claim 9 and a carrier.

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- 11. An antibody directed against the polypeptide of claim 9.
- 12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
  - 14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
  - 15. A method for detecting the polypeptide of claim 9 in a sample, comprising:
  - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
  - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.
- 16. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:
  - a) contacting the compound with the polypeptide of claim 9 under conditions sufficient to form a polypeptide/compound complex; and
  - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

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17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

- a) contacting the compound with the polypeptide of claim 9, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

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- 18. A method of producing the polypeptide of claim 9, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.
  - 20. The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.

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- 21. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-948.
- 22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.

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23. The collection of claim 22, wherein the array detects full-matches to any one of the polynucleotides in the collection.

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- 24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 25. The collection of claim 21, wherein the collection is provided in a computer-readable format.
- 26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.